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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS
OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces
5 lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher
10 concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards
15 such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types
20 make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is
25 the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent
30 can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment..

5 The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often
10 spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack ofv effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

 Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of
15 lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

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SUMMARY OF THE INVENTION

 The present invention provides nucleotide sequences of genes that are up- and down-regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate lung cancer, such as
25 antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include early detection of lung cancers, monitoring and early detection of relapse following treatment of lung cancers, monitoring response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy,
30 selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous lesions of the lung. Examples of benign or precancerous lesions include: atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

5 DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or
10 modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in
15 analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis,
20 nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

25 In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which
30 use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5877). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols. A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

"Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

- 5 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is
- 10 characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.
- 15 Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

 The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-

20 regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine

25 the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,

30 which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

 Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

 A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

 For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

5

Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxeavanis and Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and
5 software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at
10 least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample
15 source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU
20 data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern
25 encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in
30 or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can
5 be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a
10 collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

15 **Characteristics of lung cancer-associated proteins**

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication
20 (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve
25 as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In
30 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure
5 and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their
10 cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may
15 also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful
20 in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic
25 markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

30 In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, and wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding
10 sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in
15 accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

 In general, transcriptional and translational regulatory sequences may include, but are
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

 Promoter sequences may be either constitutive or inducible promoters. The promoters
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

 In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two
30 organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable
5 marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung
10 cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate
15 growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae*
20 and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and
25 adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and
30 polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Kluyveromyces fragilis and *K. lactis*, *Pichia guilliermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue,
10 although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be
15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive
25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid
5 residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully
10 described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

15 Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal
20 amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns
25 can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence
30 lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

5 Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

10 Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent
15 Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric
20 molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung
25 cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

30 Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or
5 may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate,
10 and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide
15 means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another
20 aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction
25 in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include
30 radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

5

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening
10 assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

15 In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or
20 by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be
25 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are
5 randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription
20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as,
25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin
30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used
5 to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as
10 cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and
15 incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using
20 PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein
25 promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual
30 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein
20 or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test
5 compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the
10 label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of
15 competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a
20 first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the
25 agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein
30 are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

- 5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
- 10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.
- 15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

- Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a
- 25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a
- 30 normal phenotype and become contact inhibited and would grow to a lower density.

 In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

5 Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g.,
15 Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.

Various techniques which measure the release of these factors are described in
20 Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and
30 invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

30 **Methods of identifying variant lung cancer-associated sequences**

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

- 5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

10 The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

- 15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

- In one embodiment, a therapeutically effective dose of a lung cancer protein or
25 modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
5 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly,
10 intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the
15 pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid,
20 sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases
25 such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic
30 ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms
5 suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by
10 packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions
15 are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate
20 and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

25 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
30 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to
5 accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the
10 patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be
15 used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can
20 be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present
25 invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for
30 introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

 Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

5 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

 The present invention also provides for kits for screening for modulators of lung
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and
5 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as
described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-
993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAccn	UnigenelD	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		Immunoglobulin Heavy Chain, VdJc Reg	2.68	3.28
10	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitter)	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta receptor	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
15	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
20	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
25	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
	103280	X79981	Hs.76205	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; i	1.86	1
	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
30	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
	104865	AA045136	Hs.22575	ESTs	1.23	0.49
35	104989	AA102098	Hs.118615	ESTs	0.63	0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398506	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
40	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (tr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.45	0.43
	106797	AA478962	Hs.169943	ESTs	1.18	0.32
45	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidyl	1.05	0.14
	106954	AA495980	Hs.204038	ESTs	1.25	0.33
	107054	AA500150	Hs.14366	ESTs	1.11	0.4
	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
50	107994	AA036811	Hs.165030	ESTs	0.7	0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
55	108435	AA078787	Hs.194101	ESTs	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
	109613	F03031	Hs.27519	ESTs	1.01	0.29
60	109837	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H	1.1	0.22
65	111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.95	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
	113195	T57112		yc20g11.61 Stratagene lung (#937210)	1.22	0.35
70	113238	T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
	113695	T95965	Hs.17948	ESTs	1.54	0.28
75	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
	115279	AA279760	Hs.63671	ESTs	1.79	0.91
80	115565	AA398083	Hs.43977	ESTs	0.86	0.2
	115865	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16

5	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		***yr30g11.s1 Soares fetal liver spleen	1.32	0.53
10	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
	119861	W80715		ESTs; Moderately similar to !!!!! ALU SUB	1.83	0.45
	120041	W82775	Hs.59368	ESTs	1.23	0.55
	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0885 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
15	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
	123978	C20653	Hs.170278	ESTs	1.52	0.32
20	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		***yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
	125167	W45550	Hs.102541	ESTs	1.46	0.69
	125174	W51835	Hs.231082	EST	3.07	3.76
25	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AA417667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		***HUM145B09B Clontech human fetal brain	0.94	0.36
	127002	R35380	Hs.24979	ESTs	3.02	4.06
	127307	AA369367	Hs.126712	ESTs; Weakly similar to pIL2 hypotheica	1.01	0.69
30	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AJ302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.33
	128624	AA479209	Hs.102647	ESTs	1.46	0.58
	128789	AA486567	Hs.105695	ESTs	1.1	0.34
35	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
40	129402	T63781		***yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
	129583	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp566L0120 (f	1.3	0.42
	129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!!! ALU SUBFAM1	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ublqu	1.58	1
45	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
50	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24850	regulator of G-protein signalling 5	2.34	2.82
	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
55	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T2630	Hs.258675	EST	1.86	2.09
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Crl-du-chat regi	1.73	0.58
	132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
60	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57056	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
65	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50683	Hs.82028	transforming growth factor, beta recepto	1.21	0.67
70	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
	134696	H88354	Hs.8881	ESTs	1.35	0.33
	134749	L10956	Hs.89485	carbonic anhydrase IV	0.89	0.2
75	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134859	T35288	Hs.90421	ESTs; Moderately similar to !!!!! ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
80	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
85	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*caltonin/alpha-CGRP, all transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, all transcript 12	0.85	1.9
	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45

	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simplex)	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase)	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homolog	1	1
5	101124	L10343	Hs.112341	*Protease inhibitor 3, skin-derived (SKA)	0.62	2.67
	101175	L18920	Hs.36980	*Melanoma antigen, family A, 2	1	1
	101204	L24203	Hs.82237	Alaxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 18 (cornutin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex)	0.61	8.83
10	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Cardioembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		*Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	1	8.98
15	101748	M76482	Hs.1925	Desmoglein 3 (permphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	*Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
	101809	M86849		*Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
20	101845	M93426	Hs.78867	*Protein tyrosine phosphatase, receptor-	1	1
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	*Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	*Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
25	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
	102623	U68083	Hs.37110	*Melanoma antigen, family A, 9 (MAGE-9)	1	1
30	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
	102696	U74612	Hs.239	Forthead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.69
	102913	X07696	Hs.80342	keratin 15	0.7	4.72
35	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
	102963	X15943	Hs.37058	*Calcitonin/calcitonin-related polypepti	1	1
	103021	X33587	Hs.85266	*Integrin, beta 4	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
	103058	X57348	Hs.184510	Stratfin	1.25	4.17
40	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
	103119	X63629	Hs.2877	*Cadherin 3, P-cadherin (placental)	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	*Alcohol dehydrogenase 7 (class IV), mu	1	1
	103312	X82693	Hs.3185	*Lymphocyte antigen 6 complex, locus D;	0.92	1.28
45	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	ST4 Oncofetal antigen	1	3.93
	103594	Z31560	Hs.816	*SRY (sex determining region Y)-box 2, p	0.71	7.23
50	103768	AA089997		*ESTs, Highly similar to integral membra	0.99	1.8
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
55	104733	AA019498	Hs.23071	ESTs	1.18	1.88
	104906	AA055809	Hs.26802	Protein kinase domains containing prote	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!!!! ALU SUBFAM	1.64	2.89
	105012	AA116036	Hs.9329	*Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
	105263	AA227926	Hs.6682	ESTs	0.95	2.87
60	105298	AA233459	Hs.26369	ESTs	1	1.13
	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
65	106012	AA411621	Hs.8895	ESTs; same as BFH67	0.94	2.04
	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
70	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
75	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61480	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
	108857	AA133250	Hs.62180	ESTs	1	1
80	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabtkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
	109565	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
85	109970	H09281	Hs.13234	ESTs	1.13	2.16

	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
5	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kD)*	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
	113970	W86748	Hs.8109	ESTs	1.17	1.73
15	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
20	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density l	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
	115522	AA331393	Hs.47378	ESTs	0.5	3.29
25	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
30	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456988	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
35	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
45	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
	120102	W95428	Hs.132927	*ESTs, Moderately similar to p63 regulat	1	1
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
50	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983	AA398209	Hs.97587	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405557	Hs.128791	CGI-09 protein	1	1.8
55	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP6-850E9 on chromosome 20	1.19	1.64
60	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R05041	Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmbl	1.52	2.26
	125972	AA434562	Hs.35406	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
70	126645	A167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
	127221	A1354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	A1204246		KIAA1085 protein	1.8	3.16
75	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
80	129404	AA172056	Hs.111128	ESTs	1	1
	129466	L42583		*Genbank Homo sapiens keratin 6 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
85	130080	X14850	Hs.147097	*H2A histone family, member X*	0.98	1.96
	130385	AA126474	Hs.155223	stanniocalcin 2	1	1

	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	"Doublecortin; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
15	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	"laminin gamma2 chain gene (LAMC2), exon	1	1
20	132659	Z75190	Hs.54481	"Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132890	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69511	Hs.64311	"A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.286145	"SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp5641922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	"collagen, type XI, alpha 1"	0.76	2.86
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	"Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family, member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
50	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.58
55	115206	AA262491	Hs.186572	ESTs	1	1
	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307860	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102456	survival of motor neuron protein interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133558	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
70	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.28
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		"Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (a	1.13	2.09
	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.82	1.78
80	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		"Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
	100398	D84557	Hs.155462	minichromosome maintenance deficient (mi	1.08	1.9
85	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Glia-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Epican, All. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor, arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutr	1.35	2.73
	101181	L19686	Hs.737398	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family, member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-60) alpha I	0.69	2.78
	101342	L76191	Hs.182018	interleukin-1 receptor-associated kinase	1.04	1.84
	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
20	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
25	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
	101853	M94362	Hs.76084	lamin B2	0.84	1.19
30	101977	S83364		***putative Rab5-interacting protein (cl	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discooidin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U82136		***Homo sapiens enterocyte differential	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activa	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78565	Hs.204133	hexabrachion (tenascin C; cytostatin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	tipocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
	103668	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
75	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
80	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024561	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
85	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	105280	AA232215	Hs.14500	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26562	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
15	106103	AA421104	Hs.12094	ESTs	1.04	1.44
	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA426582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to p112 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA509145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.s	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.59	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
	111337	N79512	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777023 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.57
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finge	0.96	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
	120242	Z98443	Hs.86366	ESTs	0.83	2.01

	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
5	121376	AA405599	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST	1.93	2.33
	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186892	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ [Hsapiens]	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
15	123398	AA521265	Hs.105514	ESTs	1	1.93
	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
20	124447	N46000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
	125756	W25458	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	A1382972	Hs.82128	ST4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DP1)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
30	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombination	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
	128733	AA328993	Hs.104558	ESTs	1.34	1.94
40	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435655	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
45	129703	AA401348	Hs.179999	ESTs	0.97	1.63
	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-GalbetaGlcNAc beta 1;4-galactosylt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
55	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.65	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3593	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.06	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

5	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.60666	KIAA1112 protein	1.16	1.53
	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
10	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
15	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158875	ribosomal protein L14	0.85	1.18
	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45
	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
20	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DP1; DP11)	0.7	6.21
	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
25	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
30	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
35	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
	134193	F09570	Hs.7980	ESTs	0.98	1.48
	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
40	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64
	134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
45	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
	134693	N70361	Hs.8854	ESTs	1.09	1.82
	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
50	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
	134914	U29615	Hs.91093	chitinase 1 (chitinotrioidase)	1.16	1.29
	134953	L10678	Hs.91747	profilin 2	0.95	1.76
	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
55	135051	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

Table 1B shows the accession numbers for those pkeys in Table 1A lacking unigenes. For each probe set we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Pkey: Unique Eos probe set identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
65	100661	23182_1
	100667	26401_3
70		BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655
		L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700
75	100668	26401_3
		AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066
80		AI783934 AW377727 BE163715 ALD47291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153
		BE548944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700
85	101332	25130_1
		AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171
		AI675961 AW804172 AA778841 ALD48050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196
		AA513211 AA411052 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414
		AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565571 C00444
		AA054555
		L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700
		AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066
		AI783934 AW377727 BE163715 ALD47291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153
		BE548944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700
		AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171
		AI675961 AW804172 AA778841 ALD48050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196
		AA513211 AA411052 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414
		AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565571 C00444
		AA054555
		J04088 NM_001067 AF071747 AJ011741 NB5424 ALD42407 AA218572 BE295748 BE083981 ALD40877 AW499918 AW675045 H17813
		BE081283 AA670403 AW504327 BE094229 AA104024 AJ471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI765534

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Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
 R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
 R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
 R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

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Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
100138	U83508	Hs.2463	angiotensin 1			2.30					
100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
100306	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
100458	S74019	Hs.247979	Vpre-B	42.40							
100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
101032	BE208854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
101081	AF047347	Hs.4880	amyloid beta (A4) precursor protein-bind				34.60				
101088	X70697	Hs.553	solute carrier family 6 (neurotransmitter)				193.20				
101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
101180	U11874	Hs.846	interleukin 8 receptor; beta				54.86				
101308	L41390		*Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
101346	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
101397	M26380	Hs.180878	lipoprotein lipase								3.54
101414	NM_000066	Hs.38069	complement component 8; beta polypeptide							3.81	
101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				34.60				
101507	X16896	Hs.82112	interleukin 1 receptor; type I				37.60				
101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar								4.25
101537	AJ469059	Hs.184915	zinc finger protein; Y-linked			2.54					
101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
101560	AW958272	Hs.83733	intercellular adhesion molecule 2, exon								3.38
101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
101605	M37984	Hs.118845	tropontin C; slow								3.80
101621	BE391804	Hs.62661	guanylate binding protein 1; interferon-	30.20							
101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon							2.75	
101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium						3.37		
101842	M93221	Hs.75182	mannose receptor; C type 1				38.20				
101961	AW004056	Hs.168357	*Hs-TBX2=T-box gene (T-box region) [huma			2.32					
101994	T92248	Hs.2240	uteroglobin								6.85
102020	AJ077315	Hs.154970	transcription factor CP2			2.45					
102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
102112	AW025430	Hs.155591	forkhead box F1	54.60							
102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.98
102202	NM_000507	Hs.574	fructose-bisphosphatase 1								3.62
102241	NM_007351	Hs.268107	Mutimerin			2.32					
102310	U33839		Accession not listed in Genbank		7.00						
102397	U41898		*Human sodium cotransporter NKST1 mRNA,	29.40							
102571	U60115	Hs.239069	*Homo sapiens skeletal muscle LIM-protein								3.75
102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
102636	U67092		*Human ataxia-telangiectasia locus prote			2.40					
102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15					
102675	U72512	Hs.7771	*Human B-cell receptor associated protel						3.56		
102698	M18667	Hs.1867	progastrin (papsinogen C)								4.51
102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
103098	M86361		Human mRNA for T cell receptor; clone IG					10.00			
103117	X63578	Hs.295449	pervalbumin		6.00						
103241	X76223		Hsapiens MAL gene exon 4			2.47					
103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

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	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	5.97
	103508	Y10141		*Hsapiens DAT1 gene, partial, VNTR	3.27
	103561	NM_001843	Hs.143434	contactin 1	
	103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.40
5	103575	Z26256		*Hsapiens isoform 1 gene for L-type cal	2.99
	103627	Z48513		Hsapiens XG mRNA (clone PEP6)	4.18
	103767	BE244667	Hs.296155	CGI-100 protein	3.44
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR	2.25
	104078	AA402801	Hs.303276	ESTs	46.55
10	104326	AW732659	Hs.143067	ESTs	3.05
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	3.54
	104398	AA239330	Hs.36790	ESTs; Weakly similar to putative p150 [H	3.16
	104473	AA904823	Hs.31297	ESTs	
	104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC	3.38
15	104496	AW975687	Hs.292979	ESTs	2.47
	104595	AI799603	Hs.271568	ESTs	
	104597	AA364504	Hs.93967	ESTs; Weakly similar to Sli-1 protein [3.42
	104659	AW969769	Hs.105201	ESTs	6.00
20	104686	AA010539	Hs.18912	ESTs	34.00
	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	11.00
	104764	AI039243	Hs.278585	ESTs	58.80
	104776	AA026349		ESTs	60.40
	104825	AA035613	Hs.141883	ESTs	34.20
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C	3.03
25	104942	NM_016348	Hs.10235	ESTs	41.20
	104989	R65998	Hs.285243	ESTs	
	105062	AW954355	Hs.36529	ESTs	40.00
	105101	H63202	Hs.38163	ESTs	
30	105173	U54617	Hs.8364	ESTs	34.20
	105194	R06780	Hs.19800	ESTs	16.00
	105226	R58958	Hs.26608	ESTs	
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr	2.34
	105394	BE245812	Hs.8941	ESTs	2.72
35	105647	Y08306	Hs.30148	homeodomain-interacting protein kinase 3	2.61
	105789	AF105941	Hs.18142	arrestin; beta 2	33.60
	105817	AA397825		synaptophysin	
	105847	AW964490	Hs.32241	ESTs	35.40
	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi	3.43
40	105999	BE268786	Hs.21543	ESTs	7.00
	106075	AA045290	Hs.25930	ESTs	
	106178	AL049935	Hs.301763	KIAA0554 protein	34.80
	106381	AB040916	Hs.24106	ESTs	12.00
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2	
45	106536	AA329648	Hs.23804	ESTs	96.40
	106569	R20909	Hs.300741	sorcin	47.20
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	220.40
	106842	AF124251	Hs.26054	novel SH2-containing protein 3	2.55
	106844	AA485055	Hs.158213	sperm associated antigen 6	
50	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl	39.20
	106943	AW888222	Hs.9973	ESTs	2.28
	106954	AF128847	Hs.204038	ESTs	
	107106	AA862496	Hs.28482	ESTs	10.45
	107163	AF233588	Hs.27018	ESTs	
55	107201	D20378	Hs.30731	EST	2.57
	107238	D59362	Hs.330777	EST	8.00
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospho	10.67
	107530	Y13622	Hs.85087	latent transforming growth factor beta b	2.32
	107688	AW082221	Hs.60536	ESTs	34.60
60	107706	AA015579	Hs.28276	ESTs	28.40
	107723	AA015967		EST	
	107727	AA149707	Hs.173091	DKFZP434K151 protein	80.80
	107750	AA017291	Hs.60781	ESTs	51.40
	107751	AA017301	Hs.235390	ESTs	
65	107873	AK000520	Hs.143811	ESTs	9.00
	107899	BE019261	Hs.83869	ESTs; Weakly similar to !!! ALU SUBFAM	
	107994	AA036811	Hs.48469	ESTs	44.60
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c	32.00
	108041	AW204712	Hs.61957	ESTs	30.80
70	108048	AI797341	Hs.165195	ESTs	
	108338	AA070773		*zm53p11.s1 Stratagene fibroblast (#9372	2.33
	108434	AA078899		*zm64b1.s1 Stratagene colon HT29 (#93722	
	108447	AA079126		*zm92a11.s1 Stratagene ovarian cancer (#	
	108480	AL133092	Hs.68055	ESTs	34.00
75	108499	AA083103		*zn1b12.s1 Stratagene hNT neuron (#93723	
	108535	R13949	Hs.226440	Homo sapiens clone 24681 mRNA sequence	19.00
	108550	AA084867		*zn11b.s1 Stratagene hNT neuron (#93723	12.00
	108604	AA934589	Hs.49696	ESTs	
	108625	AW972330	Hs.283022	ESTs	
80	108629	AA102425		*zn24c6.s1 Stratagene neuroepithelium NT	
	108655	AA099960		*zm65c6.s1 Stratagene fibroblast (#93721	7.00
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f	6.05
	108864	AI733852	Hs.199957	ESTs	28.80
	108895	AL138272	Hs.62713	ESTs	32.80
85	108921	AI568801	Hs.71721	ESTs	57.80
	108967	AA142989	Hs.71730	ESTs	28.80

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	109001	AJ056548	Hs.72116	ESTs; Moderately similar to hedgehog-int	2.57			
	109003	AA147497	Hs.71825	ESTs			2.11	
	109004	AA156235	Hs.139077	EST	5.60			
	109065	AA161125	Hs.252739	EST		10.00		
5	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA			3.44	
	109490	AA233416	Hs.139202	ESTs			2.92	
	109510	AJ788863	Hs.87191	ESTs	2.40			
	109578	F02208	Hs.27214	ESTs	10.00			
	109601	F02695	Hs.311662	EST		40.80		
10	109613	H47315	Hs.27519	ESTs		54.40		
	109650	R31770	Hs.23540	ESTs	31.20			
	109682	H18017	Hs.22869	ESTs	8.40			
	109724	D59899	Hs.127842	ESTs		29.40		
	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene		8.00		
15	109833	R79864	Hs.29889	ESTs	10.00			
	109837	H00656	Hs.29792	ESTs	6.49			
	109977	T64183	Hs.282982	ESTs			2.75	
	109984	AJ796320	Hs.10299	ESTs		107.00		
	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 18			2.22	
20	110271	H28985	Hs.31330	ESTs			3.48	
	110280	AW874263	Hs.32468	ESTs	44.20			
	110420	R93141	Hs.184261	ESTs		32.00		
	110578	T62507	Hs.11038	ESTs	28.40			
	110634	R98905	Hs.35992	ESTs		20.00		
25	110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-			4.15	
	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H		56.80		
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfamily				
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic	5.33			
	110971	AJ760098	Hs.21411	ESTs		44.60		
30	111023	AV655386	Hs.7645	ESTs	32.40			
	111057	T79639	Hs.14629	ESTs		17.14		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein			3.42	
	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [Hsap			3.91	
35	111442	AW449573	Hs.181003	ESTs		33.20		
	111737	H04607	Hs.9218	ESTs		53.00		
	111747	AJ741471	Hs.23666	ESTs	46.20			
	111807	R33508	Hs.18827	ESTs	16.00			
40	111862	R37472	Hs.21559	EST			3.91	
	112045	AJ372588	Hs.8022	TU3A protein			2.74	
	112057	R43713	Hs.22945	EST			4.92	
	112214	AW148852	Hs.167398	ESTs		13.00		
	112263	R52393	Hs.25917	ESTs				
45	112314	AW206093	Hs.748	ESTs	9.00	2.43		
	112324	R55965	Hs.26479	limbic system-associated membrane protein			14.00	
	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H		2.49		
	112380	H63010	Hs.5740	ESTs		2.34		
	112425	AA324998	Hs.321677	ESTs; Weakly similar to [!!!] ALU SUBFAM	8.00			
50	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9			4.53	
	112492	N51620	Hs.28694	ESTs		29.80		
	112541	AF038392	Hs.116674	ESTs			3.62	
	112620	R80552	Hs.29040	ESTs		2.37		
	112623	AW373104	Hs.25094	ESTs		2.26		
55	112867	T03254	Hs.167393	ESTs		12.00		
	112894	T08188	Hs.3770	ESTs	6.50			
	112954	AA928953	Hs.6655	ESTs	7.00			
	113029	AW081710	Hs.7369	ESTs; Weakly similar to [!!!] ALU SUBFAM				4.39
	113086	AA346839	Hs.209100	DKFZP434C171 protein				4.47
	113140	T50405	Hs.175967	ESTs		10.00		
60	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	14.00			
	113257	AJ821378	Hs.159367	ESTs			3.72	
	113394	T81473	Hs.177894	ESTs			3.60	
	113437	T85349	Hs.15923	EST	35.00			
	113454	AJ022166	Hs.16188	ESTs	6.00			
65	113502	T89130		ESTs	39.60			
	113552	AJ654223	Hs.16026	ESTs				3.88
	113645	T96358	Hs.333181	ESTs			2.58	
	113691	T96935	Hs.17932	EST		38.20		
70	113706	AA004693	Hs.269192	ESTs			3.09	
	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro		2.31		
	113924	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40			
	114035	W92798	Hs.269181	ESTs		13.00		
	114058	AK002016	Hs.114727	ESTs				5.00
	114084	AA708035	Hs.12248	ESTs		40.60		
75	114121	H05785	Hs.25425	ESTs		2.31		
	114124	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)	7.00			
	114275	AW515443	Hs.306117	interleukin 13 receptor; alpha 1	6.00			
	114297	AA149707	Hs.173091	DKFZP434K151 protein		48.80		
80	114427	AA017176	Hs.33532	ESTs; Highly similar to MZ-1 protein [H			3.45	
	114449	AA020736		*ze53b11.s1 Soares retina N2b4HR Homo sa		10.00		
	114452	AI369275	Hs.243010	ESTs; Moderately similar to RTCO_HUMAN G	14.00			
	114609	AA079505		*zm97a5.s1 Stratagene colon HT29 (#93722			3.13	
	114648	AA101056		*zm25b3.s1 Stratagene neuroepithelium NT		35.40		
85	114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy			3.42	
	114762	AA146979	Hs.288464	ESTs	33.00			

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	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00			
	115302	AL109719	Hs.47578	ESTs			12.00		
	115365	AW976252	Hs.258391	ESTs				3.32	
	115559	AL079707	Hs.207443	ESTs			48.00		
	115566	AI142336	Hs.43977	ESTs			56.20		
10	115583	AF255910	Hs.54650	ESTs; Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [Hsa			33.60		
	115819	AA486620	Hs.41135	Endomucin 2			74.40		
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs			388.80		
15	116035	AA621405	Hs.184564	ESTs			33.20		
	116049	AA454033	Hs.41644	ESTs			45.80		
	116081	AI190071	Hs.55278	ESTs				3.57	
	116082	AB029495	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tufelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular teldi			30.00		
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20				
25	116835	N39230	Hs.38218	ESTs			41.20		
	116970	AB023179	Hs.9059	KIAA0962 protein				11.00	
	117023	AW070211	Hs.102415	ESTs			91.00		
	117027	AW085208	Hs.130093	ESTs	49.40				
	117036	H88908	Hs.41192	EST			32.60		
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs			30.60		
	117325	N23599	Hs.43396	ESTs				9.29	
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
35	117543	BE219453	Hs.42722	ESTs		16.00			
	117567	AW444761	Hs.44565	ESTs			12.00		
	117570	N48649	Hs.44583	ESTs			11.00		
	117600	N34963	Hs.44676	EST					3.74
	117730	N45513	Hs.46608	ESTs		6.00			
40	117791	N48325	Hs.93956	EST		9.00			
	117929	N51075	Hs.47191	ESTs			29.20		
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109667	Hs.124154	Homo sapiens mRNA full length insert cDN		2.40			
	118446	N66361	Hs.269121	ESTs		2.28			
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs					3.10
	118549	N68163	Hs.322954	EST					3.41
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs					3.58
	118935	AI979247	Hs.247043	KIAA0525 protein			33.00		
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!! ALU SUBFAM				11.43	
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastos			52.60		
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank					3.50
	119824	W74536	Hs.184	advanced glycosylation end product-speci		2.75			
60	119831	AL117664	Hs.58419	DKFZP586L2024 protein					3.21
	119861	W78816	Hs.49943	ESTs; Moderately similar to !!! ALU SUB			33.80		
	119889	W84346	Hs.58671	ESTs			30.03		
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs					3.80
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)			36.60		
	120378	AA223249	Hs.285728	ESTs		12.00			
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40				
	120504	AA256837		ESTs			8.00		
	120512	N55761	Hs.194718	ESTs	33.00				
70	120667	AA287740	Hs.78335	microtubule-associated protein; RPI/EB fa					4.18
	120777	AA287702	Hs.10031	KIAA0955 protein			46.60		
	121082	AA398722		ESTs			39.00		
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST					5.08
75	121363	AI287280	Hs.97933	ESTs			12.00		
	121366	AI743515		ESTs			20.00		
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev					3.32
	121518	AA412155		ESTs			30.20		
	121545	AA412442	Hs.98132	ESTs		2.29			
80	121622	AA416931	Hs.126065	ESTs		9.00			
	121665	AA416556	Hs.98234	ESTs			34.80		
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs					38.80
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs					3.61

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5	121835	AB033030	Hs.300670	ESTs	2.34				
	121841	AA427794	Hs.104864	ESTs	2.61				
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
	121938	AA428659	Hs.98610	ESTs			46.80		
10	121950	AA429515		EST			31.40		
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98746	EST				3.58	
	122211	AA300900	Hs.98849	ESTs; Moderately similar to biithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
15	122247	AA436676	Hs.98890	EST			39.80		
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro	9.00				
	122266	AA436840	Hs.98907	EST				3.60	
	122285	AA436981	Hs.121602	EST				3.14	
	122409	AA446830	Hs.99081	ESTs	30.80				
20	122485	AA524547	Hs.160318	phospholemman		2.65			
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fls, clone MA	15.00				
	122772	AW117452	Hs.99489	ESTs	6.67				
	122831	AJ857570	Hs.5120	ESTs				3.37	
	122913	AJ638774	Hs.105328	ESTs			32.20		
25	123049	BE047680	Hs.211869	ESTs			41.80		
	123076	AJ345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs				2.58	
	123309	N52937	Hs.102679	ESTs				19.00	
	123455	AA353113	Hs.112497	ESTs			82.80		
30	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST					
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	35.40				
	123837	AJ807243	Hs.112893	ESTs	58.00				
	123844	AA938905	Hs.120017	olfactory receptor; family 7; subfamily		2.63		32.40	
35	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR			70.60		
	124013	AJ521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
	124160	R40290	Hs.124685	ESTs				13.00	
	124205	H77570	Hs.108135	ESTs				4.74	
40	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270962	ESTs			29.40		
	124348	AJ796320	Hs.10299	ESTs	17.00				
	124358	AW070211	Hs.102415	gamma35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AJ814166	Hs.107197	ESTs				3.14	
45	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate		2.48			
	124468	N51413	Hs.109284	ESTs			30.80		
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph		2.50			6.03
	124519	AJ670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO					
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
50	124866	AJ768289	Hs.304389	ESTs		8.00			
	124874	BE550182	Hs.127826	ESTs			37.60		
	125097	AW576389	Hs.335774	ESTs			10.00		
	125179	AW206468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs					2.79
55	125299	T32982	Hs.102720	ESTs			34.20		
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20				
	126176	BE242256	Hs.2441	KIAA0022 gene product		12.00			
	126303	D78841		HUM525A05B Human placenta polyA+ (TFu)			33.60		
60	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu			29.80		
	126773	AA648284	Hs.187584	ESTs					
	127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypotheica	39.60				
	127462	AA760776	Hs.293977	aa59b04.s1 NCL CGAP_GCB1 Homo sapiens c	28.80		34.40		
65	127486	AW002846	Hs.105468	ESTs		9.00			
	127572	AA594027	Hs.191788	ESTs		2.36			
	127609	X80031	Hs.530	ESTs			29.40		
	127832	AW976035	Hs.292396	ESTs			37.20		
	127898	AA774725	Hs.128970	ESTs				4.42	
70	128073	AW340720	Hs.125983	ESTs			38.40		
	128101	AA905730	Hs.128254	ESTs		7.33			
	128149	NM_012214	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-				2.58	
	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)		3.09			
	128333	W68800	Hs.12126	ESTs; Weakly similar to LRS [H.sapiens]			34.40		
75	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT		10.00			
	128426	AJ265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
	128634	AA464918		ESTs; Moderately similar to !!! ALU SUB			41.60		
	128687	AW271273	Hs.23767	ESTs			87.00		
80	128726	AJ311238	Hs.104476	ESTs				4.02	
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp			9.00		
	128833	W26667	Hs.184581	ESTs				3.76	
	128870	H39537	Hs.75309	eukaryotic translation elongation factor		2.66			
	128878	R25513	Hs.10683	ESTs				3.10	
85	128885	AF134803	Hs.180141	catilin 2 (muscle)			11.00		
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh					3.68
	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
	129098	AW580945	Hs.330466	ESTs	34.60				

	129210	AL039940	Hs.202949	KIAA1102 protein				4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29			
	129262	BE222198	Hs.109843	ESTs			3.30	
5	129301	AF182277	Hs.330780	Human cytochrome P450-UB (hIIB3) mRNA;				4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93			
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80		
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD			10.00	
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1			3.40	
	129782	AW016932	Hs.104105	EST	9.00			
	129950	F07783	Hs.1369	decay accelerating factor for complement		87.80		
	129958	R27496	Hs.1378	annexin A3		44.60		
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque	2.72			
15	130160	AA305688	Hs.267695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr		42.20		
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	2.54			
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr		51.60		
	130312	AF056195	Hs.15430	DKFZP586G1219 protein			3.16	
	130436	NM_001928	Hs.155597	D component of complement (adipsin)				4.11
	130523	AA999702	Hs.214507	ESTs			4.77	
20	130799	AB028945	Hs.12695	ESTs	6.00			
	130885	NM_005883	Hs.20912	adenomatous polyposis coli like			3.54	
	131002	AL050295	Hs.22039	KIAA0758 protein				3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00			
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20			
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40		
	131066	AW169287	Hs.22588	ESTs		29.60		
	131082	AJ091121	Hs.246218	ESTs; Weakly similar to zinc finger prot		9.00		
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding				3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfam			3.14	
	131179	AA171388	Hs.184482	DKFZP586D0624 protein			3.80	
	131182	AJ824144	Hs.23912	ESTs				3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98			
	131277	AA131466	Hs.23767	ESTs	3.15			
35	131281	AA251716	Hs.25227	ESTs		32.20		
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma				3.44
	131285	AJ567943	Hs.25274	ESTs; Moderately similar to putative sev			6.40	
	131355	R52804	Hs.25956	DKFZP564D206 protein	8.00			
	131391	AW085781	Hs.26270	ESTs	10.00			
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80			
	131487	FI13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f				4.03
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin 6a [39.00			
	131545	AL137432	Hs.28564	ESTs		11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity		10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47			
	131675	H15205	Hs.30509	ESTs			3.06	
	131676	AJ126821	Hs.30514	ESTs	45.80			
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	2.28			
	131717	X94630	Hs.3107	CD97 antigen				3.78
50	131756	AA443966	Hs.31595	ESTs		40.60		
	131762	AA744902	Hs.107757	ESTs; Moderately similar to CaM-KII inh				3.67
	131821	AA017247	Hs.164577	ESTs	2.87			
	131839	AB014533	Hs.33010	KIAA0633 protein				3.48
	131861	AL095858	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	54.00			
55	132015	AJ418006	Hs.3731	ESTs		49.20		
	132070	BE622641	Hs.38489	ESTs		34.80		
	132242	AA332697	Hs.42721	ESTs	2.68			
	132334	AW080704	Hs.45033	lacrimal proline rich protein	4.66			
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20			
60	132490	NM_001290	Hs.4980	LIM binding domain 2	2.66			
	132533	AJ922998	Hs.172510	ESTs	13.00			
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60		
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin lig			4.02	
	132652	N41739	Hs.61260	ESTs			3.18	
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1			11.43	
	133028	R51604	Hs.300842	ESTs	2.37			
	133071	BE384932	Hs.64313	ESTs	2.27			
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63			
	133129	AA428580	Hs.65551	ESTs				5.49
70	133147	AA026533	Hs.66	Interleukin 1 receptor-like 1	6.20			
	133151	NM_014051	Hs.94896	ESTs			3.69	
	133213	AA903424	Hs.6786	ESTs		31.40		
	133276	AW978439	Hs.69504	ESTs			9.00	
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20			
75	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20			
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)			3.72	
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr				3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65			
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80		
80	133779	T58486	Hs.222566	ESTs			3.05	
	133978	AF035718	Hs.78061	transcription factor 21	2.92			
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec				3.45
	134000	AW175787	Hs.334841	selenium binding protein 1				4.05
	134111	A1372588	Hs.8022	TU3A protein	4.49			
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f			3.27	
	134204	AJ873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [40.80		

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	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept				3.76
	134577	AA251363	Hs.177711	ESTs		15.00	32.20	
	134745	NM_000685	Hs.89472	angiotensin receptor 1B			3.05	
5	134749	T28499	Hs.89485	carbonic anhydrase IV				
	134785	T29618	Hs.89640	angiotensin 1 receptor; TEK tyrosine ki				57.80
	134825	U33749	Hs.197764	thyroid transcription factor 1				3.73
	134978	AI829008	Hs.333383	ficollin (collagen/fibrinogen domain-cont		2.52		
	135010	N50465	Hs.92927	ESTs			31.60	
	135053	AW795190	Hs.93678	ESTs				3.21
10	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80			
	135091	AA493650	Hs.94367	ESTs				4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associata	8.00			
	135203	C15737	Hs.268386	ESTs				4.31
	135236	AI636208	Hs.96901	ESTs	43.00			
15	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd				6.42
	135346	NM_000928	Hs.992	phospholipase A2; group IB (pancreas)		3.82		
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-		4.15		
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20			
	135388	W27965	Hs.99865	EST	38.80			
20	135402	L12398	Hs.99922	dopamine receptor D4				4.21

TABLE 2B shows the accession numbers for those primekeys lacking unigenelD's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	108447	43452_7 AA079126
	108550	120073_1 AA084857 AA084996
	108655	127522_1 AA099960 AA113013
	102397	44371_1 U41898
	126303	1525933_1 D78841 D78880
40	125810	1554054_1 H00083 R81062
	103627	2615_2 Z48513 Z48512
	121366	280401_1 A1743515 AA405617 AW276706
	114609	116777_1 AA079505 AA079537
	115272	172113_1 AW015947 AA211890 AA279425
45	108338	112186_1 AA070773 AA070774
	108434	114012_1 AA078899 AA078782 AA075788
	123802	genbank_AA620448 AA520448
	102310	NOT_FOUND_entrez_U33839 U33839
	102636	entrez_U67092 U67092
50	104776	genbank_AA026349 AA026349
	120504	genbank_AA256837 AA256837
	113502	genbank_T89130T89130
	108499	genbank_AA083103 AA083103
	101308	entrez_L41390 L41390
55	108629	genbank_AA102425 AA102425
	103098	221_215 M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223
	103508	entrez_Y10141 Y10141
	103575	entrez_Z26256 Z26256
60	119514	NOT_FOUND_entrez_W37937 W37937
	121082	genbank_AA398722 AA398722
	128634	AA464918_at AA464918
	105817	genbank_AA397825 AA397825
	121518	genbank_AA412155 AA412155
65	114449	genbank_AA020736 AA020736
	114648	genbank_AA101056 AA101056
	121950	genbank_AA429515 AA429515
	107723	genbank_AA015967 AA015967

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigeneID:	Unigene number					
	Unigene Title:	Unigene gene title					
10	R1:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.					
	R2:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas					
15	R3:	70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples					
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3
20	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW288244	Hs.293507	ESTs	12.40		
	135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67		
25	134951	BE305081	Hs.169358	hypothetical protein		8.00	
	134799	M36821	Hs.89590	GRO3 oncogene		8.20	
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous)			
	134772	NM_000829	Hs.163597	glutamate receptor, ionotropic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
30	134696	BE326276	Hs.8861	ESTs			
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 facio-gen			1.92
35	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		
	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
	134343	D50683	Hs.82028	transforming growth factor, beta recepto			
40	134323	BE170651	Hs.8700	deleted in liver cancer 1			
	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
	134299	AW580939	Hs.97199	complement component C1q receptor			
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60		
	134182	D52059	Hs.7972	KIAA0871 protein	12.20		
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
	133978	AF035718	Hs.78061	transcription factor 21			
	133835	AI677897	Hs.76640	RGC32 protein			
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2			
	133633	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	15.20		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			
	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAI/L			1.77
	133488	AA335295	Hs.74120	adipose specific 2			
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	
55	133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
	133153	AF070592	Hs.66170	HSKM-B protein	30.60		
	133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
60	132836	AB023177	Hs.29900	KIAA0960 protein			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
	132548	X12630	Hs.193400	interleukin 6 receptor		7.20	
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Crt-du-chat regi		4.76	
	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
65	132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs.165084	ESTs	15.20		
	131751	T96555	Hs.31562	ESTs			1.76
70	131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-II	27.80		
	131694	NM_000246	Hs.3076	MHC class II transactivator		4.00	
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2			
	131676	AI126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589	C18825	Hs.29191	epithelial membrane protein 2			
	131536	AA019201	Hs.269210	ESTs		9.40	
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59	
	131355	R52804	Hs.25956	DKFZP564D206 protein		4.48	
	131253	R71802	Hs.24853	ESTs	15.00		
80	131207	AF104266	Hs.24212	latrophilin			1.75
	131156	AI472209	Hs.323117	ESTs			1.84
	131066	AW169287	Hs.22588	ESTs		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein			
	131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr			1.93
85	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		
	130762	D84371	Hs.1898	paraoxonase 1	12.00		

	130657	AW337575	Hs.201591	ESTs			
	130655	AU831962	Hs.17409	cysteine-rich protein 1 (intestinal)			
	130589	AL110226	Hs.16441	DKFZP434H204 protein		2.08	
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled)		1.91	
	130555	R59743	Hs.116774	integrin, alpha 1	9.60		
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60		
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	6.60		
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator		1.91	
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20		
	129958	R27496	Hs.1378	annexin A3	5.05		
	129898	AI672731	Hs.13256	ESTs			
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60		
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas			
15	129626	F13272	Hs.111334	feritin, light polypeptide			
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63		
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f			
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		2.53	
	129527	AA769221	Hs.270847	delta-tubulin	39.20		
20	129402	W72052	Hs.11112	ESTs		2.11	
	129385	AA172106	Hs.110950	Rag C protein	15.20		
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40		
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83		
	129240	AA361258	Hs.237868	interleukin 7 receptor		1.95	
	129210	AL039940	Hs.202949	KIAA1102 protein			
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	4.20		
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)			
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20		
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2			
30	128789	AW368576	Hs.139851	caveolin 2		2.24	
	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20		
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40		
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamma		1.78	
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH		2.51	
35	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00		
	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80		
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	4.00		
	128458	H55864	Hs.56340	ESTs			
40	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20		
	127968	AA830201	Hs.124347	ESTs	21.30		
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60		
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40		
	127896	AI669586	Hs.222194	ESTs	7.00		
45	127859	AA761802	Hs.291559	ESTs	14.00		
	127817	AA838641	Hs.163085	ESTs	14.00		
	127742	AW293496	Hs.180138	ESTs	11.00		
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10		
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			
50	127582	AA908954	Hs.130844	ESTs	19.60		
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40		
	127535	AA568424	Hs.164450	ESTs	17.50		
	127404	AI379920	Hs.270224	ESTs	14.60		
	127396	L31958	Hs.187991	DKFZP564A122 protein	15.40		
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60		
	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00		
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN81_HUMAN ZINC	15.80		
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5			
	127242	AW390395	Hs.181301	cathepsin S	22.60		
60	127167	AA625590	Hs.190272	ESTs	21.40		
	127046	AA321948	Hs.293968	ESTs	41.20		
	126928	AA480902	Hs.137401	ESTs	11.00		
	126900	AF137386	Hs.12701	plasmalipin		1.78	
65	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60		
	126816	AA248234		gb:csq2228.seq.F Human fetal heart, Lamb	12.20		
	126812	AB037860	Hs.173933	nuclear factor IIA	17.19		
	126666	AA648886	Hs.151999	ESTs	13.57		
	126645	AA316181	Hs.61635	sbx transmembrane epithelial antigen of	15.40		
70	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	4.67		
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00		
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77		
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60		
	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	3.50		
	126182	AA721331	Hs.293771	ESTs	13.40		
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20		
	126142	H86261	Hs.40568	ESTs	14.00		
	126077	M78772	Hs.210836	ESTs	16.59		
	125994	AB90529	Hs.270799	ESTs	17.40		
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00		
80	125847	AW161885	Hs.249034	ESTs	49.57		
	125831	H04043		gb:yl45c03.r1 Soares_placenta Nb2HP Homo			
	125731	R61771	Hs.26912	ESTs	13.20		
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20		
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S			
85	125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypothet	12.60		
	125489	HA9193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40		

	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AA422996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	10.60	
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
	124578	N58321	Hs.231500	EST	21.43	
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:yyw37g07.s1 Morton Fetal Cochlea Homo	14.64	
	124306	AW973078	Hs.293039	ESTs		4.00
15	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
	123961	AL050184	Hs.21610	DKFZP4348203 protein		1.79
20	123936	NM_004673	Hs.241519	angiotensin-like 1	15.80	
	123902	AA620448		gb:aae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602964		gb:nc097c02.s1 NCI_CGAP_Py2 Homo sapiens	33.60	
	123596	AA421130	Hs.112640	EST	10.93	
25	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
	123073	AA485081	Hs.105652	ESTs	31.20	
30	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcriptase		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg		
	122553	AA451884	Hs.190121	ESTs	40.00	
35	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
	122011	AA431082		gb:czw78a10.s1 Soares_testis_NHT Homo sap		1.89
40	121992	AI860775	Hs.98506	ESTs	3.60	
	121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193767	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:cz74e03r1 Soares_testis_NHT Homo sap	14.80	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Py1 Homo sapiens	21.20	
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:xb39a05.s1 NCI_CGAP_GC81 Homo sapiens	20.00	
	120484	AA253170	Hs.95473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST	7.20	
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
	119824	W74536	Hs.184	advanced glycosylation end product-speci		
65	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	trypsin beta 1		
	119126	R45175	Hs.117183	ESTs	12.60	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis	10.00	
	118901	AW292577	Hs.94445	ESTs	3.96	
	118661	AL137554	Hs.49927	protein kinase NYD-SP15	9.60	
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to		1.90
	118416	N66028	Hs.49105	FKBP-associated protein	16.20	
	118379	N64491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy6201.s1 Soares_multiple_sclerosis_	6.60	
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s	3.80	
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113		1.86
	118032	N52802	Hs.47544	EST	5.00	
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence	4.00	
85	117404	N39725	Hs.15220	zinc finger protein 106		1.90
	117314	N32498	Hs.42829	ESTs	14.20	

	117209	W03011	Hs.306881	MSTP043 protein		
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen	20.20	
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	3.51	
	116766	AJ608657	Hs.95097	ESTs	16.20	
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60	
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	19.40	
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S		
	116166	AL039940	Hs.202949	KIAA1102 protein	2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106	1.75	
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11	
15	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	2.36	
	115955	AF263613	Hs.44198	intracellular membrane-associated caldu	18.20	
	115844	AJ373062	Hs.332938	hypothetical protein MGC5370	18.57	
	115683	AF255910	Hs.54650	junctional adhesion molecule 2	23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fts, clone HE	11.82	
20	115672	AJ889110	Hs.73251	ESTs	10.60	
	115566	AJ142336	Hs.43977	Human DNA sequence from clone RP11-196N1	1.76	
	115313	AA808001	Hs.184411	albumin	25.20	
	115279	AW964897	Hs.290825	ESTs	8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fts, clone L	1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20	
	114999	BE246481	Hs.87856	ESTs	19.20	
	114930	AA237022	Hs.188717	ESTs	5.60	
	114822	AA235672	Hs.87491	ESTs	3.60	
	114837	BE244930	Hs.166895	ESTs	43.70	
30	114769	AA143060	Hs.296100	ESTs	11.00	
	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00	
	114736	AJ610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A	4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71	
	114518	AW163267	Hs.106469	suppressor of var1 (Scerivisiae) 3-like	20.40	
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40	
	114452	AJ369275	Hs.243010	Homo sapiens cDNA FLJ14445 fts, clone HE	17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5	2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fts, clone OV	12.40	
40	114251	H15261	Hs.21948	ESTs	2.00	
	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	11.40	
	114124	W57554	Hs.125019	ESTs	6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fts, clone PL	1.82	
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALU8_HUMAN !!!		
45	113606	NM_013343	Hs.278951	NAG-7 protein	2.15	
	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.60	
	113560	T91015	Hs.268626	ESTs	32.00	
	113552	AJ654223	Hs.16026	hypothetical protein FLJ23191		
	113540	AW152618	Hs.16757	ESTs		
50	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H	8.35	
	113288	AJ076838	Hs.12967	ESTs	12.40	
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	4.27	
	113238	R45467	Hs.189813	ESTs		
	113203	AA743563	Hs.10305	ESTs	21.20	
	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	1.92	
55	113089	T40707	Hs.270862	ESTs	14.33	
	113076	AF033199	Hs.8198	zinc finger protein 204	6.00	
	113009	T23699	Hs.7246	ESTs	9.40	
	112937	AJ694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-B	10.57	
60	112794	R97018		gb:yp74b08.s1 Soares fetal liver spleen	26.60	
	112691	R88708	Hs.220647	ESTs	15.33	
	112602	AW004045	Hs.203365	ESTs	15.60	
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40	
	112210	R49645	Hs.7004	ESTs	14.00	
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00	
	111998	R42379	Hs.138283	ESTs	11.00	
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40	
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.77	
	111737	H04607	Hs.9218	ESTs	1.86	
70	111605	T91081	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00	
	111510	R07856	Hs.16355	ESTs	11.02	
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	1.88	
	111280	AA373527	Hs.19385	CGI-58 protein	18.40	
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (f		
75	111232	AJ247763	Hs.16928	ESTs	27.60	
	110942	R63503	Hs.28419	ESTs	14.80	
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71	
	110837	H03109	Hs.108920	HT018 protein	2.18	
	110824	AJ767183	Hs.26942	ESTs	12.20	
80	110776	AB032417	Hs.19545	frizzled (Drosophila) homolog 4	1.75	
	110576	H00869	Hs.37889	ESTs	13.00	
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761	5.60	
	110099	R44557	Hs.23748	ESTs	2.31	
	109984	AJ796320	Hs.10299	Homo sapiens cDNA FLJ13545 fts, clone PL		
85	109958	AA001266	Hs.133521	ESTs	11.25	
	109893	AA884208	Hs.30484	ESTs	2.68	

5	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to 138022 hypothet		17.20	3.91
	109796	A080515	Hs.12024	ESTs		9.60	
	109688	R41900	Hs.22245	ESTs			
	109648	H17800	Hs.7154	ESTs	22.80		
10	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs			1.89
	109472	AK001989	Hs.91165	hypothetical protein		6.00	
	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
15	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128554		gbczn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	11.00		
	108573	AA086005		gbczl84c04.s1 Stratagene colon (937204)	26.00		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			
20	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fs, clone NT		11.40	
25	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
30	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
	107230	A034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
35	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase			1.76
40	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
45	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fs, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60		
	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106567	AW360847	Hs.16578	ESTs			
50	106505	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp5648076 (fr		2.40	
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5		1.78	
	106552	AL031846	Hs.152151	plateophilin 4		1.76	
	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot		2.19	
	106533	AL134708	Hs.145998	ESTs	23.20		
55	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
60	105894	AI904740	Hs.25691	receptor (calcitonin) activity modifying			1.94
	105847	AW864490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm			2.47
	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H48612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
65	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H53202	Hs.38163	ESTs		8.30	
	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
70	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinase		5.40	
	104903	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
	104855	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fs, clone C			
	104825	AA035613	Hs.141883	ESTs			1.87
75	104781	AA099904	Hs.21610	DKFZP434B203 protein			1.93
	104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH	10.20		
	104691	U29590	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone	4.20		
80	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fs, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein			1.91
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
	103749	AL135301	Hs.8768	hypothetical protein FLJ10949	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
85	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD			1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

5	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		1.76
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhotabolin-like 1)		2.15
	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t		
	102698	M18667	Hs.1867	progastricsin (pepsinogen C)		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
10	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	7.40	
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
15	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M93221	Hs.75182	mannose receptor, C type 1		
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		
	101764	A1198560	Hs.81256	S100 calcium-binding protein A4 (calcium		1.78
	101716	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80	
20	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a1		2.22
	101447	M21305		gbchuman alpha satellite and satellite 3	504.80	
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	31.00	
	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N		1.75
	101345	NM_005795	Hs.152175	calcitonin receptor-like		
25	101336	NM_005732	Hs.75578	FBJ murine osteosarcoma viral oncogene h		2.24
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gbchuman dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5		2.01
30	101102	NM_003243	Hs.79059	transforming growth factor, beta receptio		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.52	
	101056	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocytes		1.91
	100893	BE245294	Hs.180789	S164 protein	15.40	
35	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	H1R (histone cell cycle regulation defec	14.80	
	100555	M69181		gbchuman nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
40	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri	4.00	
	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik	4.24	
	100351	D64158			6.20	
	100299	D49493	Hs.2171	growth differentiation factor 10	21.20	
	100134	AA305746	Hs.49	macrophage scavenger receptor 1		
	100108	U09577	Hs.76673	hyaluronoglucosaminidase 2		1.79
45	100095	Z97171	Hs.78454	myoclin, trabecular meshwork inducible	5.40	
	100066				11.29	

TABLE 3B shows the accession numbers for those primers lacking unigenetID's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
125831	1522905_1	H04043 D60988 D60337
126816	122973_1	AA248234 AA090985
126852	136135_1	AA399961 AA128347
121059	273450_1	AA393283 AA398628
120637	200885_1	AA811804 AA809404 AA286907 AW977624
122011	7617_2	AA431082
120934	177521_1	AA226198 AA226513 AA383773
123802	genbank_AA620448	AA620448
116814	genbank_H50834	H50834
118329	genbank_N63520	N63520
104404	H58762_at	H58762
104776	genbank_AA026349	AA026349
113502	genbank_T89130T89130	
101262	entrez_L35854 L35854	
108573	genbank_AA086005	AA086005
101447	entrez_M21305 M21305	
124357	genbank_N22401	N22401
108781	genbank_AA128654	AA128654
112794	genbank_R97018	R97018
100351	entrez_D64158 D64158	
100555	tigr_HT2245 M69181 M81105 U51039	

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Atymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
10	R1:	average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
15	100210	D26361	Hs.3104	KIAA0042 gene product	20.40
	100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
	100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
	100877	X80821	Hs.27973	KIAA0874 protein	35.56
20	100893	BE245294	Hs.180789	S164 protein	43.40
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
	101447	M21305		gb:Human alpha satellite and satellite 3	193.60
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
25	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
	101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
30	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
	102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
	102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
	102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
	102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
35	102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
	102829	NM_006183	Hs.80962	neurotensin	116.80
	103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
	103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
40	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (tr	42.60
	104896	AW015318	Hs.23165	ESTs	29.40
	105038	AW503733	Hs.9414	KIAA1488 protein	21.50
45	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
	106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
	106205	AW965058	Hs.111583	ESTs, Weakly similar to t38022 hypotheti	32.00
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60
50	106533	AL134708	Hs.145998	ESTs	59.80
	106575	AW970602	Hs.105421	ESTs	43.40
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
	106851	AA58823		gb:td04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
55	106995	AB023139	Hs.37892	KIAA0922 protein	20.88
	107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (tr	57.20
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
	108609	BE409857	Hs.69499	hypothetical protein	19.67
	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
60	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines	59.20
	109260	AW978515	Hs.131915	KIAA0863 protein	28.60
	109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
	109292	AW975746	Hs.188662	KIAA1702 protein	
65	109384	AA219172	Hs.86849	ESTs	21.00
	109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
	109445	AA232103	Hs.189915	ESTs	24.20
	109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
	109633	AW003785	Hs.170267	ESTs	20.40
70	109786	AI989482	Hs.146286	kinesin family member 13A	19.60
	109958	AA001266	Hs.133521	ESTs	24.00
	110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
	111084	H44186	Hs.15456	PDZ domain containing 1	61.20
75	111132	AB037807	Hs.83293	hypothetical protein	24.60
	111229	AW389845	Hs.110855	ESTs	27.20
	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
	111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
80	112885	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
	112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
	112897	AW206453	Hs.3782	ESTs	22.00
	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
85	113073	N39342	Hs.103042	microtubule-associated protein 18	55.40

	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113850	AL267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (Scerensiaae) 3-like	23.60
10	114824	AA950961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
15	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115809	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI591147	Hs.61232	ESTs	20.80
20	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yy16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
	118138	AA374756	Hs.83560	Homo sapiens mRNA for KIAA1771 protein,	22.00
25	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypothe	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1619	achate-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
40	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:nc97c02.s1 NCL_CGAP_Py2 Homo sapiens	28.80
	124005	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20
50	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125834	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126566	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:UL-H-B13-ata-e-12-0-UL.s1 NCL_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW283496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809572	Hs.123304	ESTs	20.54
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AK022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3857243, mRNA	20.40
	128509	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	28.60
85	129785	H19006	Hs.184780	ESTs	72.20
	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

5	130149	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase domain	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone A	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	AJ879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0548 protein	21.00
15	131860	BE383576	Hs.334	Rho guanine nucleotide exchange factor (33.40
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132094	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
20	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AJ076916	Hs.5398	guanine morphosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothe	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AA499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
35	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	69.33
	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pr	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A45010 X-fin	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
45	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primers lacking unigenes for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325605 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359
		BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AA58623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigeneID:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5
	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076557	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
40	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
45	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
	100906	AU076916	Hs.5398	guanine monophosphate synthetase					5.16
55	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
	101045	J05614		gb:Human proliferating cell nuclear anti					4.69
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101175	U82571	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (5.69
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	oploid receptor, mu 1			6.40		
	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
65	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
	101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
70	101369	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (comelin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
75	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetrati				12.00	
	101502	M26958		gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
80	101535	X57152	Hs.99853	fibritarin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW859908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

	101695	M69136	Hs.135626	chymase 1, mast cell	4.79		
	101724	L11690	Hs.620	bulbous pemphigoid antigen 1 (230/240kd)	15.21		
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	55.50		
5	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino)		18.57	4.10
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant			
	101804	M86699	Hs.169840	TTK protein kinase	4.50		
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00		
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56		
10	101842	M83221	Hs.75182	mannose receptor, C type 1		12.80	
	101851	BE260964	Hs.82045	mitokine (neurite growth-promoting factor			5.88
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80		
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			4.35
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)		7.40	
	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4			5.12
15	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,		12.00	
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20		
	102154	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kallinin	2.62		
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85		
	102217	AA829978	Hs.301613	JTV1 gene			6.18
20	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu			4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1			5.80
	102251	NM_004398	Hs.41706	DEAD/HD (Asp-Glu-Ala-Asp/His) box polypep	4.50		
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)			5.15
	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta			4.17
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gra		9.33	
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87		
	102368	U39817	Hs.36820	Bloom syndrome	15.91		
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma		19.20	
30	102404	NM_005429	Hs.79141	vascular endothelial growth factor C		14.00	
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family		12.00	
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2			4.57
	102606	AI435128	Hs.181369	ubiquitin fusion degradation 1-like			3.98
	102610	U65011	Hs.30743	preferentially expressed antigen in mela	77.50		
	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50		
35	102642	AA205847	Hs.23016	G protein-coupled receptor		22.00	
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence	12.00		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein		12.80	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50		
	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50		
40	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C			9.24
	102696	BE540274	Hs.239	forkhead box M1			5.54
	102768	U82321		gbHomo sapiens clone 14.98 mRNA sequenc	6.60		
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e			3.78
45	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat		14.40	4.26
	102824	U08016	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			
	102829	NM_006183	Hs.80962	neurotensin	8.00		
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1			5.50
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin		6.70	
50	102913	NM_002275	Hs.80342	keratin 15	4.64		
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93		
	102951	X15218	Hs.2969	v-eld avian sarcoma viral oncogene homol		11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)			7.26
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01		
55	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90		
	103038	AA926960	Hs.334883	CDC28 protein kinase 1			8.79
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin			4.27
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro	9.80		
	103119	X53629	Hs.2677	cadherin 3, type 1, P-cadherin (placenta	4.05		
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastric/intest	3.07		
	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm			5.62
	103192	M22440	Hs.170009	transforming growth factor, alpha	7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			4.70
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		100.00	
65	103316	X83301	Hs.324728	SMA5		9.80	
	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71		
	103378	AL036166	Hs.323378	coated vesicle membrane protein	14.00		
	103385	NM_007069	Hs.37189	similar to rat HREV107		11.00	
	103391	X94453	Hs.114366	pyrolysine-5-carboxylate synthetase (glut	2.93		
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,			5.15
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr			3.98
	103446	X98834	Hs.79971	sel (Drosophila)-like 2		21.40	
	103476	U77071	Hs.293007	aminopeptidase puromycin sensitive	13.00		
	103477	AJ011812	Hs.119018	transcription factor NRF		6.40	
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02		
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50		
	103558	BE616547	Hs.2785	keratin 17	6.41		
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp			3.84
	103587	BE270266	Hs.82128	ST4 oncogene/trophoblast glycoprotein	78.50		
80	103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51		
	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50		
	103768	AF086009		gbHomo sapiens full length insert cDNA			4.48
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468	8.00		
	103847	AF219946	Hs.102237	tubby super-family protein	10.40		
85	103913	AW967500	Hs.133543	ESTs		15.60	
	104094	AA418187	Hs.330515	ESTs	6.60		

WO 02/086443			PCT/US02/12476		
5	104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034	26.00
	104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80
	104261	AW248364	Hs.5409	RNA polymerase I subunit	3.98
	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80
	104415	BE410992	Hs.258730	hemo-regulated initiation factor 2-alpha	10.29
10	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	15.79
	104558	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H	17.40
	104660	BE298665	Hs.14846	Homo sapiens mRNA: cDNA DKFZp564D016 (tr	6.40
	104689	AA204050	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	6.55
15	104754	AJ206234	Hs.155924	cAMP responsive element modulator	10.00
	104758	BE560269	Hs.7010	NPD002 protein	4.47
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87
	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86
20	105026	AA809485	Hs.124219	hypothetical protein FLJ12934	11.00
	105076	AJ598252	Hs.37810	hypothetical protein MGC14833	5.01
	105132	AA148164	Hs.247280	HBV associated factor	3.99
	105143	AJ368636	Hs.24608	ESTs, Weakly similar to I38022 hypothei	11.00
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	16.00
25	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00
	105264	AA227934		gbcr57e08.s1 Soares_NhlhMPu_S1 Homo sapi	10.00
	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	9.20
30	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,	7.80
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	27.00
	105848	AW954064	Hs.24951	ESTs	7.60
35	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha	4.14
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome	16.80
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	23.40
	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50
	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00
40	106159	AK001301	Hs.3487	hypothetical protein FLJ10439	3.95
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36	6.04
	106260	AJ097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S	13.20
	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso	5.02
	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 (6.60
45	106318	AA025610	Hs.9805	cleavage and polyadenylation specific fa	5.04
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced	7.25
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	13.80
	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75
	106586	AA243837	Hs.57787	ESTs	10.84
50	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (tr	45.60
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00
	106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00
	106813	C05766	Hs.181022	CGI-07 protein	11.40
	106895	AK001826	Hs.25245	hypothetical protein FLJ11269	6.00
55	106913	AJ219346	Hs.86178	M-phase phosphoprotein 9	6.55
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.27
	107054	AJ076459	Hs.15978	KIAA1272 protein	34.80
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71
	107098	AJ823593	Hs.27688	ESTs	24.80
60	107104	AJ076640	Hs.15243	nucleolar protein 1 (120kD)	7.05
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60
	107198	AV657225	Hs.9846	KIAA1040 protein	19.20
	107203	D20426	Hs.41639	programmed cell death 2	7.60
	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50
65	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.71
	107516	X57152	Hs.99853	fibrillarin	4.33
	107529	BE515065	Hs.296585	nucleolar protein (NKE/D repeat)	4.00
	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80
70	107851	AA022953	Hs.61172	EST	8.00
	107901	L42612	Hs.335952	keratin 6B	3.40
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88
	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50
	108015	AW298357	Hs.49927	protein kinase NYD-SP15	23.40
75	108056	AA043675	Hs.62633	ESTs	12.80
	108075	AJ887370	Hs.139709	hypothetical protein FLJ12572	12.80
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00
	108295	N31256	Hs.161623	ESTs	6.60
	108305	AA071391		gbznm61e06.r1 Stratagene fibroblast (937	11.80
80	108393	AA075211		gbznm86a08.r1 Stratagene ovarian cancer	11.80
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	20.80
	108554	AA084948		gbznm13b09.s1 Stratagene hNT neuron (937	6.40
	108573	AA086005		gbznl84c04.s1 Stratagene colon (937204)	25.40
	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	9.60
85	108597	AK000292	Hs.278732	hypothetical protein FLJ20285	14.60
	108695	AB029000	Hs.70823	KIAA1077 protein	3.00
	108699	AA121514	Hs.70832	ESTs	10.00
	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c	11.00
	108780	AJ076442	Hs.117938	collagen, type XVII, alpha 1	11.21

	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
	108860	AA133334	Hs.129911	ESTs	6.09			
5	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-hi	3.00			
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines	10.58			
10	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
	109418	AJ866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-li		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
15	109543	AA564994	Hs.222851	ESTs		12.67		
	109648	H17800	Hs.7154	ESTs			10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gbJHSC33H092 normalized infant brain cDN			16.00	
	109704	AJ743880	Hs.12876	ESTs		11.00		
20	109792	R49625		gbcyg61103.s1 Soares infant brain 1N1B H			12.60	
	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00			
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
25	110500	AA907723	Hs.36962	ESTs	4.50			
	110551	AW450381	Hs.14529	ESTs		8.60		
	110561	AA378597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10507 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
30	110916	BE178102	Hs.24349	ESTs		6.80		
	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AJ476429	Hs.19238	ESTs			10.40	
35	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
	111597	R11499	Hs.189716	ESTs			9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence	6.80			
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
	112054	R43590		gb.yc85g02.s1 Soares infant brain 1N1B H	10.80			
40	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
	112382	R59904		gb.yh07g12.s1 Soares infant brain 1N1B H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00			
45	112539	R70318	Hs.339730	ESTs			37.20	
	112772	AJ992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin				4.83
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
50	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein	7.00			
55	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0563 gene product			9.40	
	113702	T97307		gb.ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AJ369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE			13.91	
	113984	R96696	Hs.35598	ESTs	7.80			
60	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20		
	114182	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42			
	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
65	114313	H18456	Hs.27946	ESTs			10.00	
	114339	AA782845	Hs.22790	ESTs	7.80			
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f			4.14	
	114560	AJ452469	Hs.165221	ESTs		9.80		
	114699	AA127386		gb.zn90d09.r1 Stratagene lung carcinoma		7.60		
70	114767	AJ859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb.zo76c03.s1 Stratagene pancreas (93720		6.00		
	114833	AJ477215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3				4.03
75	115097	AA256213	Hs.72010	ESTs			35.40	
	115113	AA256460		gb.zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m				4.19
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
80	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AJ142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
85	115545	AJ207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H		6.00		

	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81			
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14			
	115793	AA424883	Hs.70333	hypothetical protein MGC10753			11.80	
5	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL			9.71	
	115892	AA291377	Hs.50831	ESTs		27.40		
	115906	AI767758	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53			
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82			
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970			34.29	
10	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g			8.23	
	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00			
	116090	AI591147	Hs.61232	ESTs	5.17			
	116096	AA682382	Hs.59982	ESTs		8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60		
	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17				
15	116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypothe			5.82	
	116278	NM_003686	Hs.47504	exonuclease 1	9.50		4.08	
	116335	AK001100	Hs.41690	desmocollin 3	3.67			
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00		
20	116503	AI925318	Hs.212617	ESTs			12.60	
	116674	AI768015	Hs.92127	ESTs		32.00		
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp	7.60			
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F	9.80			
	116993	AA17023	Hs.40478	ESTs			10.20	
25	117079	H92325		gbys8505.s1 Soares retina N2b4HR Homo			15.20	
	117317	AI263517	Hs.43322	ESTs			13.40	
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,			20.60	
	117396	W20128	Hs.296039	ESTs			10.60	
	117412	N32535	Hs.42645	ESTs			16.00	
	117519	N32528	Hs.146286	kinesin family member 13A			9.11	
30	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42			4.01	
	117721	N46100	Hs.93939	EST			19.80	
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71			
	117903	AA768283	Hs.47111	ESTs			17.80	
35	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f			4.17	
	118013	AI674126	Hs.94031	ESTs		8.82	10.60	
	118017	AI813444	Hs.42197	ESTs				
	118186	N22886	Hs.42380	ESTs	7.00			
	118325	AI868065	Hs.166184	intersectin 2			13.80	
40	118367	N54269	Hs.48946	EST		6.14		
	118368	N54339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14			
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3		12.40		
	118709	AA232970	Hs.293774	ESTs			12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50			
45	119027	AF086161	Hs.114511	hypothetical protein FLJ11808	3.22			
	119052	R10889		gbcyf38d02.s1 Soares fetal liver spleen	9.60			
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome		6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593			10.80	
	119243	T12603		gbCHR90123 Chromosome 9 exon II Homo sa			9.44	
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot			11.80	
	119499	AI918906	Hs.55080	ESTs		14.80		
	119599	W45552		gbzcc26d03.s1 Soares_senescent_fibroblas		12.60		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00			
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50			
55	119941	AA699485	Hs.58896	ESTs		8.00		
	119994	AA642402	Hs.59142	ESTs	7.73			
	120102	W67363	Hs.170218	KIAA0251 protein		39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91			
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par		8.20		
60	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73			
	120599	AA804448	Hs.104463	ESTs	7.00			
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos			10.00	
	120715	AA292700		gbzcs59a06.s1 NC1_CGAP_G081 Homo sapiens	9.40			
	120821	Y19062	Hs.96870	slaufen (Drosophila, RNA-binding protein			13.80	
65	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	9.00			
	120880	AA360240	Hs.97019	EST	15.60			
	120983	AA398209	Hs.97587	EST		27.66		
	121034	AL389951	Hs.271623	nucleoporin 50kD		20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like	22.80			
70	121313	AA402713	Hs.97872	ESTs			10.00	
	121369	AW450737	Hs.128791	CGI-09 protein	25.71			
	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte			5.42	
	121476	AA412311	Hs.97903	ESTs	8.30			
	121509	AA868939	Hs.97888	ESTs	8.59			
75	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50			
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00			
	121838	AA425680	Hs.98441	ESTs			10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00			
	121991	AA430058	Hs.98649	EST			12.20	
80	122089	AW016543	Hs.98682	hypothetical protein FKSG32		8.60		
	122105	AW241685	Hs.98699	ESTs		6.14		
	122163	AA435702	Hs.98829	EST			10.40	
	122318	AA429743		gbzv60b05.r1 Soares_testis_NHT Homo sap			18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50			
	122338	AA443311	Hs.98998	ESTs	4.80			
85	122414	AI313473	Hs.99087	ESTs, Weakly similar to S47073 finger pr	8.00			

	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.40	
	122702	AU220089	Hs.99439	ESTs	9.20		
	122852	AI580056	Hs.98992	ESTs		10.40	
5	122925	AW268962	Hs.111335	ESTs	6.80		
	123005	AW369771	Hs.52620	integrin, beta 8		12.60	
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro			5.35
	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypothe		6.06	
	123315	AA495369		gbzv37d10.s1 Soares ovary tumor NbHOT H		12.40	
10	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po		11.80	
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein		13.00	
	123519	AW015887	Hs.112574	ESTs	12.20		
	123614	AK000492	Hs.98806	hypothetical protein		7.80	
15	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L			10.60
	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490		7.00	
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma		9.80	
	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
20	123900	AA621223	Hs.112953	EST		12.80	
	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.02		
	124069	AF134160	Hs.7327	claudin 1		27.80	
25	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha			35.80
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
	124297	AL080215	Hs.102301	Homo sapiens mRNA: cDNA DKFZp586J0323 (f			11.00
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo			16.00
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)			6.08
30	124674	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog			21.00
	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
	124969	AI650360	Hs.100256	ESTs			10.80
	125000	T58615	Hs.110640	ESTs			9.80
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypothe	7.60		
	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
35	125299	T32982	Hs.102720	ESTs			9.57
	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC			14.00
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p	8.20		
	125418	AA777690	Hs.188501	ESTs			13.20
40	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.96		
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225			11.20
	125756	BE174587	Hs.289721	growth arrest specific transcript 5			4.31
45	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass			15.60
	125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20		
	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1NIB H	7.40		
50	125924	BE272506	Hs.82109	syndecan 1			4.23
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein			3.98
	126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen		10.80	
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yy23f06.s1 Soares fetal liver spleen	6.57		
55	126435	AW614529	Hs.285847	CGI-19 protein			10.60
	126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino			4.38
	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi			14.80
	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g			4.01
60	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares fetal liver spleen			11.60
	126627	AA497044	Hs.20887	hypothetical protein FLJ10392			14.60
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
	126795	AW976076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
65	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
	126892	AF121855	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs			22.83
	126979	AA210954		gb:czq89h10.r1 Stratagene hNT neuron (937			11.80
70	126986	AI279892	Hs.46801	sorting nexin 14			11.60
	126992	AI809521		gb:zw30e03.x1 Soares_NFL_T_GBC_S1 Homo s			20.80
	127066	R25066		gb:yg42c07.r1 Soares infant brain 1NIB H			27.60
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens			21.60
	127139	AA830233	Hs.293585	ESTs			11.20
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene fami	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
	127225	AA315933	Hs.120879	ESTs			16.80
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,			13.60
	127500	AW971353	Hs.162115	ESTs	11.20		
80	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin		7.80	
	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs			13.80
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			28.00
	127662	W80755	Hs.8294	KIAA0196 gene product			19.80
85	127668	AA343257	Hs.139993	ESTs			11.20

5	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836541	Hs.163085	ESTs			24.60
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fs, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
10	127969	F06498	Hs.53748	Homo sapiens cDNA FLJ14676 fs, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
	128077	AI310330	Hs.128720	ESTs			9.60
	128166	NM_006147	Hs.11801	interferon regulatory factor 6			9.24
15	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954958	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
	128539	R48163	Hs.258618	ESTs	12.60		
20	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9			10.00
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2		16.80	
	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
	128796	AJ000152	Hs.105924	defensin, beta 2	8.12		
25	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plekrophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
	129008	AL079648	Hs.301088	ESTs	8.80		
	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
30	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein	8.00		
	129229	AF013758	Hs.109543	polyadenylate binding protein-interactin	4.00		
	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
35	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
	129466	L42583	Hs.334309	keratin 6A	12.84		
	129494	AI148976	Hs.112062	ESTs			11.00
40	129505	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129641	AI911527	Hs.11805	ESTs			12.00
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA158214	Hs.12152	APMCF1 protein			5.71
45	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-GalbetaGlcNAc beta 1,4-galactosylt	2.56		
	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein			4.03
	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34		7.00	
50	130026	T40480	Hs.332112	EST	6.40		
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
	130149	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	2.74		
	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (ubiquitin-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
55	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein			9.60
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
60	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
	130648	AI458165	Hs.17286	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
65	130744	H59696	Hs.18747	POPT (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130857	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
	130869	J03626	Hs.2057	uridine monophosphate synthetase (orotat			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein			9.60
70	130994	W17044	Hs.327337	ESTs		12.40	
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP,	10.21		
	131031	NM_001650	Hs.288650	aquaporin 4			9.80
	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
75	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
	131185	BE280074	Hs.23960	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
80	131219	W25005	Hs.24395	small inducible cytostine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521563	Hs.334644	hypothetical protein FLJ14668	15.00		
85	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11

	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00		
	131885	BE502341	Hs.3402	ESTs	6.48		
	131921	AA456093	Hs.34720	ESTs		8.40	
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00		
	131958	NM_014062	Hs.3566	ART-4 protein			3.82
	131965	W79283	Hs.35962	ESTs	3.03		
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80	
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30		
10	132109	AW190902	Hs.40088	cysteine knot superfamily 1, BMP antagonist	21.00		
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40	
	132162	AA315805	Hs.94560	desmoglein 2			12.25
	132164	AJ752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70		
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71		
15	132181	AW961231	Hs.16773	Homo sapiens clone TCC01A00427 mRNA sequ	3.83		
	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50		
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50		
	132328	NM_014787	Hs.44896	DnaI (Hsp40) homolog, subfamily B, membe			9.20
	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60	
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40	
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38		
	132544	L19778	Hs.51011	H2A histone family, member P		7.00	
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64		
	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60	
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95		
	132638	AJ798870	Hs.54277	DNA segment on chromosome X (unique) 692		8.20	
30	132653	Z15008	Hs.54451	laminin, gamma 2 (necalin (100kD), kafini	4.38		
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	4.60		
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71		
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83
	132892	AW834050	Hs.9973	tensin			12.00
	132906	BE613337	Hs.234896	germinin	3.09		
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87
	132982	AA576635	Hs.6153	CGI-48 protein	3.50		
40	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18		
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19		
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96		
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55		
	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00
45	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96
	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28
	133155	M58583	Hs.662	cerebellin 1 precursor		10.80	
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00		
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50	
	133421	AF134160	Hs.7327	claudin 1	2.85		
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p			4.66
	133453	AJ659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80	
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14		
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11	
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07		
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1			4.60
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyl			13.00
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56		
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20	
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00		
70	134160	T88162	Hs.79432	fibrillin 2 (congenital contractural ara		24.60	
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40	
	134272	X76040	Hs.278614	protease, serine, 15	4.50		
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00	
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40
	134367	AA339449	Hs.82285	phosphoribosylglycylamide formyltransfer	2.80		
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68		
	134423	H53497	Hs.83006	CGI-139 protein			3.84
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60	
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70
	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio			4.63
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00		

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	134724	AF045239	Hs.321576	ring finger protein 22		12.00	
	134743	AA044163	Hs.89463	potassium large conductance calcium-act	4.00		
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20	
5	134806	AD001528	Hs.89718	spermine synthase			4.58
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle			4.79
	134859	D26488	Hs.90315	KIAA0007 protein		6.20	
	134891	RS1083	Hs.90787	ESTs		7.40	
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00		
	134993	BE409809	Hs.301005	purine-rich element binding protein B			4.48
10	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50		
	135080	AI761180	Hs.94211	rod1 (required for cell differentiation,	5.00		
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00	
	135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin			4.01
	135184	U13222	Hs.96028	forkhead box D1		7.00	
15	135242	AI583187	Hs.9700	cyclin E1	13.50		
	135286	AW023482	Hs.97849	ESTs	6.46		
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80	
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00		
20	135371	NM_006025	Hs.997	protease, serine, 22	8.00		
	135393	L11244	Hs.99886	complement component 4-binding protein,		14.60	

TABLE 5B shows the accession numbers for those primekeys lacking unigenes/D's for Table 5A. For each probe set we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Key: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Key	CAT number	Accessions
35	117079	1621717_1 H92325 T97125
	124305	242183_1 AW963221 AA344870 AA344871 H93331
	101502	18202_6 M26958
	109792	754958_1 R49625 F10674
	126034	1598157_1 H60340 N91637
40	102768	44641_1 U82321 H66077
	126345	1653833_1 N49713 N49819 W03810
	127066	1703458_1 R25066 R20144 R20145 Z43845
	127099	244301_1 AA347668 AW955810 Z44271 F07065 F07064 R13505
	119243	1774795_1 T12603 T12604
45	125876	1566433_1 H14480 N98295
	112054	1538292_1 R43590 F10439
	126979	171411_1 AA210954 AA211007
	126992	880655_1 AJ809521 H12174 Z42556
	122318	292419_1 AA429743 AA442754
50	114699	135322_1 AA127386 R15644 AA127404
	114793	150742_1 AA158245 AA158235
	108305	111550_1 AA071391 AA069892 AA069891
	108393	113411_1 AA075211 AA075245 AA075126 AA074946
	100867	tigr_HT4586 U14622
55	123731	genbank_AA609839 AA609839
	109700	genbank_F09609 F09609
	120715	genbank_AA292700 AA292700
	113702	genbank_T97307 T97307
	115113	genbank_AA256460 AA256460
60	101045	entrez_J05614 J05614
	108554	genbank_AA084948 AA084948
	108573	genbank_AA086005 AA086005
	119052	149538_1 R10889 R10888
	126522	416020_1 W31912 AI167491
65	126605	439280_1 AA676910 AA778853 AA778865 W86800
	103768	46922_1 W42667 AI580740 AI690440 AI561350 AW467906 AW151450 AI825927 AI041716 AI885600 AI742213 AW248624 AI955498 AA033947
		AA845593 AI623711 N68583 C00064 AA193567 AW083668 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
		AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
		AI199673 AI811765 AI275832 AI422233 AI191852 AI066682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
		H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881
70		AW362477 AA089997 AI350265 W93479 N96688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214
		AI970774 AI857712 AI683081 AI855584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375
		AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
		AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881
		AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
75		AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AA92005 AA677429 AA996334 AI693771 AI950039 AI245629 AI285515
		AI856186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492
		AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843189
		AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339
		AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255
80		AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R50788
		AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219546 W61039 W93907 AW385050 W37967
		W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009549 C03892 AW149454 AA310963 AA219693
		AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409
85		AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
		W07688 AA193645 AA378994 AA489273 F32267 W93903 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 RG0282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849
 AI288629 AA843996 W15260 AI188286 AW248079 R15836

5 119599 genbank_W45552 W45552
 112382 genbank_R59904 R59904
 105264 genbank_AA227934 AA227934
 100071 entrez_A28102 A28102
 123315 714071_1 AA496369 AA496546

10

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Altymatrix Hu03 Genachip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

20

R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
25 100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
101174	L17330	Hs.280	pro-T/NK cell associated protein	15.00	
101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasis)		2.68
30 101972	S82472		gb:beta-pol-DNA polymerase beta (exon a)		2.11
102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose)	7.50	
102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	7.50	
102832	U92015		gb:Human clone 143789 defective mariner	13.50	
103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
35 103439	X98266		gb:HLsaplens mRNA for ligase like protei		2.50
103563	L02911	Hs.150402	activin A receptor, type I	9.00	
103857	AJ076795	Hs.45033	lactoferrin rich protein		3.94
104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
40 104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
106131	BE514788	Hs.296244	SNARE protein		2.17
106672	H47233	Hs.30643	ESTs	7.00	
106872	T56887	Hs.18282	KIAA1134 protein	11.50	
45 106960	AA156238	Hs.32501	ESTs		2.38
106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protei		2.95
108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
108599	AB018549	Hs.69328	MD-2 protein	13.00	
50 108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothe		2.40
109247	AA314907	Hs.85950	ESTs	7.00	
109630	R44607	Hs.22672	ESTs		5.00
110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
110234	H24458	Hs.32085	EST	16.50	
55 110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
111057	T79639	Hs.14629	ESTs	16.50	
111850	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
112291	R53972	Hs.26026	ESTs		3.00
112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
60 113009	T23699	Hs.7246	ESTs		4.50
113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
113121	T48011	Hs.8764	EST		2.21
65 113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
113757	AA703095	Hs.18631	ESTs		2.65
113948	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
113894	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
70 114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
114987	AA251016	Hs.87808	EST		6.00
115460	AW958439	Hs.38613	ESTs		2.27
115722	W91892	Hs.59609	ESTs		9.00
116261	AA481788	Hs.190150	ESTs	9.50	
75 116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
117178	H98675	Hs.269034	ESTs		2.68
117757	AF088019	Hs.46732	EST	7.50	
118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
80 118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
118657	AI822106	Hs.49902	ESTs		2.39
120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [Hsapi		3.50
120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
85 120524	AA261852	Hs.192905	ESTs	6.00	
120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fts, clone L	17.92	

	121558	AA412497	gb:z89g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146	ESTs	10.00
	121936	AI024600	Hs.98612	ESTs	15.00
	121938	AA428659	Hs.98610	ESTs	14.00
5	122177	AA435789	Hs.98833	EST	8.93
	123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.04
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap		11.50
	123756	AA609971	Hs.112795	EST	11.00
	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
10	124371	N24924	Hs.188601	ESTs	6.50
	127477	BE328720	Hs.280651	ESTs	4.33
	127591	AI190540	Hs.131092	ESTs	3.02
	128252	AA455924	Hs.192228	ESTs	7.00
	128426	AI265784	Hs.145197	ESTs	
15	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	2.11
	128945	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	15.50
	129235	AW977238	Hs.126084	KIAA1055 protein	4.25
	129506	AB020684	Hs.11217	KIAA0877 protein	6.50
20	129595	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	10.00
	130160	AA305688	Hs.267695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr	20.00
	130340	D82326	Hs.239106	solute carrier family 3 (cystine, dibasi	11.50
	131220	AB023194	Hs.300855	KIAA0977 protein	17.50
	131430	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.10
25	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein	6.15
	132458	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	5.58
	132647	NM_006927	Hs.54432	sialyltransferase 4B (beta-galactosidase	7.50
	132655	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.53
	132682	AI077500	Hs.54900	serologically defined colon cancer antig	2.50
30	132747	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	2.83
	132812	R50333	Hs.92186	Leman coiled-coil protein	3.82
	133337	AF085983	Hs.293676	ESTs	5.00
	133876	AL134906	Hs.771	phosphorylase, glycogen; liver (Hers dis	3.00
	134119	AW157837	Hs.79226	fasciculation and elongation protein zet	2.06
35	134464	AA302983	Hs.239720	CCR4-NOT transcription complex, subunit	2.27
	134542	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	11.50
	135002	AA448542	Hs.251677	G antigen 7B	87.00
	135305	AA203555	Hs.98288	Homo sapiens cDNA FLJ14903 fis, clone PL	6.50

TABLE 6B show the accession numbers for those primekeys lacking unigenelD's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
55	108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
	103439	35330_1	X98266 N41124
	123551	genbank_AA608837	AA608837
	123861	genbank_AA620840	AA620840
	102832	entrez_U92015	U92015
	101972	entrez_S82472	S82472
60	121558	genbank_AA412497	AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Key:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.			
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.			
	Key	ExAccn	UnigeneID	Unigene Title	R1 R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80
	101046	K01160		(NONE)	672.00
20	101066	AW970254	Hs.889	Charot-Leyden crystal protein	66.00
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	77.20
	101497	W05150	Hs.37034	homeo box A5	62.80
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20
	102125	NM_006456	Hs.288215	siylaltransferase	103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	65.70
	102796	AL079546	Hs.107019	sympleskin; Huntingtin interacting protei	58.80
	102829	NM_006183	Hs.80962	neurotensin	268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	212.10
	103260	X78416	Hs.3155	casein, alpha	130.70
	103351	X89211		gb:Hsapiens DNA for endogenous retrovir	64.60
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40
	105024	AA126311	Hs.9879	ESTs	68.20
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S	74.60
45	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	71.10
	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp5548076 (tr	83.80
	106614	AA648459	Hs.335951	hypothetical protein AF301222	62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	202.40
	106999	H93261	Hs.10710	hypothetical protein FLJ20417	89.60
50	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c	66.40
	108810	AW295647	Hs.71331	hypothetical protein MGC5350	95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	63.40
	109597	AA989362	Hs.293780	ESTs	85.00
	109691	T65568	Hs.12860	ESTs	58.70
55	109704	AI743880	Hs.12876	ESTs	60.60
	110942	R63503	Hs.28419	ESTs	76.40
	111722	R23924	Hs.23596	EST	74.60
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-II	64.80
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	76.70
	113073	N39342	Hs.103042	microtubule-associated protein 18	120.20
	114251	H15261	Hs.21948	ESTs	127.20
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	91.00
65	115815	AW905328	Hs.180842	ribosomal protein L13	66.40
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	226.60
	115955	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00
70	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20
	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo	63.50
	120484	AA253170	Hs.96473	EST	81.60
	120983	AA398209	Hs.97587	EST	81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD	66.20
75	121423	AW973352	Hs.290585	ESTs	64.40
	122553	AA451884	Hs.180121	ESTs	60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	80.20
	124472	N52517	Hs.102670	EST	71.00
	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	104.80
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	72.00
	125731	R61771	Hs.26912	ESTs	69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00
	126020	H79863	Hs.114243	ESTs	62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	62.80
85	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	60.10

	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
5	127987	AI022103	Hs.124511	ESTs	96.60	
	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		105.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
10	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
	130090	H97678	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stannocalcin 2		139.60
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
15	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fs, clone HE	76.20	
	131775	AB014548	Hs.31921	KIAA0548 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
20	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30
	133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 protein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
25	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
	135047	AI134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primekeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
103207	30635_4	X72790
106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
116571	genbank_D45652	D45652
118466	genbank_N66741	N66741
101046	entrez_K01160 K01160	
101941	entrez_S77583 S77583	
103351	entrez_X89211 X89211	
123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Altymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

10

R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung
 R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
15	300097	AJ916973	Hs.213603 ESTs	5.46	4.69
	300117	AW189787	Hs.147474 ESTs	0.58	0.56
	300197	AJ686661	Hs.218286 ESTs	4.26	5.44
	300201	AJ308300	gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
	300225	AJ989963	Hs.197505 ESTs	1.68	1.75
20	300247	AW274682	Hs.161394 ESTs	1.08	2.28
	300256	AJ69095	Hs.298241 Transmembrane protease, serine 3	0.65	1.00
	300337	AJ707881	Hs.202090 ESTs	5.80	9.09
	300362	Z42308	gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
	300374	AJ859947	Hs.314158 ESTs	2.99	4.38
25	300387	AW270150	Hs.254516 ESTs	1.50	2.53
	300440	AJ421541	Hs.146164 ESTs	3.98	5.25
	300441	R10367	Hs.307921 EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
	300449	AJ362967	Hs.132221 hypothetical protein FLJ12401	0.43	0.62
	300469	AW135830	Hs.233955 hypothetical protein FLJ20401	0.16	0.83
30	300552	X85711	Hs.21838 hypothetical protein FLJ11191	4.10	9.75
	300627	W27363	gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
	300630	AW118822	Hs.128757 ESTs	2.91	5.86
	300716	AJ216113	Hs.126280 hypothetical protein FLJ23393	1.00	0.92
	300738	AJ623332	Hs.130541 KIAA1542 protein	1.82	1.71
35	300777	AA235361	Hs.96840 KIAA1527 protein	4.48	8.22
	300790	AJ92471	Hs.188270 ESTs	1.29	1.18
	300832	AJ688147	Hs.220615 ESTs, Weakly similar to T03829 transcrip	5.51	8.56
	300838	Z44942	Hs.22958 calcium channel alpha2-delta3 subunit	4.90	6.34
	300838	AJ582897	Hs.192570 hypothetical protein FLJ22028	1.70	2.81
40	300878	AW449802	Hs.285901 Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
	300897	AJ890356	Hs.127804 ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
	300926	AA504860	gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
	300960	AJ041019	Hs.152454 ESTs	2.74	4.46
	300961	AW204069	Hs.312716 ESTs, Weakly similar to unnamed protein	1.00	1.00
45	300962	AA593373	Hs.293744 ESTs	1.46	1.51
	300967	AA565209	Hs.269439 ESTs	0.39	1.30
	300987	AW450840	Hs.148590 ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
	300988	AJ927208	Hs.208952 ESTs	0.16	0.37
	301050	AW136973	Hs.288516 ESTs, Weakly similar to S69890 mitogen I	3.23	1.94
50	301098	AA677570	Hs.185918 ESTs	6.76	14.28
	301157	AA729905	Hs.231916 ESTs	3.16	8.85
	301162	AJ142118	Hs.129004 ESTs	1.68	7.18
	301170	AA737594	Hs.247606 ESTs	4.40	6.42
	301192	AJ088751	Hs.121188 ESTs	6.38	11.59
55	301193	AA758115	Hs.128350 ESTs, Weakly similar to JCS423 2-hydroxy	4.35	7.78
	301267	AW297762	Hs.255690 ESTs	1.56	1.61
	301281	AA843986	Hs.190586 ESTs	2.19	1.78
	301341	AJ819188	Hs.208229 ESTs	0.76	0.76
	301382	AA912839	Hs.163369 ESTs	1.00	1.81
60	301407	AW450466	Hs.126830 ESTs	1.48	1.51
	301452	AA975688	Hs.159955 ESTs	0.51	1.46
	301483	AW272467	Hs.254655 Unfilled	2.40	5.02
	301494	AJ678034	Hs.131099 ESTs	2.79	3.41
	301521	AJ733621	Hs.133011 zinc finger protein 117 (HPF9)	0.67	0.67
65	301531	AJ077462	Hs.134084 ESTs	2.52	3.76
	301580	AJ878959	Hs.73737 splicing factor, arginine/serine-rich 1	7.41	11.92
	301676	Z43570	Hs.27453 ESTs, Moderately similar to G01251 Rar p	8.31	10.70
	301690	F05865	Hs.108323 ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
	301718	F07744	Hs.7987 DKFZP434F162 protein	4.20	8.78
70	301799	AA384252	Hs.286132 D15F37 (pseudogene)	5.83	7.04
	301804	AA581004	Hs.62180 anillin (Drosophila Scrape homolog), act	1.70	0.76
	301822	X17033	Hs.271988 Integrin, alpha 2 (CD49B, alpha 2 subunit)	1.58	1.36
	301846	R20002	Hs.6823 hypothetical protein FLJ10430	1.00	1.00
	301868	T71508	Hs.13861 ESTs, Weakly similar to pH sensitive max	2.88	5.49
75	301882	T78054	gb:yc97g09.r1 Soares infant brain 1NIB H	2.28	3.80
	301905	AJ991127	Hs.117202 ESTs	1.00	1.00
	301948	AA344647	Hs.116724 aldo-keto reductase family 1, member B11	5.28	2.28
	301960	AW070252	Hs.27973 KIAA0874 protein	5.38	6.48
	302011	T91418	Hs.125156 transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
80	302016	N40834	Hs.23495 hypothetical protein FLJ11252	1.00	1.25
	302041	NM_001501	Hs.129715 gonadotropin-releasing hormone 2	0.71	0.99
	302072	AJ238381	Hs.132576 paired box gene 9	1.60	1.71
	302094	AJ286176	Hs.6786 ESTs	0.52	1.20
	302095	AW044300	Hs.137506 Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
85	302148	AW269618	Hs.23244 ESTs	3.04	3.87

	302155	AJ088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ066276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal4betaGlcNAc beta 1,4-galactosyl	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfamily	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (tr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155155	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
15	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (tr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:alpha-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
20	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
30	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180769	S164 protein	0.80	0.95
	302679	H55022		gbyu66g11.1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gbtHomo sapiens mRNA for immunoglobulin	4.25	8.13
	302705	U09060		gbtHuman immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gbtHuman autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gbtHomo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gbtHomo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gbtHsapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.283961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gbtHsapiens rearranged Ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
50	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gbtHomo sapiens clone 2A1 scFV antibody	1.41	1.86
	303013	F07899	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	0.72	0.76
55	303077	AF163305		gbtHsapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146288	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHz168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359789	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gbtEST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474186	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
	303978	AW513315		gbtgc43c12x1 NCL CGAP_U11 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU 6	2.83	4.06
	303990	AW515465		gbtgc471a11x1 NCL CGAP_Kid8 Homo sapiens	1.15	2.35
	303998	AW516449		gbtgc68f05x1 NCL CGAP_U12 Homo sapiens	2.20	9.35
85	303999	AW516611		gbtgc70b11x1 NCL CGAP_Ov39 Homo sapiens	4.85	6.28
	304006	AW517947		gbtgc65h02x1 NCL CGAP_U12 Homo sapiens	3.21	4.07

	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yo04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1N1B H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
15	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78456	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304456	AAA11240		gb:zv26g05.s1 Soares_NbHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zd82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zd02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA485074	Hs.297581	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nm13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304956	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zb89h08.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nt01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptide	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCI_CGAP_GC81 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GC80 Homo sapiens4.49	8.71	8.71
	305690	AA813477		gb:ai67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kd6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84e08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA864374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCI_CGAP_Kd5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s1.56	1.12	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kd3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferase	2.20	2.70
	306242	AA932805		gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:oo53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4562 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kd6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:og35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67	7.44
	306446	AA977348		gb:og72e12.s1 NCI_CGAP_Kd6 Homo sapiens	3.92	6.27

5	306458	AA978186		gbcp33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306457	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gbcor84d07.s1 NCL_CGAP_Lu5 Homo sapiens	1.00	1.00
	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gbcou57e08.s1 NCL_CGAP_Br2 Homo sapiens	16.20	31.83
10	306572	AA995686		gbcos25c12.s1 NCL_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gbcos18c10.s1 NCL_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gbcou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
15	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gbcov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
	306751	AI032589		gb:cw70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
20	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093957		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
	306956	AI125111		gb:am56f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
25	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
30	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
35	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307426	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:qj72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
	307551	AI281556		gb:qu52f11.x1 NCL_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
40	307608	AI290285		gb:qm01r02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:tb17b01.x1 NCL_CGAP_Ov37 Homo sapiens	1.59	1.31
	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RJ	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
45	307730	AI336092		gb:qt43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:qt127f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	AI342731		gb:qp26a07.x1 NCL_CGAP_Lu5 Homo sapiens	4.52	12.58
	307783	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:qt118f09.x1 NCL_CGAP_GC4 Homo sapiens	6.57	9.61
50	307807	AI351799		gb:qt109d02.x1 NCL_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:qt109g03.x1 NCL_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:qt194a11.x1 NCL_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:qz08g05.x1 NCL_CGAP_CLL1 Homo sapiens	3.18	5.21
55	307902	AI380462		gb:tg02h05.x1 NCL_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
	308011	AI439473		gb:ti60a08.x1 NCL_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
60	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:ti77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2.38	8.72	8.72
65	308122	AI480123	Hs.309411	EST	2.70	3.86
	308154	AI500600		gb:tn93d08.x1 NCL_CGAP_UI2 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schizofen4 [M.mu	2.48	4.86
	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (K-1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_ED4.r tumor2 Homo sapiens cD	3.34	3.79
70	308216	AI557135		gb:PT2.1_13_HD6.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
75	308413	AI636253	Hs.196511	ESTs	3.16	4.82
	308450	AI650860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB5 Homo	3.90	5.64
	308599	AI718893		gb:as47d07.x1 Barstead aorta HPLRB5 Homo	3.32	5.12
80	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12.x1 NCL_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCL_CGAP_CLL1 Homo sapiens	0.82	0.99
	308697	AI767143		gb:wi97a07.x1 NCL_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
85	308778	AI811109		gb:tr04c11.x1 NCL_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCL_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
	308875	AI832332		gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	303879	AJ832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	303886	AJ833240		gb:at76d10.x1 Barstead colon HPLR87 Homo	3.06	2.65
	303898	AJ858945		gb:wt32d10.x1 NCI_CGAP_Ut1 Homo sapiens	2.45	3.44
5	303934	AJ855023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
	303966	AJ870704		gb:wt47h01.x1 NCI_CGAP_Ut1 Homo sapiens	1.00	1.00
	303979	AJ873111		gb:wt52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15	11.10
	303945	AJ910902		gb:tg39f01.x1 NCI_CGAP_Ut1 Homo sapiens	0.61	0.59
	303951	AJ911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
10	303969	AJ917366	Hs.17202	SWI/SNF related, matrix associated, act	3.27	5.88
	303983	AJ922426	Hs.119598	ribosomal protein L3	2.39	3.34
	3039105	AJ925503	Hs.265884	ESTs	5.54	17.78
	3039122	AJ928178		gb:wt095a11.x1 NCI_CGAP_Kd11 Homo sapien	1.00	2.92
	3039128	AJ928816	Hs.180842	ribosomal protein L13	1.38	5.55
15	3039164	AJ937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
	3039177	AJ951118		gb:wt63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
	3039288	AJ991525	Hs.299426	ESTs	4.86	7.48
	3039299	AW003478		gb:wtq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	3039303	AW004823		gb:wt53a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
20	3039411	AW085201	Hs.244144	EST	4.30	7.14
	3039437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	3039459	AW117645	Hs.65114	keratin 18	2.88	4.55
	3039476	AW129368		gb:wt014b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6.60
	3039499	AW135325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
25	3039529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
	3039532	AW151119		gb:wtg33e10.x1 NCI_CGAP_Ut1 Homo sapiens	1.18	4.40
	3039526	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	3039641	AW194230	Hs.253100	EST, Moderately similar to GH1U Ig gamm	1.47	1.39
	3039675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
30	3039693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	3039695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	3039700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	3039747	AW264889		gb:wtq35h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	3039769	AW272346		gb:wt513e10.x1 NCI_CGAP_Kd11 Homo sapien	5.76	11.90
35	3039782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	3039783	AW275401	Hs.254798	EST	1.00	4.11
	3039799	AW276964		gb:wtq58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
	3039866	AW299916		gb:wt544c01.x1 NCI_CGAP_Kd11 Homo sapien	3.02	5.04
40	3039903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
	3039923	AW340684		gb:wt05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	3039928	AW341418		gb:wt08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	3039931	AW341683		gb:wt013d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	3039933	AW341936		gb:wtb73f10.x1 NCI_CGAP_Ut2 Homo sapiens	4.90	18.29
	3039964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
45	310002	AJ439095	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (tr	0.20	0.47
	3100096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	3100098	AJ685841	Hs.161354	ESTs	0.31	0.76
	310109	AJ203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310115	AJ611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195542	Hs.148901	ESTs	1.00	2.71
	310146	AJ206614	Hs.197422	ESTs	9.50	15.31
	310193	AJ627653	Hs.147562	ESTs	2.85	4.18
55	310255	AW450439	Hs.153378	ESTs	4.26	10.63
	310261	AJ240483	Hs.201217	ESTs	3.28	4.40
	310264	AJ915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AJ242102	Hs.213636	ESTs	5.43	8.19
	310282	AJ243332	Hs.156055	ESTs	3.15	8.06
60	310290	AW013815	Hs.149103	ESTs	2.19	3.12
	310333	AJ253200	Hs.145402	ESTs	1.17	1.91
	310346	AJ261340	Hs.145517	ESTs	4.81	9.95
	310385	AJ263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW195632	Hs.252956	ESTs	0.85	1.01
65	310446	AJ275715	Hs.145926	ESTs	2.18	3.85
	310468	AJ984074	Hs.196398	ESTs	3.39	5.19
	310477	AJ948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AJ681145	Hs.160724	ESTs	3.30	7.33
70	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AJ302654	Hs.208024	ESTs	3.26	3.46
	310584	AJ653007	Hs.156304	ESTs	2.39	4.08
	310608	AJ962234	Hs.196102	ESTs	5.60	6.49
	310624	AJ341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AJ814373	Hs.164175	ESTs	1.85	1.71
	310648	AJ347863	Hs.156672	ESTs	0.17	0.69
	310694	AJ654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	AJ472124	Hs.157757	ESTs	4.82	6.27
	310714	AJ418446	Hs.157882	ESTs	1.76	3.51
80	310722	AJ989803	Hs.157289	ESTs	1.14	6.85
	310756	AJ916560	Hs.158707	ESTs	8.46	13.01
	310764	AJ376769	Hs.167172	ESTs	4.76	7.37
	310848	AJ459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AJ421677	Hs.161332	ESTs	6.37	7.94
	310858	AJ871000	Hs.161330	ESTs	6.07	9.84

5	310864	AJ924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AJ560210	Hs.263912	ESTs	10.08	17.66
10	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AJ521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
	311034	AJ564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
15	311134	AJ990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	periazdn	0.65	0.95
	311187	AJ638374	Hs.224189	ESTs	2.46	2.78
	311220	AJ556040	Hs.196532	ESTs	1.10	2.52
	311230	AJ989808	Hs.197663	ESTs	1.41	1.75
20	311236	AJ653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AJ671221	Hs.199887	ESTs	1.00	1.41
	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
	311294	AA826425	Hs.291829	ESTs	1.04	2.69
25	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AJ682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
	311405	AW280961	Hs.201815	ESTs	3.80	11.66
	311409	AJ698839	gbwd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94	
30	311420	AJ936291	Hs.209867	ESTs	5.30	12.56
	311443	AJ791521	Hs.192206	ESTs	4.39	6.09
	311467	AJ934909	Hs.175377	ESTs	1.00	1.04
	311479	AJ933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	artaplin 1	2.50	5.73
35	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
	311537	AJ805121	Hs.211828	ESTs	3.69	5.85
	311543	AJ681360	Hs.201259	ESTs	1.73	1.34
40	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AJ819230	Hs.211238	Interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AJ922143	Hs.211334	ESTs	2.39	3.32
45	311586	AJ827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450675	Hs.212709	ESTs	1.00	1.00
	311621	AJ924307	Hs.213464	ESTs	4.16	6.74
	311635	AJ928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
50	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
	311714	AW131785	Hs.246831	ESTs, Weakly similar to CLK_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144587	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
55	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AJ682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AJ056769	Hs.133512	ESTs	1.34	3.97
	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
60	311823	AJ089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.85	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
	311896	AW206447	gb:U1-H-B11-efg-g-02-0-ULs1 NCI_CGAP_Su	1.66	1.13	
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
65	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AJ597863	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AJ382726	Hs.182434	ESTs	5.80	8.14
70	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78	4.92
	312046	AJ580018	Hs.268591	ESTs	4.11	7.32
	312056	T83748	Hs.268594	ESTs	2.36	3.08
75	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
	312094	Z78390	gb:HSZ76390 Human fetal brain S. Meier-E	3.05	4.48	
	312097	AJ352096	Hs.112180	zinc finger protein 148 (pH2-52)	4.52	9.70
80	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AJ052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89655	Hs.195648	ESTs	0.67	1.03
	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AJ052572	Hs.269864	ESTs	2.41	3.32
85	312201	AJ928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613	gb:za65a07.s1 Soares fetal liver spleen	4.28	11.13	
	312252	AJ128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	312318	AW235092	Hs.143981	ESTs	3.45	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R65210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gbt43h12x1 NCI_CGAP_Bm52 Homo sapien	2.37	3.98
	312437	AA995028		gbtRC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 [f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.146924	ESTs	1.11	1.00
15	312507	AI168177	Hs.143653	ESTs	5.89	8.24
	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
20	312599	AI865073	Hs.125720	ESTs	3.75	5.29
	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240582	Hs.214578	ESTs	0.98	2.03
	312689	AW450461	Hs.203565	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
30	312925	N90868	Hs.271695	ESTs	2.50	4.25
	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
35	312984	N25871	Hs.177337	ESTs	2.03	2.13
	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419280	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
40	313056	AI651930	Hs.135684	ESTs	1.51	2.04
	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
45	313136	N59284	Hs.288010	ESTs	0.49	1.36
	313153	AI240838	Hs.132750	ESTs	5.35	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	VI19632	Hs.124170	ESTs	1.00	3.87
50	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular teldj	0.74	2.06
	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [Hs	2.00	4.32
55	313325	AI420511	Hs.127832	ESTs	1.20	2.27
	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
60	313417	AA741151	Hs.137323	ESTs	0.63	3.01
	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
65	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
	313690	AI483591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gbznm58c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
80	313835	AI538438	Hs.159087	ESTs	5.74	8.88
	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.05
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
85	313883	AI949384		gbznu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.90	10.91
	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00

	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431	Hs.194628	gbnc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
15	314128	AA935633	Hs.194628	ESTs	2.90	6.35
	314151	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
25	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419	Hs.132801	gb:EST391378 MAGE resequences, MAGP Homo1.42	1.36	1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AI754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.184002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735	Hs.153279	gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31	1.02
	314943	AA767977	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AA74433	Hs.179556	ESTs	5.37	9.36
	315353	AA452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	fidgetin-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473	Hs.156919	gb:zh36102.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.84
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI581671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
85	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
	315526	AI193048	Hs.126685	ESTs	1.67	1.78

	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
	315562	AA737415	Hs.152826	ESTs	2.66	2.48
5	315577	AW513545	Hs.17283	hypothetical protein FLJ10690	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.56
	315634	AA837085	Hs.220585	ESTs	0.50	1.40
10	315658	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932652	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
15	315730	H25899	Hs.201591	ESTs	0.11	0.60
	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gbcd115a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	AI652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
	316232	AW297853	Hs.251203	ESTs	1.48	1.60
35	316275	AI671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
	316346	AI028478	Hs.157447	ESTs	3.51	6.69
40	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
	316514	AA768037	Hs.291671	ESTs	4.70	6.04
45	316519	AI929097		gbcd10c11.s1 NCL_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
50	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
	316891	AW298119	Hs.202536	ESTs	1.64	2.97
60	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
	317137	AW341567	Hs.125710	ESTs	2.82	5.12
70	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc1osteonectin, cwcv and kazal-like d	2.74	0.88
	317266	AA906289	Hs.203614	ESTs	1.00	1.00
75	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
	317320	AA927151	Hs.130452	ESTs	3.58	8.13
80	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972955	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126860	ESTs	1.88	4.15
	317521	AI824338	Hs.126891	ESTs	3.12	4.55
85	317529	AI916517	Hs.126865	ESTs	2.73	3.34

	317570	AJ733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
5	317627	AJ346110	Hs.132553	ESTs	1.50	1.39
	317650	AJ733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	AJ307659	Hs.174794	ESTs	5.33	9.59
	317701	AJ674774	Hs.128014	ESTs	1.00	1.00
	317711	AJ733015	Hs.272189	ESTs	5.13	7.81
	317722	AJ733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	AJ143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AJ98273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AJ368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AJ820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
20	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865	AJ298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AJ827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
	317890	AJ915599	Hs.129225	ESTs	4.68	7.48
25	317899	AJ952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	AJ005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AJ016694	Hs.256921	ESTs	1.86	4.50
30	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	AJ024540	Hs.131574	ESTs	1.21	1.27
	318117	AJ208304	Hs.250114	ESTs	0.86	1.17
	318187	AJ792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90	6.98
35	318223	AJ077540	Hs.134090	ESTs	1.05	0.90
	318240	AJ085377	Hs.143610	ESTs	3.10	2.40
	318255	AJ082692	Hs.134662	ESTs	0.02	1.05
	318266	AJ554341	Hs.271443	ESTs	6.12	10.55
	318330	AJ093840	Hs.143758	ESTs	4.98	7.90
40	318369	AJ493501	Hs.170974	ESTs	2.46	5.62
	318428	AJ949409	Hs.194591	ESTs	0.77	0.45
	318458	AJ149783	Hs.158438	ESTs	3.54	4.92
	318467	AJ151395	Hs.144834	ESTs	4.56	5.62
	318473	AJ939339	Hs.146883	ESTs	2.08	4.05
	318476	AJ693927	Hs.265165	ESTs	4.22	8.07
45	318487	AJ167877	Hs.143716	ESTs	1.47	1.05
	318488	AJ217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTH1188 HTCCL1 Homo sapiens cDNA 5/3	2.58	5.20
50	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
55	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596	AJ470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
65	318711	AJ936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AJ962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24953	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865	H10818		gb:ym04f10.r1 Soares infant brain 1N1B H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
75	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AJ219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.269522	ESTs	5.84	9.79
80	318985	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13678	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12639	ESTs	5.87	7.26

5	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6918	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
	319279	T65094	Hs.12677	OGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
10	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
	319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
15	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39i07.r1 Soares fetal liver spleen	4.28	8.81
20	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	AJ809337	Hs.116417	ESTs	1.76	5.65
	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
25	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	AL382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
	319523	T69499	Hs.191184	ESTs	1.55	3.25
	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
30	319546	R09692		gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82988	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
35	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1N1B H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HTO	2.51	3.55
	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
40	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
	319708	R15372	Hs.22664	ESTs	1.00	1.22
	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
45	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydcm	4.63	6.56
	319812	N74880	Hs.264330	N-acetylphosphoglycine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
50	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
	319935	H79450	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
55	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RPS-850E9	1.81	1.57
	320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
	320018	T83263		gb:yd40h08.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
60	320032	AI699772	Hs.292564	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
	320053	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320096	H58138	Hs.117915	ESTs	2.08	4.47
65	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
	320188	AW419200	Hs.172318	ESTs	1.26	1.00
	320193	AA831259	Hs.17132	ESTs	2.58	6.23
70	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N116 (f	0.84	1.18
	320219	AA327564	Hs.127011	tbubointersitilal nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	teklin 2 (testicular)	0.18	1.09
75	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (tr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
80	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	AI167978	Hs.139851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141680	chloride channel 2	2.17	1.26
	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320388	H16055	Hs.31286	ESTs	1.00	3.22
85	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
	320436	AA253352	Hs.293663	ESTs	2.22	3.49
	320438	W24548	Hs.5869	ESTs	3.53	8.14

	320448	AI240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folistatin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 f1s, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34572	Hs.324522	ESTs	3.16	5.63
	320536	AA331732	Hs.137224	ESTs	2.83	5.83
10	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80508	small nuclear ribonucleoprotein polypept	1.00	6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AA45591		gb:yg04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
25	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 Inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
30	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AI473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uroplakin 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
	320927	AI205786	Hs.213923	ESTs	0.18	1.46
35	320957	AI878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
45	321130	H43750	Hs.125494	ESTs	1.00	3.14
	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
50	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 f1s, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF058654		gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
55	321270	R83560		gb:yy76c06.s1 Soares fetal liver spleen	3.80	5.26
	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.83
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
60	321356	R93443	Hs.271770	ESTs	3.10	4.66
	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:Hsapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 f1s, clone H	1.60	3.11
65	321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
	321468	AA514198	Hs.38540	ESTs	2.46	6.50
	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
70	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108551	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06	7.19
	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
75	321581	AA019964	Hs.28803	ESTs	4.88	6.73
	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
80	321642	AW085917	Hs.247084	ESTs	1.52	1.38
	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb:at70c12.r1 Soares_NhlMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 f1s, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
85	321700	N55160	Hs.167260	ESTs	4.57	7.46
	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	A1694875	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.00	1.00
5	321777	A1637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.69
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29458	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	A1651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp554O1278	1.00	1.90
20	322044	AW340926		gbxy61b10.x1 NCL_CGAP_Lu34.1 Homo sapie	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	A1341937		gbxqt10e03.x1 NCL_CGAP_GC4 Homo sapiens	4.69	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
	322091	AU198863	Hs.106243	ESTs	1.69	1.75
25	322125	R93901		gbxyq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gbxyr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52567		gbxyt85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gbxyt88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gbxyt94c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
35	322212	AF087995	Hs.134877	ESTs	3.42	4.84
	322221	AU890619	Hs.179562	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AJ640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gbztd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
40	322284	AJ792140	Hs.49265	ESTs	0.66	2.76
	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
	322320	AF086419		gbztd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gbzbd18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AJ394663	Hs.122116	ESTs, Moderately similar to Ost2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AU15730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AJ916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AJ828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:z103g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AJ110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	AJ110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23507	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AJ608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	AJ962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AJ377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
80	322887	AJ965306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
	322913	AJ733737	Hs.68837	ESTs	2.38	6.61
	322926	AJ825940	Hs.211192	ESTs	4.02	5.79
	322929	AJ365585	Hs.146246	ESTs	0.30	1.14
	322958	AJ905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
85	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	A1733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	AI700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
15	323232	AA148722	Hs.224680	ESTs	0.45	1.35
	323256	AW003382	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	AI697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	AI336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
	323359	AA234172	Hs.137418	ESTs	0.34	1.18
25	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	AI672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
30	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD (Hsapien	0.43	0.80
	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo.2.21		3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	AI185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
40	323678	AL042121	Hs.20980	ESTs	3.33	5.10
	323691	AA317551	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
45	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	AI869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AI472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	AI381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
	324275	AA429088	Hs.98523	ESTs	3.62	5.38
65	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	AI198841	Hs.128173	ESTs	4.06	5.91
70	324325	AL138153	Hs.300410	ESTs	5.88	8.25
	324338	AL138357	Hs.145078	regulator of differentiation (in S. pombe	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.78	1.64
	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	AI924953	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152912	ESTs	2.73	2.17
	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	AI148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
5	324801	AJ819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
	324804	AJ692552		glbwrd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
10	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
	324886	AA805794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUMML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
15	324958	AA525076	Hs.132892	protocadherin 20	5.12	9.81
	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
20	325114	D83901	Hs.315562	ESTs	2.73	3.17
	325146	AJ064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653682	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
25	325235				2.64	4.12
	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
30	325389				0.88	1.05
	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
35	325559				7.48	21.40
	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
40	325597				2.98	13.40
	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
45	325739				0.59	0.88
	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
50	325895				7.78	15.98
	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
55	325971				4.88	7.42
	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
60	326163				3.27	5.70
	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
65	326274				1.00	8.09
	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
70	326589				9.20	13.49
	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
80	326964				0.41	1.70
	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
85	327053				3.55	6.31
	327075				1.59	1.40

	327085	2.50	12.57
	327130	5.38	8.04
	327155	3.74	6.58
5	327220	1.28	1.54
	327224	6.55	12.91
	327268	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
	327361	2.69	4.41
10	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
	327467	6.58	18.01
15	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
	327606	2.06	3.61
20	327611	5.90	14.26
	327642	4.06	8.74
	327654	1.05	2.08
	327734	1.00	1.00
	327775	1.46	11.79
25	327796	3.47	5.65
	327840	3.26	6.64
	327940	5.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.59
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
35	328113	0.72	0.91
	328157	5.58	6.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
	328299	2.20	3.06
40	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328806	0.22	0.78
	328851	3.68	10.54
	328908	6.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329067	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	6.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00

	329764			5.78	15.50
	329816			2.09	5.44
	329860			3.13	10.77
	329953			7.83	14.21
5	330020			5.58	13.12
	330036			3.32	5.57
	330052			4.31	7.97
	330085			1.34	1.76
	330088			4.70	12.46
10	330093			0.44	1.06
	330100			3.47	4.83
	330106			2.14	3.61
	330107			3.17	6.87
	330120			5.61	11.89
15	330123			4.50	12.74
	330208			1.55	7.62
	330263			13.10	23.38
	330300			2.81	4.98
	330313			3.00	4.41
20	330366			0.67	0.76
	330372			4.76	11.82
	330385	AA449749	Hs.182971	2.14	2.15
	330397	D14659	Hs.154387	0.40	1.15
25	330468	L10343	Hs.112341	1.11	0.94
	330472	L24203	Hs.82237	1.67	1.17
	330478	L38486	Hs.296049	0.46	1.07
	330493	M27826	Hs.267319	1.07	0.95
	330495	M31328	Hs.71642	0.97	0.96
	330506	M61806	Hs.6241	0.17	3.66
30	330512	M80563	Hs.81256	0.60	1.06
	330537	U19765	Hs.2110	2.81	2.07
	330547	U32989	Hs.183671	3.91	1.49
	330551	U39840	Hs.299867	1.15	1.03
	330568	U56244		2.83	4.79
35	330599	U90437		2.08	1.54
	330601	U90916	Hs.82845	0.89	1.35
	330605	X02419	Hs.77274	1.87	1.55
	330609	X04741	Hs.76118	1.83	1.30
	330617	X53587	Hs.85266	1.54	1.15
40	330630	X78669	Hs.79088	1.39	1.19
	330644	Y07755	Hs.38991	3.83	1.13
	330650	Z58228	Hs.2340	1.25	0.95
	330660	AA347868	Hs.139293	15.50	29.07
	330692	AA017045	Hs.6702	1.00	1.00
45	330707	AA133891	Hs.293690	0.20	1.35
	330715	AA233707	Hs.11571	0.12	1.40
	330717	AA233926	Hs.52620	6.62	5.42
	330722	AA243560	Hs.34382	1.40	1.65
	330740	AA287746	Hs.22654	0.27	2.04
50	330742	AA400979	Hs.25691	0.44	0.90
	330744	AA406142	Hs.12393	0.71	3.23
	330751	AA428286	Hs.29643	1.66	1.52
	330760	AAA48663	Hs.30469	0.52	0.90
	330763	AA450200	Hs.274337	0.37	0.97
55	330786	D60374	Hs.49136	0.78	0.84
	330790	T48536	Hs.105807	0.23	3.17
	330814	AA015730	Hs.265398	0.37	2.07
	330827	AA040332	Hs.12744	1.60	1.00
	330844	AA063037	Hs.65803	0.93	1.16
60	330901	AA157818	Hs.267319	1.02	1.03
	330931	F01443	Hs.284256	0.24	0.88
	330952	H02855	Hs.29567	0.08	1.31
	330961	H10998	Hs.7164	1.29	1.26
	330968	H16568	Hs.23748	0.48	0.96
65	331014	H98597	Hs.30340	0.29	0.74
	331046	N65563	Hs.191358	0.99	8.56
	331060	N75081	Hs.157148	1.24	1.00
	331099	R36671	Hs.83937	0.75	1.03
	331108	R41408	Hs.21983	1.00	2.75
70	331131	R54797		6.04	10.68
	331135	R61398	Hs.4197	0.80	0.96
	331170	T23461	Hs.159293	2.63	4.29
	331180	T32446	Hs.6640	1.78	2.71
	331183	T40769	Hs.8469	1.00	3.01
75	331203	T82310		1.70	3.80
	331271	AA059347	Hs.82226	1.20	3.19
	331306	AA252079	Hs.63931	0.31	1.30
	331327	AA281076	Hs.109221	2.09	2.41
	331341	AA303125	Hs.23240	0.72	2.43
80	331359	AA416979	Hs.46901	0.09	0.91
	331363	AA421562	Hs.91011	1.02	0.87
	331378	AA448881	Hs.49282	1.03	1.23
	331384	AA456001	Hs.93847	1.40	1.00
	331402	AA505135	Hs.44037	1.80	3.93
85	331422	F10802	Hs.163628	1.65	1.89

	331490	N32912	Hs.25813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:od74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.249989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331658	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member l	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
15	331718	AA191404	Hs.104072	ESTs	6.80	11.77
	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331959	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:aa41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
30	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamma	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
35	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	nectin 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.111112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	trypsin beta 1	0.51	1.00
50	332504	AA053917	Hs.15106	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XGA (steroid	0.98	1.70
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA495035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52

	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
5	333260	0.75	1.01
	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
15	333628	1.90	1.90
	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.96
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333894	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
	333966	8.10	14.30
35	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
	334934	4.01	7.43
60	334945	1.04	2.96
	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
65	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.96	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17

	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
	335814	1.13	1.48
5	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
	335868	2.98	6.43
10	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
	335995	0.37	1.17
15	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336065	0.54	1.63
	336107	0.95	0.70
20	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
	336419	0.65	0.79
25	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
	336636	2.13	1.83
30	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
	336684	1.50	1.14
35	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
	336900	6.14	12.73
40	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
	337054	2.78	7.35
45	337128	7.20	16.14
	337162	3.45	5.34
	337183	5.72	11.41
	337184	3.72	5.90
	337192	1.27	1.06
50	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
	337325	2.76	3.72
55	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
	337549	1.66	2.31
60	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
	337786	5.07	9.73
65	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
	338008	1.48	1.12
70	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
	338145	1.70	1.97
75	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
	338182	3.32	4.63
80	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66

	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.57
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
25	338937	6.55	12.26
	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.36	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenes/D's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the 'Accession' column.

Key: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
	322044	187363_1 AW340926 AA249053 N86075
50	322060	44320_1 A1341937 AW003063 U34725 AA904742
	321430	42705_1 X57414 X57415
	321467	43034_1 X13075 X13076
	322125	46779_1 R93901 AF075073 R93902
	322166	46861_1 H69434 AF085958 H69846
55	322173	46873_1 H52567 H52557 AF085970 H52164
	322178	46882_1 H56535 AF085980 H56712
	322179	46885_1 H92891 AF085982 H92777
	321577	1615102_1 H84849 H84252 H84260 H86664 H85320
	321587	1615333_1 H95531 H95521 H84529
60	313723	111953_1 AA070412 AA102346 AA081885
	320997	627492_1 H22544 H46842 A1204929
	322278	47271_1 W69304 AF066283 W69200
	321687	218439_1 AA625149 AA313030 AA313052 H97463
	313883	129439_1 AA665089 AA135130 AA484059 AA102419 AW877765
65	322320	47422_1 W79150 AF086419
	322339	814584_1 A1668646 A1734214 W17348
	314648	293660_1 AW979268 AA878419 AA431342 AA431628
	300201	682222_1 A1308300 A1308296
	306897	25196_2 A1093967
70	323155	979809_1 AL120701 AL135041 AL121524
	322527	38927_1 AF147359 T58511 T58560
	322585	473768_2 W88919 W89125
	300362	1574395_1 Z42308 H23514
	322635	82296_1 AA005129 AA679084 AA694399
75	322664	85042_1 AA011522 AA702841 AA011691 AA330797
	315454	380580_1 A1239454 A1239473 AA625812 A1208703
	322687	37372_1 AF074666 A1110759 AF090902
	314852	327472_1 A1903735 AA491283 A1694953 AW976903 AA761362
	307783	697809_1 A1347274 AW844024
80	324072	269032_1 AA381722 AA381829 AW963906 AW963902 AA381242
	300627	221345_1 AA488472 W27363 AA317053 BE082689 AW967036 BE079872
	323505	196389_1 AW970512 AA280251 A1652267 BE466438 A1650725 AA551854 AA281574 AW571481
	315791	403558_1 AA678177 AA677034
	324303	233842_1 AL118754 AA333202 H38001
85	316519	442885_1 AA847835 AA768378
	300926	333127_1 AA504860 AA504911

	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	L08442 D51348
	302742	458_39	L12061
	318499	364430_1	T25451 AA585296 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AJ341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_-5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909260 AI909259
	312094	797889_1	Z78390 T97427
15	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
	312389	902067_1	AI863140 W80703 R43474
25	319611	1566863_1	H14957 R56522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131
			AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717
			AW063311 AA429538
30	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203697 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572
			AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_-3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
40	306442	AA976899	
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	306510	AA988546	
	306557	AA994530	
45	306572	AA995686	
	306582	AA996248	
	306656	AI004024	
	306686	AI015615	
	306751	AI032589	
50	308011	AI439473	
	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	308956	AI125111	
55	306958	AI125152	
	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
60	308599	AI719893	
	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
65	308808	AI818289	
	308875	AI832332	
	308886	AI833240	
	308898	AI858845	
	308966	AI870704	
	308979	AI873111	
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	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
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75	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
	303998	AW518449	
80	303999	AW516611	
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5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
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	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
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	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307561	AI282207	
20	307609	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
	307796	AI350556	
25	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
30	307820	AI355761	
	307852	AI365541	
	309122	AI928178	
	309164	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
	302679	311853_1	H55022 AA186889
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	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
	302705	31765_1	U09060 U09061
50	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
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	304203	N56929	
	304234	W81608	
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	304430	AA347682	
65	304456	AA411240	
	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
70	304760	AA580401	
	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
75	306109	AA911861	
	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
	330568	NOT_FOUND_entrez	U56244
80	330599	15323_-12	U90437
	331131	genbank_R54797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	457396_1	AA828597 N54811
85	332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those PKeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, L. et al.	Plus	73381-73768
15	332816	Dunham, L. et al.	Plus	359844-360030
	332906	Dunham, L. et al.	Plus	1923101-1923205
	332911	Dunham, L. et al.	Plus	1961767-1961858
	332912	Dunham, L. et al.	Plus	1962120-1962246
	332922	Dunham, L. et al.	Plus	2009620-2009738
20	332956	Dunham, L. et al.	Plus	2510528-2510658
	332959	Dunham, L. et al.	Plus	2518145-2518213
	333138	Dunham, L. et al.	Plus	3369205-3369323
	333139	Dunham, L. et al.	Plus	3369495-3369571
	333221	Dunham, L. et al.	Plus	3978070-3978187
	333380	Dunham, L. et al.	Plus	4904775-4904846
25	333387	Dunham, L. et al.	Plus	4910935-4910997
	333512	Dunham, L. et al.	Plus	5560510-5560564
	333524	Dunham, L. et al.	Plus	5612620-5612780
	333585	Dunham, L. et al.	Plus	6234778-6234894
30	333618	Dunham, L. et al.	Plus	6562391-6562566
	333627	Dunham, L. et al.	Plus	6620584-6620903
	333628	Dunham, L. et al.	Plus	6629004-6629233
	333650	Dunham, L. et al.	Plus	6795852-6797128
	333678	Dunham, L. et al.	Plus	7068223-7068288
	333750	Dunham, L. et al.	Plus	7608165-7608234
35	333763	Dunham, L. et al.	Plus	7692491-7692630
	333767	Dunham, L. et al.	Plus	7694407-7694623
	333768	Dunham, L. et al.	Plus	7695440-7695697
	333769	Dunham, L. et al.	Plus	7696625-7696707
40	333772	Dunham, L. et al.	Plus	7706773-7706902
	333777	Dunham, L. et al.	Plus	7746805-7746916
	333846	Dunham, L. et al.	Plus	8008623-8008757
	333884	Dunham, L. et al.	Plus	8153960-8154161
	333887	Dunham, L. et al.	Plus	8154882-8155025
45	333891	Dunham, L. et al.	Plus	8156437-8156709
	333892	Dunham, L. et al.	Plus	8156825-8157001
	333948	Dunham, L. et al.	Plus	8583497-8583627
	333954	Dunham, L. et al.	Plus	8563186-8563335
	333966	Dunham, L. et al.	Plus	8655643-8655826
50	333968	Dunham, L. et al.	Plus	8681004-8681241
	334061	Dunham, L. et al.	Plus	9586941-9587077
	334094	Dunham, L. et al.	Plus	9889953-9890105
	334113	Dunham, L. et al.	Plus	10282459-10282597
	334161	Dunham, L. et al.	Plus	10599033-10599180
55	334219	Dunham, L. et al.	Plus	12716160-12716384
	334239	Dunham, L. et al.	Plus	13056569-13056893
	334333	Dunham, L. et al.	Plus	13603544-13603657
	334378	Dunham, L. et al.	Plus	13907239-13907370
	334382	Dunham, L. et al.	Plus	13915866-13916036
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	334588	Dunham, L. et al.	Plus	15032740-15032817
	334616	Dunham, L. et al.	Plus	15176123-15176470
	334633	Dunham, L. et al.	Plus	15333206-15333305
	334866	Dunham, L. et al.	Plus	18872214-18872317
	334891	Dunham, L. et al.	Plus	19299770-19299944
65	334934	Dunham, L. et al.	Plus	20103970-20104058
	335015	Dunham, L. et al.	Plus	20582792-20582945
	335120	Dunham, L. et al.	Plus	21436286-21436384
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	335179	Dunham, L. et al.	Plus	21634405-21634526
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	335379	Dunham, L. et al.	Plus	22899306-22899420
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	335416	Dunham, L. et al.	Plus	23237354-23237465
	335496	Dunham, L. et al.	Plus	24164386-24164545
	335497	Dunham, L. et al.	Plus	24167666-24167869
	335558	Dunham, L. et al.	Plus	24740167-24740347
	335586	Dunham, L. et al.	Plus	24990333-24990497
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	335823	Dunham, L. et al.	Plus	26365925-26366004
	335983	Dunham, L. et al.	Plus	27939868-27939970
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	336638	Dunham, I. et al.	Plus	991906-993240
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	337184	Dunham, I. et al.	Plus	23973949-23974016
	337268	Dunham, I. et al.	Plus	28011979-28012034
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	337389	Dunham, I. et al.	Plus	31401509-31401579
	337493	Dunham, I. et al.	Plus	33330760-33330981
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	337871	Dunham, I. et al.	Plus	5443027-5443101
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	338872	Dunham, I. et al.	Minus 28300921-28300790
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	339229	Dunham, I. et al.	Minus 32722330-32722199
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	325235	6381943 Minus	162154-162264
	329588	3962484 Plus	1169-1619
	329560	3962491 Plus	2095-2990
70	329541	3983503 Minus	2765-3059
	325328	5866875 Plus	86780-86854
	325340	6017033 Minus	166656-166819
	325373	5866920 Minus	1136686-1136777
	325367	5866920 Minus	922881-922958
	325389	5866921 Plus	239672-239759
75	325436	5866939 Minus	29778-29907
	325498	5866967 Plus	173372-173930
	325471	6017034 Minus	289268-289342
	325557	6056302 Plus	50921-51050
80	325559	6249595 Minus	118590-119172
	325560	6249595 Minus	133794-133981
	325569	6249599 Plus	78927-80217
	325587	6682462 Plus	126724-126967
	325585	6682462 Plus	73476-73574
	325597	5866992 Plus	1065020-1065089
85	325639	5867002 Plus	253525-253608

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	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62829
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301858-301972
	330052	4567182	Plus	352660-352963
35	330036	6042048	Plus	117120-117216
	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	95187-95248
50	326605	5867637	Plus	24656-24749
	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
55	326693	6682502	Minus	335002-335095
	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	76340-76456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
65	327130	6531976	Plus	20247-22343
	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
70	327224	5867534	Plus	188468-188544
	327321	6249562	Minus	99745-99836
	327361	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611	5867868	Minus	175053-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97564-97710
	327734	5867940	Minus	31003-31583

	327775	5867964	Minus	130791-130871
	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
5	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73515
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
15	327984	5868216	Plus	66611-66677
	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905852	Minus	3246-3302
20	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38989-40010
	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
25	328666	5868254	Minus	778-901
	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
30	328743	5868289	Plus	274638-274726
	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
35	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335406
	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
45	328934	5868500	Plus	846342-846448
	328949	6456765	Minus	43552-43619
	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
50	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
	329037	5868562	Minus	32466-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
60	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26289
	329337	5868806	Minus	467155-467222
	329011	6582532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigeneID's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
400195			NM_007057:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265:Homo sapiens RAD21 (S. pombe)	15.80	398.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	UV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586:g[16330167]kb[BAA86477.1] (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457:g[17512178]pb[1730337 polypr	1.00	400.00
401411			ENSP000000247172:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397:g[17498898]pb[1733295] hypoth	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP000000241802:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP000000251056:Plasma membrane calcium	1.00	1.00
402260			NM_001436:Homo sapiens fibrillarin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823:g[110432400]emb[CAC10290.1] (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP000000231844:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813:g[112737279]ref[XP_012163.1] k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP000000237855:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020:Homo sapiens CGI-75 protein (14.29	91.00
404101			C8000950:g[1423560]pb[1447318] RNA-bind	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP000000244562:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005938:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058:Homo sapiens H2B histone fami	1.00	1.00

	404287		C6001909:gi704441 kbj BAA18909.1 (D298	29.71	42.00
	404298		C6001238:gi121715 sp P26697 GTA3_CHICK	1.30	1.00
	404347		Target Exon	1.00	1.00
	404440		NM_021046:Homo sapiens melanoma antigen,	1.00	15.00
5	404721		NM_005596:Homo sapiens nuclear factor I	1.00	60.00
	404794	NM_000078	cholesteryl ester transfer protein, plas	1.07	1.38
	404854		Target Exon	1.61	2.01
	404877		NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
	404927		Target Exon	1.00	1.00
10	404996		Target Exon	1.00	1.00
	405449		CY000047:gi11427234 ref XP_009399.1 z	1.00	1.00
	405568		NM_031413:Homo sapiens cat eye syndrome	1.00	78.00
	405572		Target Exon	0.76	1.14
15	405646		C12000200:gi14557225 ref NP_000005.1 el	1.01	1.28
	405676	BE336714	cytochrome c-1	1.13	2.89
	405770		NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
	405932		C15000305:gi13806122 gb AAC69198.1 (AF0	1.99	1.99
	406137		NM_000179:Homo sapiens mutS (E. coli) h	2.77	2.38
	406360		Target Exon	1.00	35.00
20	406399		NM_003122:Homo sapiens serine protease	1.00	39.00
	406467		Target Exon	1.00	1.00
	406621	X57809	Hs.181125 immunoglobulin lambda locus	1.41	1.74
	406642	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
	406663	U24683	Hs.293441 immunoglobulin heavy constant mu	2.07	2.93
25	406671	AA129547	Hs.285754 mel proto-oncogene (hepatocyte growth fa	15.00	51.00
	406673	M34996	Hs.198253 major histocompatibility complex, class	0.98	3.09
	406676	X58399	Hs.81221 Human L2-9 transcript of unrearranged im	1.30	1.53
	406678	U77534	gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
	406685	M18728	gb:Human nonspecific crossreacting antig	1.46	2.85
30	406687	M31126	Hs.272822 pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540	Hs.220529 carcinoembryonic antigen-related cell ad	226.37	350.00
	406698	X03068	Hs.73931 major histocompatibility complex, class	1.01	2.52
	406815	AA833930	Hs.288036 tRNA Isopentanyltiprophosphate transferas	20.25	32.00
	406851	AA609784	major histocompatibility complex, class	0.75	1.91
35	406964	M21305	gb:Human alpha satellite and satellite 3	38.15	1114.00
	406967	M24349	gb:Human parathyroid hormone-like protel	1.00	1.00
	406974	M57293	gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881	Hs.256301 hypothetical protein MGC13170	1.77	1.10
40	407128	R83312	Hs.237260 EST	1.00	1.00
	407137	T97307	gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168	R45175	Hs.117183 ESTs	2.16	18.00
	407239	AA076350	Hs.67846 leukocyte immunoglobulin-like receptor,	1.10	1.57
	407242	M18728	gb:Human nonspecific crossreacting antig	1.12	2.85
45	407244	M10014	Hs.75431 fibrinogen, gamma polypeptide	3.24	15.38
	407289	AA135159	Hs.203349 Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
	407300	AA102616	Hs.120769 gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
	407366	AF026942	Hs.271530 gb:Homo sapiens ctp33 mRNA, partial sequ	0.06	8.25
	407378	AA293264	Hs.57776 ESTs, Moderately similar to I38022 hypot	1.00	26.00
50	407430	AF169351	gb:Homo sapiens protein tyrosine phospho	1.00	25.00
	407453	AJ132087	gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
	407577	AW131324	Hs.246759 hypothetical protein MGC12538	1.00	1.00
	407634	AW016569	Hs.136414 UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
	407710	AW022727	Hs.23615 ESTs	1.00	28.00
55	407720	AB037776	Hs.38002 KIAA1355 protein	1.89	1.31
	407746	AK001962	hypothetical protein FLJ11100	1.00	1.00
	407756	AA116021	Hs.38260 ubiquitin specific protease 18	4.51	5.00
	407758	D50915	Hs.38365 KIAA0125 gene product	1.00	28.00
	407782	AA508956	Hs.112619 ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
60	407788	BE514982	Hs.38991 S100 calcium-binding protein A2	7.88	3.83
	407790	AJ027274	Hs.288941 Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
	407811	AW190902	Hs.40098 cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144	Hs.161566 ESTs	173.91	108.00
	407944	R34008	Hs.239727 desmocollin 2	111.30	70.00
65	408000	L11690	Hs.620 bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
	408031	AA081395	Hs.42173 Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
	408063	BE086548	Hs.42346 caldesmonin-binding protein calsarcin-1	195.78	231.00
	408070	AW148852	gb:cd05d05.x1 NCL CGAP_Bm35 Homo sapien	1.00	1.00
	408101	AW968504	Hs.123073 CDC2-related protein kinase 7	37.84	61.00
	408122	AJ432652	Hs.42824 hypothetical protein FLJ10718	0.85	1.71
70	408212	AA297567	Hs.43728 hypothetical protein	5.88	7.91
	408243	Y00787	Hs.624 interleukin 8	4.27	9.98
	408349	BE546947	Hs.44276 homeo box C10	3.79	3.46
	408353	BE439838	Hs.44298 mitochondrial ribosomal protein S17	1.88	1.65
75	408354	AJ382803	Hs.159235 ESTs	1.00	73.00
	408369	R38438	Hs.182575 solute carrier family 15 (H777 transport	1.41	16.50
	408380	AF123050	Hs.44532 diubiquitin	15.19	37.22
	408482	NM_000676	Hs.45743 adenosine A2b receptor	1.65	1.19
	408522	AJ541214	Hs.46320 Small protein-rich protein SPRK (human,	1.98	1.24
80	408538	AW381532	Hs.135188 ESTs	1.55	1.50
	408545	AW235405	Hs.253690 ESTs	1.00	1.00
	408572	AA055611	Hs.226558 ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408633	AW963372	Hs.46677 PRO2000 protein	107.16	56.00
	408660	AA525775	ESTs, Moderately similar to PC4259 ferri	1.00	1.00
85	408761	AA057264	Hs.238936 ESTs, Weakly similar to (define not ava	52.24	141.00
	408771	AW732573	Hs.47584 potassium voltage-gated channel, delayed	3.05	109.00

	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, deli	1.00	89.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AJ979168	Hs.344096	glycoprotein (transmembrane) numb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
15	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50956	carbamoyl-phosphate synthetase 1, mitocho	1.00	1.00
	409228	AG64298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AJ879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.80	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI561173	Hs.67688	ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gbczm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
	409719	AJ769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW676258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:UL-HF-BR0p-ajr-4-11-0-ULr1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
45	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	1.08	1.90
75	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adlican	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 18	23.34	34.00
80	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219591	Hs.73625	RAB6 interacting, kinesin-like (rabkinase	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
85	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	412659	AW753865	Hs.74376	alpha2-macroglobulin related ER localized protein	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
5	412811	H06382		ESTs	1.00	11.00
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subunit	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22	1.88
	413048	M53221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein)	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
15	413223	AI732182	Hs.191856	ESTs	5.73	27.00
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE553085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516	fidgin-like 1	1.00	1.00
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
25	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
	413690	BE157489		gbr:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
30	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cyt)	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin)	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntrophin 1A (brain)	1.23	1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor	2.02	2.51
40	414142	AW358397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
45	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W070171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	Insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S)	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AW346699	Hs.77356	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian)	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77697	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW964064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
75	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	30.84	63.00
80	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit	1.48	1.39
	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypotheti	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-L	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415889	AI267700		ESTs	78.89	1.00

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
5	416177	AA174069	Hs.187607	ESTs	1.00	9.00
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA681386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.09	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
	417034	NM_006183	Hs.60962	neurotensin	1.00	1.00
20	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fs, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
25	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1078	small proline-rich protein 1B (cornuifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
30	417428	N87579	Hs.278871	gbl.L2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
	417542	JD4129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
35	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.85366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	58.00
	417791	AW965339	Hs.111471	ESTs	39.98	18.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	cathepsin K (pycnodystosis)	3.96	5.16
60	418300	AI433074	Hs.86582	Homo sapiens cDNA: FLJ21578 fs, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibitor	1.00	1.00
	418379	AA218940	Hs.137516	fidgetin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
70	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmoolin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancerhesis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
80	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
	418712	Z42183		gbl.HSCDBF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
85	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AJ538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor I	1.10	1.14
	419183	U60689	Hs.89653	cytochrome P450, subfamily X04V (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
15	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gbrHUM316G108 Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
20	419474	AW968619	Hs.155849	ESTs	13.63	62.00
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.66	3.63
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitinotriostidase)	1.47	4.98
	419569	AJ971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AJ793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
30	419729	AA586442	Hs.21411	gbrno53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419936	AJ792788		gbr:091d05.y5 NCI_CGAP_Kd5 Homo sapiens	1.00	1.00
	419937	A9040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	V55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271108	Hs.133294	ESTs	3.15	1.43
	420047	AJ478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	AJ623693	Hs.323494	ESTs	45.04	54.00
45	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibitor	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin 1 precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
50	420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AJ683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AJ659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF118030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AJ684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AJ913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
70	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.78
	421505	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
	421582	AJ910275		trifoli factor 1 (breast cancer, estrogen	1.23	1.00
80	421633	AF121850	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
	421773	V69233	Hs.112457	ESTs	1.12	1.14
85	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.108643	polyadenylate binding protein-interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gbc:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
15	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
	422424	AI186431	Hs.295638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AJ076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
30	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
	422656	AI870435	Hs.1569	UIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AA409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
35	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	53.00
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
40	422963	AA401369	Hs.190721	ESTs	171.41	17.00
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gbc:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.125782	sushi-repeat protein	21.90	64.00
	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423518	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
55	423551	AA327598	Hs.233785	ESTs	3.54	4.33
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fs, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
65	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
	423787	AJ285745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151064		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13686	Hs.135348	osteoblast specific factor 2 (fascidin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fs, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
80	424120	T80579	Hs.290279	ESTs	1.00	1.00
	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gbc:EST14944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
85	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
	424340	AA339036	Hs.7033	ESTs	0.88	1.15

	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Ctk2	95.55	92.00
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
5	424420	BE614743	Hs.146688	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424503	X06256	Hs.149509	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
10	424539	U02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
15	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992282	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
	424867	AJ024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AJ076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypothe	1.00	53.00
30	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	100.77	44.00
	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	AJ751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
35	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425568	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	AJ923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	AJ077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166195	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	AJ949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
75	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	AI493134		sclerostin	1.00	1.00
85	426991	AK001536		Homo sapiens cDNA FLJ10574 fis, clone NT	3.39	2.28
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
5	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
15	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
	427562	R56424	Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
20	427666	AI791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243888	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
25	427719	AI393122	Hs.134726	ESTs	7.03	4.52
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
30	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I380222 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
35	428129	AI244311	Hs.26912	ESTs	1.00	42.00
	428169	AI928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
	428434	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratiffin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428545	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	1.00	1.00
50	428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
55	428801	AW277121	Hs.254881	ESTs	1.67	6.15
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
60	428969	AF120274	Hs.194689	artemin	1.36	1.24
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
	429164	AI688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs	1.00	7.00
	429228	AI553633	Hs.326447	ESTs	39.47	29.25
70	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	88.00
	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
75	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
	429551	AW450624	Hs.220931	ESTs	2.89	65.00
80	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
	429616	AI982722	Hs.120845	ESTs	1.00	1.00
85	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

	429663	M58874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212660	tumor necrosis factor receptor superfamily	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
5	429918	AW673986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
	430114	AA847744	Hs.99640	ESTs	1.00	1.00
10	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00	51.00
	430147	R60704	Hs.234434	hair/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AU538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
	430300	U60805	Hs.238648	oncostatin M receptor	1.00	35.00
15	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfamily	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
20	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
	430481	AA479578	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
25	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430508	AU015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
	430577	Z26317	Hs.94560	desmoglein 2	1.72	1.30
30	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	A1742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to T78885 serine/th	0.94	1.28
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	A1332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
45	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
50	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
	431548	A1834273	Hs.9711	novel protein	5.66	15.00
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	67.12	91.00
55	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uropod 18	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	61.17	46.35
60	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	A1538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	A1567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	1.00	1.00
65	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12r1 Stratagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	A1804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
75	432552	A1537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	A1243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N52096	Hs.293185	ESTs, Weakly similar to JCT328 amino aci	1.92	5.29
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
80	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGCA4485	1.22	1.34
	432867	AW016936	Hs.233364	ESTs	1.00	1.00
85	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279505	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW183534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALLB_HUMAN III	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.65	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
15	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AO94221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
20	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	1.00
	434094	AA305599	Hs.238206	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
	434217	AWD14795	Hs.23349	ESTs	14.11	57.00
25	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCI_OGAP_Ov23 Homo sapiens	1.48	1.56
	434424	AB111202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
30	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
	434792	AA649253	Hs.132458	ESTs	8.52	44.00
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
40	434928	AWD15595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00	1.00
	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
	435509	AA58679	Hs.181915	ESTs	1.00	1.00
	435525	AI831297	Hs.123310	ESTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
55	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
60	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
65	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV integration site fami	60.01	1.00
	436414	BE264533	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171355	ESTs	0.95	1.33
	436443	AW138211	Hs.128746	ESTs	1.12	9.26
70	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
	436839	AA401369	Hs.190721	ESTs	1.00	17.00
80	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268814	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
	437016	AI076916	Hs.5398	guanine monophosphate synthetase	2.35	1.78
85	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

5	437181	A305615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
	437259	A377755	Hs.120695	ESTs	1.00	205.00
	437270	R18087	Hs.323769	displatin resistance related protein CRR	1.56	1.54
10	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AL125859	Hs.112607	ESTs	1.35	1.75
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	A306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
15	437444	H45008	Hs.31518	ESTs	1.00	39.00
	437568	A954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe	1.00	3.00
	437814	AJ088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
20	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [Hsa	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
	437915	AJ637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 taratoca	74.05	35.00
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
25	437937	AJ917222	Hs.121655	ESTs	1.00	1.00
	437942	AJ888256	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
	438113	A467908	Hs.8882	ESTs	1.80	2.39
	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
30	438274	AJ918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
	438494	AA908578	Hs.130183	ESTs	2.05	80.00
	438546	AW297204	Hs.125811	ESTs	1.00	131.00
35	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AJ879064	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
	438746	AJ885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
40	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AJ865558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
45	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96696	Hs.35598	ESTs	1.00	28.00
	439128	AJ949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
50	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439265	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
55	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
60	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
	439605	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
65	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAPI_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sera domain, immunoglobulin domain (Ig),	2.36	1.88
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
70	439780	AL109588		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
75	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypothe	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AI085392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
80	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
85	440704	N69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440843	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440894	AJ160011	Hs.272068	ESTs	1.29	1.14
	441020	AA401369	Hs.190721	ESTs	142.99	17.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	441128	AA570256	ESTs, Weakly similar to T23273 hypothe	4.13	3.50
	441290	W27501	Hs.89605 cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	Hs.23044 RAD51 (S. cerevisiae) homolog (E coli Ra	130.23	43.00
5	441377	BE218239	Hs.202656 ESTs	22.03	1.00
	441390	AI692560	Hs.131175 ESTs	3.65	7.70
	441497	R51084	Hs.23172 ESTs	1.00	1.00
	441525	AW241867	Hs.127728 ESTs	1.53	1.42
	441553	AA281219	Hs.121296 ESTs	1.89	1.57
10	441607	NM_005010	Hs.7912 neuronal cell adhesion molecule	1.47	2.11
	441633	AW958544	Hs.112242 normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Hs.7921 Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	Hs.7957 adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721 ESTs	44.15	17.00
	441801	AW242799	Hs.86366 ESTs	1.00	1.00
15	441919	AI553802	Hs.128121 ESTs	1.00	122.00
	441937	R41782	Hs.22279 ESTs	0.86	1.37
	441954	AI744935	Hs.8047 Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810 CDA11 protein	1.00	48.00
20	442029	AW956698	Hs.14456 neural precursor cell expressed, develop	9.92	45.00
	442072	AI740832	Hs.12311 Homo sapiens clone Z3570 mRNA sequence	25.05	77.00
	442108	AW452649	Hs.166314 ESTs	3.61	3.14
	442117	AW664964	Hs.128899 ESTs	3.00	5.49
	442137	AA977235	Hs.128830 ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
	442159	AW163390	Hs.278554 heterochromatin-like protein 1	1.92	1.66
25	442179	AA983842	Hs.333555 chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	Hs.150614 ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178 hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Hs.176508 Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
30	442547	AA306997	Hs.217484 ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
	442556	AI137761	Hs.8379 Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447482	Hs.20183 ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	Hs.23210 ESTs	1.00	19.00
	442717	R88362	Hs.180591 ESTs, Weakly similar to T23976 hypothe	1.00	5.00
35	442875	BE623003	Hs.23625 Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
	442914	AW188551	Hs.99519 hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	Hs.8858 bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	Hs.131562 ESTs	8.45	64.00
	443068	AI188710	ESTs	1.00	27.00
40	443204	AW205878	Hs.29643 Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	Hs.143655 ESTs	12.42	2.00
	443247	BE614387	Hs.333893 c-Myc target JPO1	128.84	96.00
	443324	R44013	Hs.164225 ESTs	0.02	4.59
	443383	AI792453	Hs.166507 ESTs	1.00	47.00
	443400	R28424	Hs.250648 ESTs	18.52	61.00
45	443426	AF098158	Hs.9329 chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	Hs.9605 cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	Hs.269636 ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645 fibrinogen, B beta polypeptide	1.00	16.00
	443633	AL031290	Hs.9654 similar to pregnancy-associated plasma p	1.00	39.00
50	443648	AI085377	Hs.143610 ESTs	39.81	70.00
	443715	AI583187	Hs.9700 cyclin E1	48.74	7.00
	443723	AI144442	Hs.157144 syntaxin 6	1.29	1.30
	443802	AW504924	Hs.9805 KIAA1291 protein	1.75	1.61
55	443859	NM_013409	Hs.9914 follistatin	1.35	1.13
	443892	AA401369	Hs.190721 ESTs	1.00	17.00
	443947	V24187	gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082 potassium intermediate/small conductance	5.71	6.87
	444006	BE395085	Hs.10086 type I transmembrane protein Fn14	1.47	1.92
60	444009	AI380792	Hs.135104 ESTs	1.00	77.00
	444017	U04840	Hs.214 neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	Hs.13281 ESTs	1.00	29.00
	444129	AW294292	Hs.256212 ESTs	1.00	1.00
	444279	U62432	Hs.89605 cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	Hs.239 torhead box M1	2.91	1.14
	444378	R41339	Hs.12569 ESTs	1.00	1.00
	444381	BE387335	Hs.283713 ESTs, Weakly similar to S64054 hypothe	469.00	556.00
	444461	R53734	Hs.25978 ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217 KIAA0877 protein	24.91	90.00
	444489	AI151010	Hs.157774 ESTs	1.00	111.00
70	444619	BE538082	Hs.8172 ESTs, Moderately similar to A46010 X-lin	1.00	70.00
	444665	BE613126	Hs.47783 B aggressive lymphoma gene	30.56	139.00
	444707	AI188613	Hs.41690 desmocollin 3	1.00	1.00
	444735	BE019923	Hs.243122 hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	Hs.11950 GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	Hs.62180 anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	Hs.12457 hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	Hs.147613 ESTs	1.00	73.00
	445413	AA151342	Hs.12577 CGI-147 protein	28.14	50.00
80	445417	AK001058	Hs.12680 Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	Hs.322971 ESTs	1.00	1.00
	445462	AA378776	Hs.288649 hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830 hypothetical protein	1.67	70.00
	445537	AI245571	Hs.12844 EGF-like domain, multiple 6	1.71	2.72
85	445580	AF167572	Hs.12912 skb1 (S. pombe) homolog	1.52	1.34
	445554	X91247	Hs.13046 thioredoxin reductase 1	1.51	1.52

	445669	AI570330	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	49.42	54.00
5	445885	AI734009	Hs.127699	KIAA1603 protein	1.00	132.00
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AI347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
10	446078	AI339982	Hs.156061	ESTs	1.00	42.00
	446102	AW168057	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ110540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
15	446293	AI420213	Hs.149722	ESTs	1.00	2.00
	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AI377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
20	446574	AI310135	Hs.335933	ESTs	3.89	72.00
	446519	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446536	AC002563	Hs.15767	citrin (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
25	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
	446856	AI814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
30	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AI357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
35	447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazarus	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.53	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AI375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
	447415	AW837335	Hs.28149	ESTs, Weakly similar to KF38_HUMAN KINES	0.91	1.13
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19236	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AI538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	Integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AI955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGCS469	2.48	1.92
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked mol	2.34	1.97
75	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AI471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AI625777	Hs.344766	ESTs	8.33	44.00
	449054	AF148848	Hs.22934	myonectin	73.85	104.00
85	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 153kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	A1638293		gb.tl09b07.x1 NCL CGAP GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.66
	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
	450101	AV649889	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	A1916071	Hs.15607	Homo sapiens Fanconi anemia complementation	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
	450375	AA009647	Hs.8850	a disintegrin end metalloproteinase domain	51.26	93.00
20	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	A1701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	RA9131	Hs.26267	ATP-dependent interferon response protein	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	A1761324		gb.wt50b11.x1 NCL CGAP Co16 Homo sapiens	15.02	124.00
	451110	A1955040	Hs.265398	ESTs, Weakly similar to transformation-related	1.00	143.00
	451253	H48289	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	A1805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	A1821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
50	452194	A1894413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3806519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodomain	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613	AA461589	Hs.23459	ESTs	1.39	1.32
	452689	AW295390	Hs.213062	ESTs	1.00	26.00
	452706	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	lg superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in melanocytes	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell growth	1.55	1.00
	452834	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252756	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	trizzed (Drosophila) homolog 10	1.00	1.00
	453103	A1301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
	453160	A1263307	Hs.239884	H2B histone family, member L	1.00	30.00
85	453197	AB916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00

5	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93
	453240	AJ969564	Hs.166254	hypothetical protein DKFZp5661133	1.00	1.00
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11
	453331	AI240665	Hs.8850	ESTs	199.42	340.00
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17
	453459	BE047032	Hs.257789	ESTs	2.84	5.58
10	453563	AW608906.comp	Hs.181163	hypothetical protein MGC5629	4.58	90.00
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00
	453830	AA534296	Hs.20963	ESTs	24.92	25.00
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00
15	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcription	1.97	1.58
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00
	453964	AI961486	Hs.12744	ESTs	1.00	1.00
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81
	453976	BE463830	Hs.163714	ESTs	3.02	131.00
25	454024	AA935327	Hs.293907	hypothetical protein FLJ23403	1.00	131.00
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00
	454059	NM_003154	Hs.37048	stathurin	1.00	1.00
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
30	454241	BE144666	Hs.110826	gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04
	454417	AI244459	Hs.154320	trinucleotide repeat containing 9	4.30	7.82
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00
	455175	AW993247	Hs.816	gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00
	456237	AA203682	Hs.87225	gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00
	456321	NM_001327	Hs.95998	cancer/testis antigen	1.14	1.10
	456475	NM_000144	Hs.123469	Friedreich ataxia	1.00	48.00
	456508	AA502764	Hs.100623	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00
40	456534	X91195	Hs.1619	phospholipase C, beta 3, neighbor pseudo	2.12	1.80
	456736	AW248217	Hs.127792	achaete-scute complex (Drosophila) homolog	1.15	1.94
	456759	BE259150	Hs.171545	delta (Drosophila)-like 3	1.00	1.00
	456990	NM_004504	Hs.197764	HTV-1 Rev binding protein	16.42	84.00
	457200	U33749	Hs.14355	thyroid transcription factor 1	0.57	1.76
45	457234	AW968360	Hs.122908	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15
	457465	AW301344	Hs.127179	DNA replication factor	46.37	47.00
	457489	AI693815	Hs.112948	cryptic gene	1.12	1.35
	457646	AA725650	Hs.291971	ESTs	1.55	2.51
	457733	AW974812	Hs.35406	ESTs	1.00	55.00
50	457819	AA057484	Hs.343566	ESTs, Highly similar to unnamed protein	4.36	3.18
	458092	BE545684	Hs.7655	KIAA0251 protein	1.00	1.32
	458098	BE550224	Hs.28465	metallothionein 1E (functional)	1.00	22.00
	458207	T28472	Hs.209194	U2 small nuclear ribonucleoprotein auxiliary	2.06	1.88
	458242	BE299588	Hs.129182	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00	1.00
55	458247	R14439	Hs.129182	ESTs	7.00	9.85
	458679	AW975460	Hs.129182	ESTs	1.00	3.00
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01
	458833	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71
	459352	AW810383	Hs.206828	ESTs	12.60	63.00
60	459670	F01020	Hs.172004	titin	1.00	1.00
	459702	AI204995	gb:an03c03.x1	Stratagene schizo brain S1	1.00	237.00

TABLE 98

65	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
70	Pkey	CAT Number
	407746	10125_1
		AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461
		AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320
		D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1
	408660	107294_1
75	409522	113735_1
	409866	1156522_1
	410032	1170435_1
	411089	123172_1
80	411152	1234028_1
	412537	1304_1
		AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386
		AI679895 AA514764 AA454562 AI082392 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA566188
		BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202
		AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
		AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024
		T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AI044114 AI684577 AI809865
		AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865

			AI478773 AI160445 AI574530 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H05383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 NB6396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024596 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346518 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA458292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74175 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88990 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 NB3673 AA283672 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA456370 N28754 N28747 AI568146 AI979333 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI925845 AW945895 Z42183 T31621 T97478 D62703 AA242966 D79798 AI076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64306 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R05796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI067440 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29575 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40085 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI792788 BE142230 AA252019 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA58276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AW881145 AA490718 M85637 AA304575 T06067 AA331991 AL119930 AA320596 AW752565 AL031985 AL137241 AI792386 AI733654 AI857654 AI049911 AA337221 AA336756 AW966196 AW953120 R56325 AA349562 AI493134 AI498691 AW771508 AI498457 AI768408 AI783624 AI383985 AI580267 D79813 AA393768 AIK001536 AA191092 AW510354 AI554256 AI353968 AA134266 AA663848 AA400100 AA401424 AI038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687614 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA93675 AA837380 BE006554 BE006473 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140588 AI277175 AA425444 AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341 AA249027 AI038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI308821 AI919424 AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI578018 AI853985 D79662 BE221049 AW265018 AI589700 AW196655 N67573 AI370908 BE042393 N75017 AI698870 AW960115 AL133561 AL041090 AI117481 AI122068 AW439292 AI968826 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937 BE041395 AA491826 AA621946 AA715980 AA666102 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW686939 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821687 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AI788376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AI173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA698929 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H68088 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AA628980 AI126603 BE504035
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438091	44964_1	AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R57100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI822204 N88343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI638085 AW884528 AI024768 AI004723 AW087420 AI556133 N94964 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52439 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780984 AI985913 BE174196 AA029094 AW592159 T55581 N78072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 W76096 AW979121 AA847986 AA828098 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955584 AI346341 AI857454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077 AL109688 R23665 R26578 AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171 AI359527 AI005068 AI355567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923 AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390 W24187 W24194 R17789 Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649 AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA905264 AA041527 R01145 AI086888 BE463637 AA398795 AI354883 AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659 AI950089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595 AA096002 N83992 AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265 AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI827478 AA399460 AI760441 AA346416 BE047245 AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417 AA911497 BE537702 AI638293 AW813561 AI761324 AW880941 AW880937 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756 AL133619 AA468118 AA383064 AI476447 T09430 AI673758 AA524895 AI581345 AI300820 AW458812 AA256162 AI559724 AI685732 AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AWZ72464 AI215594 AA622747 R74039 N35031 AI804128 AW513621 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI25754 AI200813 AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316 AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130 BE144666 BE184942 AW238414 BE184946 AW993247 AW861464 AA203682 R11958 BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393 AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI205395 AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407 BE467534 BE218421 BE467767 AA589054 BE467053 AI797130 BE327781
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TABLE 9C

50	Pkey:	Unique number corresponding to an Ecs probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
55	Pkey	Ref	Strand	Nt_position
	400512	9796593	Minus	1439-1615
	400517	9796686	Minus	49956-50346
	400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
	400664	8118496	Plus	13558-13721,13942-14090,14554-14679
60	400665	8118496	Plus	16879-17023
	400666	8118496	Plus	17982-18115,20297-20456
	400749	7331445	Minus	9162-9293
	400763	8131616	Minus	35537-35784
	401027	7230983	Minus	70407-70554,71060-71160
	401093	8516137	Minus	22335-23166
65	401203	9743387	Minus	172951-173056,173868-173928
	401212	9859408	Plus	87839-88028
	401411	7799787	Minus	144144-144329
	401435	8217934	Minus	54508-55233
	401464	6682291	Minus	170688-170834
70	401714	6715702	Plus	96484-96681
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130466-130593,131097-131258,131866-131932,132451-132575,133580-134011 83126-83250,85320-85540,94719-95287 28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573 83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814 165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942 6973-7118 124054-124209 61542-61750 42904-43124,43211-43336,44607-44763,45199-45281,46337-46732 121907-122035,122804-122921,124019-124161,124455-124510,125672-126076 113765-113910,116553-115765,116808-116940 21059-21168 35279-35405,35573-35659 110326-110491
75	401760	9928699	Plus	
	401780	7249190	Minus	
	401781	7249190	Minus	
	401785	7249190	Minus	
	401797	6730720	Plus	
	401961	4581193	Minus	
	401985	2580474	Plus	
80	401994	4153858	Minus	
	402075	8117407	Plus	
	402260	3399665	Minus	
	402265	3287673	Plus	
	402297	6598824	Plus	
85	402408	9796239	Minus	

	402420	9796339	Plus	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
5	402994	2996643	Minus	4727-4969
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	116458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
15	404076	9931752	Minus	3848-3967
	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
20	404210	5006246	Plus	169925-170121
	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
25	404440	7528051	Plus	80430-81581
	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
30	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405676	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-62075
	405832	7767812	Minus	123525-123713
	406137	9166422	Minus	30487-31058
40	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

45 TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease
Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix HuO3 Genechip array.

50 Table 10B show the accession numbers for those Pkey's lacking UnigeneID's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

55 Table 10C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

60 Pkey_i Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
65	404394			ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
	404916			Target Exon	1.00	159.00
	405257			Target Exon	1.00	422.00
70	407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
	407568	AA740964	Hs.62699	ESTs	1.00	123.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	tol-like receptor 2	39.65	149.00
75	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL040178	Hs.142003	ESTs	0.10	11.90
80	414154	AW205314	Hs.323060	ESTs	0.62	2.09
	414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
	414998	NM_002543	Hs.77729	oxidized low density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
85	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypothei	0.29	2.64
	415810	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

5	416319	AJ815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
10	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87850	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
15	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrophin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
	420656	AA279088	Hs.187636	ESTs	1.65	8.07
20	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
	422426	W79117	Hs.58559	ESTs	0.03	7.44
	422652	AW967969	Hs.118958	syntactin 11	0.14	3.62
25	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X32521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
30	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425898	AJ076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
35	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17708	Hs.2223	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429496	AA453800	Hs.192793	ESTs	1.00	138.00
40	430468	NM_004673	Hs.241519	angiotensin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
	431848	A1378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
45	432519	A1221311	Hs.130704	ESTs, Weakly similar to BCHUA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AJ823593	Hs.27688	ESTs	1.00	105.00
	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
50	436532	AA721522	Hs.177043	gbmv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
	437119	A1379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	A1669586	Hs.222194	ESTs	1.00	147.00
55	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	A1302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438876	AA827640	Hs.189090	ESTs	23.32	370.00
	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
60	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
65	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446584	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N59013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
	447357	A1375922	Hs.159367	ESTs	0.46	2.64
	448106	A1800470	Hs.171941	ESTs	18.05	296.00
70	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449275	AW450848	Hs.205457	perlecan	0.56	1.38
	450400	A1694722	Hs.279744	ESTs	0.88	4.33
	450698	A1654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
75	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
	456332	A1000341	Hs.220491	ESTs	1.00	192.00
	459580	AA022888	Hs.176065	ESTs	0.20	2.98
80	400269			Eos Control	0.40	2.40
	403421			NM_016369*Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.55	1.74
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
85	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28489	Hs.89485	carbonic anhydrase IV	0.20	1.28
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alpha	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1857	progastricsin (pepsinogen C)	0.35	1.62
5	425438	T62216	Hs.270840	ESTs	0.23	9.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	0.46	2.43
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
	443709	AI082692	Hs.134662	ESTs	0.00	3.02
15	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
20	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883*gi 6753278 ref NP_033938.1 c	1.00	109.00
	401083			NM_016582*Homo sapiens peptide transpor	0.89	1.39
25	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
	402808			ENSP00000235229:SEMB	1.00	1.87
	403021			C21000030*gi 9555960 ref NP_063957.1 AT	1.00	149.00
	403438			NM_031419*Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*Homo sapiens a disintegrin-II	0.04	4.89
30	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
	404277			NM_019111*Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*Homo sapiens v-ros avian UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106			C11001637*gi 5032241 ref NP_005732.1 z	1.00	235.00
35	405381			Target Exon	1.00	93.00
	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.48
	406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
45	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA052954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine r	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
65	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12566	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N64464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
80	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
85	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
	417673	T87281	Hs.16355	ESTs	0.15	15.54

	418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
5	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronat/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
10	420256	U84722	Hs.76205	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
15	421470	R27496	Hs.1378	annexin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00	129.00
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
25	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
	423695	Z92548		Sushi domain (SCR repeat) containing	0.73	1.27
30	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
35	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	toll-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
40	428708	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	AI478578	Hs.50536	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
45	430212	AA469153		gbnc67f04.s1 NCI_CGAP_P1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
50	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AI734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	NA6466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
	432596	AJ224741	Hs.278461	matrilin 3	0.04	5.79
60	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
	434445	AI349306	Hs.11782	ESTs	0.50	1.84
65	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
70	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene fami	1.00	77.00
75	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
	442200	AW590572	Hs.235768	ESTs	0.78	5.83
80	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
	443951	F13272	Hs.111334	fertilin, light polypeptide	0.55	2.09
85	444330	AI597655	Hs.49265	ESTs	1.00	90.00

	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AJ741471	Hs.236566	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69
	446917	AI347863	Hs.156672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
15	450693	AW450461	Hs.203965	ESTs	1.00	91.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
25	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
	453390	AA862496	Hs.28482	ESTs	1.00	72.00
	453631	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	456579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK020216	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probaset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

40	Pkey	CAT Number	Accession
	408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AAB30127 AA046953 AI668930 C06094 AW104534
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
45	413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
	423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449639 T81622 T79697 T29519 R94105 T83923 R73300 AJ797007 R73380 AA961010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304820 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418952 W32571 R72840 H45409 R72085 R46356 R46758
50	423696	23112_1	AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903895 Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI857336 AA627604 H16914 AA358477 AA338009
	430212	314437_1	AA469153 AI718503 AA469225
55	436532	421802_1	AA721522 AW975443 T93070
	453531	97026_1	AA417940 AA036735 T07025
	454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probaset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	400754	7331445	Plus	144559-144684
70	401045	8117619	Plus	90044-90184,91111-91345
	401083	3242744	Plus	33192-33390
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
	403021	7547270	Plus	120799-120966
75	403421	9565041	Minus	126609-126773,139986-140205
	403438	9719679	Plus	90792-90938
	403687	7387384	Plus	9009-9534
	403764	7717105	Minus	118692-118853
	404277	1834458	Minus	91665-91946
80	404288	2769644	Plus	3512-3691
	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
	404518	8151988	Plus	84494-84603
	404916	7341826	Plus	91057-91188
	405106	8079395	Minus	80877-81418
85	405257	7329310	Plus	73121-73273
	405381	6006920	Minus	7636-8054

WO 02/086443
406387 9256180 Plus

116229-116371,117512-117651

PCT/US02/12476

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Alfymatrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigeneID's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122*Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
407869	A827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	60.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxide	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	1.00	3.00
421582	A8910275		trefoll factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	A1868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	A1015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	A1834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431988	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW509005	Hs.3697	serine (or cysteine) proteinase inhibitor	29.31	72.00
434424	A1811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome reg	1.00	1.00
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

	439759	AL358055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
	441377	BE218239	Hs.202656	ESTs	22.03	1.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
5	443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
	444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
	444931	AV652066	Hs.75113	general transcription factor IIIA	1.00	54.00
	446102	AW168067	Hs.317694	ESTs	1.00	1.00
10	446163	AA026980	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	1.00	11.00
	447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
	448243	AW369771	Hs.52620	Integrin, beta 8	15.84	1.00
15	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	452689	F33868	Hs.284176	transferrin	1.54	1.44
	453392	U23762	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
20	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
	453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

25 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

30	Pkey	CAT Number	Accession
	410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003067 AF037207 AF010126 AA633976 AA872836 BE298825 BE299889 AI016464 AI584600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AJ468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M54982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R05796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82697 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV656200 R95790 W03250 W00913 AA344136 AV660126 R97823 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343080 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71269 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
35	419502	18535_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578574 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050590 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AJ471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756

TABLE 11C

70 Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	Nt_position
	403329	8516120	Plus	96450-96598
	406399	9256288	Minus	63448-63554

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenes number
 Unigenes Title: Unigenes gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigenes Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AJ541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NIIE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	XS4232	Hs.2689	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

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PCT/US02/12476

	446282	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
5	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
	450832	AW970602	Hs.105421	ESTs	25.17	36.00
	452240	AI591147	Hs.61232	ESTs	13.42	1.00
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27
	453830	AA534296	Hs.20953	ESTs	24.92	25.00
10	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00

TABLE 12B

15	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
20	Pkey	CAT Number	Accession			
	439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW855684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077			

TABLE 12C

25	Pkey:	Unique number corresponding to an Eos probeset				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.				
	Strand:	Indicates DNA strand from which exons were predicted.				
30	NL_position:	Indicates nucleotide positions of predicted exons.				
	Pkey	Ref	Strand	NL_position		
	400666	8118496	Plus	17982-18115,20297-20456		
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573		
35	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814		
	401785	7249190	Minus	165778-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942		
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732		
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076		
40	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450		

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigenel Title	R1	R2
408562	AA36323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	midkine	1.00	157.00
436532	AA721522		gbmv54h12r1 NCL CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gbzrk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 55680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigeneID's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Pref.Utility: Preferred Utility
 Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigeneID	Unigene Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kd), kalini	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103354	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	s.m.	
412719	AWD16610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	mAb & diag & s.m.	secreted
415817	U89967	Hs.78967	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	X03272	Hs.79432	fibrillin 2 (congenital contractual ara	diag	extracellular
417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U88945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418505	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60659	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, Scerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	perforin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (perniphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.158396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M36699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
15	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	BE001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
	428969	AF120274	Hs.194689	artemin	diag	extracellular
25	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
	436481*	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	
40	437016	AJ076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothei	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.s	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF-1-i	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	s.m.	
50	442117	AW664954	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013408	Hs.9914	folistatin	diag	extracellular
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
55	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothei	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	mAb & diag	secreted
	446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
	447033	AI357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	Integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AI581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450375	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
70	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fs, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
	452747	BE153855	Hs.61460	lg superfamily receptor UNIR	mAb	plasma membrane
	452838	U65011	Hs.30743	preferentially expressed antigen in mala	CTL	nuclear
75	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AI693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

WO 02/086443

PCT/US02/12476

414883 15024_1 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AJ719075 BE270172 BE269819 AA889955 AJ204630 W25243 AJ935150
AA872039 W72395 T99630 AJ422691 H98460 N31428 BE255916 HQ3265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667
R75953 AW662396 AA662522 AI865147 AJ423153 AW262230 AA584410 AA583187 AW024595 AW069734 AJ826996 AA282997 AA876046
AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AJ423513 AI094597 H42079 R54703 AIS30359 AA617681 AA978045
AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AJ312104 AIS11822 AA416871 AI185409 AA129784 AA701623 AI075239
AI139549 AA633648 AI339996 AI336880 AA399239 AJ078708 AJ085351 AJ362835 AJ346618 AJ146955 AJ989380 AJ348243 N92892 AA765850
AI494230 AJ276887 AA962596 AJ92600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
AJ494211 AW059601 AW886710 R92790 N59755 AJ361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R376789
AA954344 H77576 R96823 AJ457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AJ161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

5 Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10 Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15	Seq ID No:	Sequence ID number			
	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
20	Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
	Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
25	Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
30	Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
	Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
	Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakkinase
35	Seq ID No: 27 & 28	423873	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
	Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
40	Seq ID No: 37 & 38	429510	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
	Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
45	Seq ID No: 47 & 48	443648	AJ085377	Hs.143610	ESTs
	Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD2_HUMAN NKGD2-
	Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,
	Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
50	Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 18 (comfalin)
	Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
	Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
	Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
55	Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter
	Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
	Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
	Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
	Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
65	Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
	Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
70	Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re
	Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
	Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
75	Seq ID No: 106 & 107	417542	J04129	Hs.82269	progesterone-associated endometrial prote
	Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratiferin
	Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
	Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
	Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
80	Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
	Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11035
	Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
85	Seq ID No: 125 & 126	424687	J06070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

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Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
Seq ID No: 129 & 130	418462	BE001596	Hs.85256	integrin, beta 4
Seq ID No: 131 & 132	100668	LO5424	Hs.169610	CD44 antigen (homing function and Indian
Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
Seq ID No: 165 & 166	413281	AA851271	Hs.222024	transcription factor BMAL2
Seq ID No: 167 & 168	444781	NM_014400	Hs.11850	GPI-anchored metastasis-associated prote
Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
Seq ID No: 177 & 178	425397	JO4088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-4
Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-4
Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-4
Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-4
Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-4
Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol
Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin 1 precursor
Seq ID No: 201 & 202	102963	X02404	Hs.274534	calbindin-related polypeptide, beta
Seq ID No: 203 & 204	100576	X00356	Hs.37058	calbindin/calmodulin-related polypeptid
Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin, lissencephaly, X-linked (d
Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 7B
Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini
Seq ID No: 221 & 222	114346	AI137256	Hs.130489	ATPase, aminophospholipid transporter-II
Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor
Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA: cDNA DKFZp547C136 (fr
Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fs, clone NT
Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca
Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
Seq ID No: 256 & 257	446292	AF081497	Hs.279582	Rh type C glycoprotein
Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor
Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
Seq ID No: 282	407137	T97307		ghybe53n05.s1 Soares fetal liver spleen
Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

5	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 297 & 298	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 299 & 300	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 301 & 302	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
10	Seq ID No: 303 & 304	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342: Homo sapiens kinesin protein 9
	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
15	Seq ID No: 312 & 313	428810	AF068236	Hs.193768	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
20	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327	403329			unnamed protein product (Homo sapiens)
	Seq ID No: 328 & 329	409993	AW247090	Hs.57101	minichromosome maintenance deficient (S.
	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
25	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	Seq ID No: 340 & 341	102910	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
30	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
35	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409469	D86407	Hs.54481	low density lipoprotein receptor-related
	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
40	Seq ID No: 362 & 363	418113	AJ272141	Hs.83484	SRP (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
45	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (comifin)
	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
	Seq ID No: 380 & 381	103768	AF086009	Hs.295398	gbc: Homo sapiens full length insert cDNA
50	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149509	Integrin, alpha 5 (fibronectin receptor,
	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
55	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
	Seq ID No: 400 & 401	423861	D13666	Hs.136348	perlestin (OSF-2os)
60	Seq ID No: 402 & 403	444381	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270266	Hs.82128	ST4 oncotetral trophoblast glycoprotein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	ST4 oncotetral trophoblast glycoprotein
	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
65	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adican
	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
70	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
75	Seq ID No: 432 & 433	432201	AJ538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
	Seq ID No: 438 & 439	431211	M86949	Hs.323733	gap junction protein, beta 2, 26kD (conn
	Seq ID No: 440 & 441	447033	AJ357412	Hs.157601	ESTs
80	Seq ID No: 442 & 443	447033	AJ357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	AJ357412	Hs.157601	ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
85	Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antag

	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ355012.1 [Hsa
	Seq ID No: 464 & 465	402075			ENSP00000251056: Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
10	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305.gij3806122[gb]AAC69198.1) (AF0
	Seq ID No: 486 & 487	405932			C15000305.gij3806122[gb]AAC69198.1) (AF0
	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
15	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
20	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
25	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gbhdh13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
30	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalini
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406590	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 18
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
45	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progestagen-associated endometrial prote
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410655	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410655	U92649	Hs.64311	a disintegrin and metalloproteinase doma
50	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2 -
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365: Homo sapiens melanoma antigen,
55	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 600 & 601	409757	NM_001838	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucina-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucina-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI633815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.59376	ESTs
	Seq ID No: 624 & 625	407242	M18728		ghb-human nonspecific crossreacting anti
	Seq ID No: 626 & 627	407242	M18728		ghb-human nonspecific crossreacting anti
85	Seq ID No: 628 & 629	407242	M18728		ghb-human nonspecific crossreacting anti
	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type 1 transmembrane protein Fn14

5	Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain
	Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
	Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrophin
	Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc
	Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy
	Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu
	Seq ID No: 644 & 645	448243	AW389771	Hs.52620	integrin, beta 8
	Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
	Seq ID No: 648 & 649	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6
10	Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
	Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
	Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
	Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
15	Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
	Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
	Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha
	Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
	Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
20	Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
	Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
	Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
	Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kallikrein 11
25	Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
	Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport
	Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
	Seq ID No: 684 & 685	422424	AJ186431	Hs.296638	prostate differentiation factor
	Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
30	Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeo box 5

TABLE 15B

35	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
40	Pkey	CAT Number	Accession	
	309931	AW341683		
	330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662	
	439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AJ346341 AI867454 N54784 AI655270 AJ421279 AW014882 AA775552 N62351 N59253 AA626243 AJ341407 BE175639 AA456968 AI358918 AA457077	
	450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532	
45			AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067	
	451320	86576_1	AW118072 AI631982 T15734 AA224195 AJ701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AJ140719 AJ720211 T03490 AJ372637 T15415 AW205836 AA630384 T03515 T33230	
			AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612	

TABLE 15C

50

Pkey:

Ref:

Strand:

NI_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

55

Pkey

Ref

Strand

NI_position

402075

8117407

Plus

121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

60

403329

8516120

Plus

96450-96598

403478

9958258

Plus

116458-116564

404440

7528051

Plus

80430-81581

404877

1519284

Plus

1095-2107

65

405770

2735037

Plus

61057-62075

405932

7767812

Minus

123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

1	11	21	31	41	51	
1	11	21	31	41	51	60
10	20	30	40	50	60	120
10	20	30	40	50	60	180
10	20	30	40	50	60	240
10	20	30	40	50	60	300
15	25	35	45	55	65	360
15	25	35	45	55	65	420
15	25	35	45	55	65	480
15	25	35	45	55	65	540
15	25	35	45	55	65	600
20	30	40	50	60	70	660
20	30	40	50	60	70	720
20	30	40	50	60	70	780
20	30	40	50	60	70	840
20	30	40	50	60	70	900
25	35	45	55	65	75	960
25	35	45	55	65	75	1020
25	35	45	55	65	75	1080
25	35	45	55	65	75	1140
25	35	45	55	65	75	1200
30	40	50	60	70	80	1260
30	40	50	60	70	80	1320
30	40	50	60	70	80	1380
30	40	50	60	70	80	1440
30	40	50	60	70	80	1500
35	45	55	65	75	85	

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

1	11	21	31	41	51	
1	11	21	31	41	51	60
10	20	30	40	50	60	120
10	20	30	40	50	60	180
10	20	30	40	50	60	240
10	20	30	40	50	60	300
10	20	30	40	50	60	360
10	20	30	40	50	60	420

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

1	11	21	31	41	51	
1	11	21	31	41	51	60
10	20	30	40	50	60	120
10	20	30	40	50	60	180
10	20	30	40	50	60	240
10	20	30	40	50	60	300
10	20	30	40	50	60	360
10	20	30	40	50	60	420
10	20	30	40	50	60	480
10	20	30	40	50	60	540
10	20	30	40	50	60	600
10	20	30	40	50	60	660
10	20	30	40	50	60	720
10	20	30	40	50	60	780
10	20	30	40	50	60	840
10	20	30	40	50	60	900
10	20	30	40	50	60	960
10	20	30	40	50	60	1020
10	20	30	40	50	60	1080
10	20	30	40	50	60	1140
10	20	30	40	50	60	1200
10	20	30	40	50	60	1260
10	20	30	40	50	60	1320
10	20	30	40	50	60	1380
10	20	30	40	50	60	1440
10	20	30	40	50	60	1500
10	20	30	40	50	60	1560
10	20	30	40	50	60	1620
10	20	30	40	50	60	1680
10	20	30	40	50	60	1740
10	20	30	40	50	60	1800
10	20	30	40	50	60	1860
10	20	30	40	50	60	1920

AATTGGCCAA TATTTTTCAA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT 1980
 TTAGGACAGT TGCAACAGTG AAAAGAAGAA AATTATTCAA ATTTGGACAT TTTAATTGTT 2040
 TAAAAATTGT ACAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100
 GTTTAAAAAG GGCAAAAGTT TTAGACTGTA CTAAATTTTA TAACCTACTG TTTAAAGCAA 2160
 AAATGGCCAT GCAGGTGAC ACCGTGTTGTA ATTTATAATA GCTTTTGTTC GATCCCACT 2220
 TTCCATTTTG TTCAATATA AAAAACCATG AATTACTGT GTTTGAAATA TTTTCTTATG 2280
 GTTTGTAATA TTTCTGTAAA TTTATTGTGA TATTTTAAGG TTTTCCCCC TTTATTTTCC 2340
 GTAGTTGTAT TTTAAAGAT TCGGCTCTGT ATTATTGTAA TCAGTCTGCC GAGAAATCCAT 2400
 GTATATATTT GAACATAAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTCTACT 2460
 CCATTATGCA CAGTTTGAGA TAAATAAATT TTTGAAATAT GGACACTGAA AAAAAAATA 2520
 AAAAAACAA AACAAAAAA CAAAAACAA AACACAGAAA AACAAAAAA AAAAAACAA 2580
 CACAACACA AACAAAAAA AAAAAAAGA AACAAACACA CAACACAAA CAACACAAA 2640
 CCACACACA AACACACA CACAGAGG

Seq ID NO: 4 Protein sequence:
 Protein Accession #: CAA83435.1

1 11 21 31 41 51
 MYNMMETELK PPGPQQTSGG GGENSTAAAA GGNQKNSPDR VKRPMNAPMV WSRGQRRKMA 60
 QENPKQHINSE ISKRLGASWK LLSETEKRPF IDEAKRLRAL HMKHPDYKY RPRKTKTLM 120
 KKKYTLPGG LLAPGNSMA SGVGVGAGLG AGVNQRMDSY ABMNGWSNGS YSMQDQLGY 180
 PQHPGLNAHG AAQMFMERY DVSAQYNSM TSSQTYMNGS PTYSMSYSQO GTPGMALGSM 240
 GSVVKSEASS SPFVVTSSSH SRAPCQAGDL RDMISMYLPG AEPPEPAAPS RLHMSQHYQS 300
 GPVPGTAING TPLFLSHM

Seq ID NO: 5 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29-541

1 11 21 31 41 51
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTATG 60
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAGAAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTTC TGAACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGAGAGAG TTCAATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCTTAC 300
 TGCTTTAGAT GGCTTTAGCT TGGAAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTTCTG ATACTGGAAA 420
 TGACAAAAAT GGAAAGGAA AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACGGCA 480
 GCTGTATGAG AATAACCCA GAAGACCCCTA CATATCTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAAATAA TCATTATTAT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTGT TGTGAAATG TGACAAACAC ACTTATCTGT CTCCTTCTCA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCRAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAATAA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:
 Protein Accession #: AAB50564

1 11 21 31 41 51
 MMAGMKIQLV CMLLLAFSSW SLCSDSEEM KALEADFLTN MHTSKISKAH VPSWRMTLLN 60
 VCSLVNNLNS PABETGEVHE EELVARRKLP TALDGFSLFA MLTIYQLHKI CHSRAFQWE 120
 LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLVENKPRRP YILKRDSEYYY

Seq ID NO: 7 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109-2940

1 11 21 31 41 51
 ACCTAAACCT TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTGCAG GTCCATTTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTAAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAACAT TAAGGAAATG 300
 ATAACTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
 ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCTTAC AATACAGAGG GTGTGGAAAA GAGGGAAAA ACATTCAATT CACACCTAAT 540
 TTCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCGAGT GTTTGTCCAT 600
 GAATGGGCCC ACCTCCGTTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTCTTAC 660
 ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGTCTCTTG CCCCAGAA AACTGTATTA TTAGTAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGGTTGA ATTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCACAA 900
 CTACAGAAC AGATGTGCAG CCTCAGAAAT GCATGGGATG TAATCACAGA CTCGTCTGAC 960
 TTTACACCA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCCAC ATTCTGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGC TCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTTGAA 1140
 ATTCTACCT TGTGGGCTT TCCAGTTTC GACAGCAAG GAGAGATCAG AGCCAGCTTA 1200
 CACCAATAA ACAGCAATGA TGATCGAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTGA GGTGGTTGAA 1320
 AAAGTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAAGCG AGATGATAAG 1380
 CTTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACATTTCA CTCCATTGCC 1440

CTGGGTTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
 TTCTTTGTTTC CAGATATATC AAATCCAAT AGCATGATTG ATGCTTTTCAG TAGAATTTCC 1560
 TCTGGAACTGC GAGACATTTT CCAGCAACAT ATTCACTTGG AAAATACAGG TGAAAAATGTC 1620
 AAACCTCACCC ATCAATTGAA AAACACAGTG ACTGTGGGATA ATACTGTGGG CAACGACACT 1680
 5 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740
 GGACGAAAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTGCGAC AGCTAGTCTT 1800
 TGGATTTCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCTGGAACAA TACCCATCAT 1860
 TCTCTGCAAG CCTGAAAGT GACAGTGACC TCTCGGSCCT CCAACTCAGC TGTGCCCOCA 1920
 10 GCACCTGTGG AAGCCTTTGT GGAAGAGAGC AGCCTCCATT TTCCTCATCC TGTGATGATT 1980
 TATGCCAATG TGAACACGGG ATTTTATCCC ATTTCTAATG CCACTGTCCAC TGCCACAGTT 2040
 GAGCCAGAGA CTGGAGATCC TGTTAOCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
 GTTATAAAAA ATGATGGAAT TTACTOGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA 2160
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAAC CCACTCTATT 2220
 CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGTAATAT TCAGATGAAT 2280
 15 GCTCCAGGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACACC TGATGTTGTT 2400
 CCACCATGCA AAATTATTGA CTTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCATCTC 2460
 TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520
 AGTAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
 20 AAGCGAATTC AGCAGCAAGC TGGCATCAGG GAGATATTTA CGTCTCCACC CCAGATTTC 2640
 ACGAATGAGC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTATGTT 2700
 GCAATACGAG CAATGAGTAT GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCGAGGCG 2760
 CCTCTGTTTA TTCCOCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 25 GGAQTITTTAA CAGCAATGGG TTTGATAGGA ATCAITTTGCC TTATTATAGT TGTGACACAT 2880
 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTGG ACTACAAAAA 3000
 CATACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCAITTAG TTTTGTGACA 3060
 ATACAGATAA GATTTTITACA TGGTAGATCA ACAATTCTTT TTGGGGTAG ATTAGAAAAC 3120
 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAGTAAT GTCTTTAAAG 3180
 30 GCAAAGGAAA GCGTAAAGTC GGACCACTGT CAAGGAAAGT TTGTTTTATT GAGGTGGAAA 3240
 AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA 3300
 TCATTGATTT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGAGTAC AGGTGTCTTG 3360
 TTTACATGAA GATCATGCTA TAITTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT 3420
 35 CTGTCTATTT TGTATTATAT ATTTTCAGAT ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
 TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACOGGT 3540
 TTTATGACAA AGGTCTATTG AATTTATTGT TMTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600
 TTTCTAAGTT TATGTCCCTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCC 3660
 TACCTAGGAA A

Seq ID NO: 8 Protein sequence:
 Protein Accession #: NP_006527.1

1 11 21 31 41 51
 45 MTQRSLIAGPI CNLKFVTLIV ALSSELPFLG AGVQLQDNGY NGLLIAINPO VPENQNLISN 60
 IKEMITEASF YLENAIKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH 120
 GDDPYTLQYR GCKKCKYIY FFPNFIINDN LTAGYGSRRG VFVEHWAHLR WGVFDEYNND 180
 KPFYINGQNI IQVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
 50 MPMSQLSSVV EFCNASTHNQ EAPNLQNMOC SLRSANDVIT DSADPHHSFP MNGTELEPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQQAEEFYLM QIVEIHTFVG IASFDSKGEI 360
 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNGKA YGSMVLVTS 420
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRIT GGLKFPVFDI SNSNSMIDAP 480
 SRISSTGDI FQHIQLEST GENVKPHEQL KNTVTVDNVT GNDTMFLVTW QASGPPEIIL 540
 55 FDPDGRKYIT NNFITNLIFR TASLWIPGTA KPGHWITYLN MTHESLQALK VTVTSRASNS 600
 AVPPATVEAF VERDLHLFFH PVMIIYANVKQ GPFYILNATV TATVEPETGD FVTLLRLDDG 660
 AGADWIKNDG IYSRVYFSAF ANGRYSKVE VNRSPSISTP AHSIPGSHAM YVPGYTANGN 720
 IQMNAPRKSV GRNEERKRWG FSRVSSGGSP SVLGVPAAGP HDVFPCKII DLEAVKVEE 780
 LTLNWTAPGE DFDQQAQTSY EIRMSKSLQN IQDDFNAIL VNTSKRNPPQ AGIREIPTFS 840
 60 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDFVPARDY 900
 LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENG T KLL

Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 336-632

1 11 21 31 41 51
 70 CTCCOCTCAC CCGGTCAGG GATGCCAGT CCCCAGACA CCTCCCACTT CCCACTGTGG 60
 CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCTCCCCCA GCTGGTGGTG 120
 GAGCTGGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAATAATGCC AAGTTGGGGG 240
 CCAGTG3GGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT 300
 75 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
 CGCTGGCTGT GCTGGTCACT ACCTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
 AGCTGAGTAA GGGGGAATG AAGGAACITC TGCACAAGGA GCTGCCCAGC TTTGTGGGGG 480
 AGAAAGTGGA TGAGGAGGGG CTGAAGAAGC TGATGGGCAG CCTGGATGAG AACAGTGACC 540
 AGCAGGTGGA CTTCCAGGAG TATGCTGTTT TCCTGGCACT CATCACTGTC ATGTGCAATG 600
 80 ACTTCTTCCA GGGCTGCCCA GACCGACCTT GAAGCAGAAC TCTTGACTTC CTGCCATGGA 660
 TCTCTTGGGC CCAGAGCTGT TGATGCCCTT GAGTTTGTGA TTCAATAAAC TTTTITTTGTC 720
 TGTGTGATAA ATTTTAATTG CTCAGTGATG TTCCATAACC CGGCTGGCTC AGCTGGAGTG 780
 CTGGGAGATG AGGGCTCCTT GGATCTCTCT CCTTCTGGG CTCTGACTCT CCTGGAAATC 840
 TCTCCAGGAC CAGAGCTATG CTTTGGTCT CAATTTTGA ATTTCAACA CCAGCAAAAA 900
 85 ATTGGAATC GAGATAGGTT GCTGACTTTT ATTTTGTCAA ATAAAGATAT TAAAAAGGC 960
 AAATACCA

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

5 1 11 21 31 41 51
| | | | | |
MMCSLEQAL AVLVITTFHKY SCQEGDKFKL SKGEMKELLE KELPSFVGEK VDEBGLKKLM 60
GSLDENSQQ VDFQYAVFL ALITVMCNDF PQGCPDRP

10 Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-626

15 1 11 21 31 41 51
| | | | | |
CTCCCCCTCAC CCGGGTCCAG GATGCCCACT CCCCACGACA CCTCCCACTT CCCACTGTGG 60
CCTGGGTGGG CTGAGGGGCT GCCTTGACC TGGCTTAGAG CCCTCCCCCA GCTGGTGGTG 120
GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTGGTTTCC TTAATAATGCC AAGTTGGGGG 240
CCAGTGGGCG CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT 300
GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
CGCTGGCTGT GCTGTGCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
AGCTGAGTAA GGGGGAAATG AAGGAACCTC TGCAACAAGG GCTGCCACGC TTTGTGGGGC 480
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GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660
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GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG TATTCAATAA ACTTTTITGG 840
TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCATATA CCGGCTGGCG TCAGCTGGAG 900
TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG GGCCTGACT CTCTGGAAA 960
TCTCTCCAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGG GAATTTCAAA CACCAGCAA 1020
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GCAATACCA

35 Seq ID NO: 12 Protein sequence:
Protein Accession #: Eos sequence

40 1 11 21 31 41 51
| | | | | |
MMCSLEQAL AVLVITTFHKY SCQEGDKFKL SKGEMKELLE KELPSFVGHG REPCAVERFR 60
VHLFNPVIGD LRNQSPEGKS DCPKITQHWR KWMRRG

45 Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 58-354

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GAGCTGCCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240
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65 Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_005969.1

70 1 11 21 31 41 51
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75 Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62-358

80 1 11 21 31 41 51
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CAGAGAGCTG CCGAGCTTGG TGGGGGAGAA AGTGGATGAG GAGGGGCTGA AGAAGCTGAT 240
GGCAGCCTG GATGAGAACA GTGACGAGCA GGTGACTTTC CAGGAGTATG CTGTTTCTCT 300
GGCACTCATC ACTGTCATGT GCAATGACTT CTCCAGGGC TGCCAGACC GACCCTGAAG 360
CAGAACTCTT GACTTCTTGC CATGGATCTC TTGGGCCAG GACTGTGTAT GCCTTTGAGT 420
TTTGATTTCA ATAACTTTT TTTGTCTGTT GATAATATT TAATGCTCA GTGATGTTCC 480
ATAACCCGGC TGGCTCAGCT GGAATGCTGG GAGATGAGGG CTTCTGGAT CTTGCTCCCT 540
TCTGGGCTCT GACTCTCTG GAAATCTCTC CAAGGCCAGA GCTATGCTT AGGTCTCAAT 600
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Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

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1 11 21 31 41 51
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10 GSLDENSDQQ VDFQYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

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CGCGGGCGCA GGGCAGCGGT TCGCGCACAC CCTAGCACAC ATGAACACGC GCAAGAGCTG 240
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25 AATTTTCTGG AGTTTCTGCC CCTGCTCTGC GTACGCCCTC AGTCACTTC GCCAGCAGTA 420
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30 GGGCCTATGA GCGACGGCGC CCGCGGAGCT CCGAGCAGCG GTAGCGCCCC CCTGTAAAGC 720
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ACCAGCTCAG CCTCTGATAA GCTGGACTCG GCACGCCCGC AACAGCACC GAGGAGTTAA 840
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35 ATGGACCGCG CATGCGCGCG CTCTGGGGCT TCTGCTGGCT GGTGTGGGG TTCTGGAGGG 1020
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50 AAGGCAACCC CAACACGCG CTTCAGTGGT TCTATAACCG GGCAATATTG AATGAGTCCA 1920
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65 TTGACCTGCA AAGTTAAAAA AAAATTAAAG TTGAGAACAG GTATAAGTGC ACACCTGAAT 2820
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80 CAGGAGTATG GCTTGTGCTG AAGAGAGGTT TGGCTATCCC CACCCCAACC CACCCCAACC 3720
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85 CAAGGCATTA ATCTTAATAA ACCAGGATCC ATTTAGGTAC CACTTGATAT AAAAAGGATA 4020
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Seq ID NO: 18 Protein sequence:
Protein Accession #: CAAS3571

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SKNIFLANLQ IPNCGLPAN LAAPNLVVEE GKSIITLSCSV AGDPVFNMYW DVGNLVSXHM 240
NETSHTQSL RINTISSDDG GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDEH 300
WCIPPTVIGN PKPALQWPNY GAILNESKYI CTKIHVTNHT EYEGCLQLDN PTHMNGDYT 360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
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Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_000228
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1 11 21 31 41 51
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Seq ID NO: 20 Protein sequence:

Protein Accession #: NP_000219

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VLRPAEKLVMT SMTKQLGDFW TRMEELRHQA RQQAARAVQA QQLAEGASEQ ALSAQEGFER 1080
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Seq ID NO: 21 DNA sequence

Nucleic Acid Accession #: NM_003722

Coding sequence: 145-1491

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TGGAGCTATT CCACTGAATC GAAGAACTC TACTGCCAAA TTGCAAGAGC ATGCCCATC 660
CAGATCAGGG TGATGACCCC ACCTCTCTAG GGAGCTGTTA TCGCGGCCAT GCCTGTCTAC 720
AAAAAAGCTG AGCACCTCAC GGAGGTGGTG AAGCGTGCC CCAACCATGA GCTGAGCGGT 780
GAATTCACAG AGGGACAGAT TGCCCTCTCT AGTCATTGTA TTGAGTAGTA GGGGAACAGC 840
CATGCCAGT ATGTAGAAGA TCCCATCACA GGAAGACAGA GTGTGCTGTT ACCTTATGAG 900
CCACCCAGG TTGGCACTGA ATTCAGGACA GTCTTGTACA ATTTCATGTG TAACAGCAGT 960
TGTGTGAGAG GGATGAACCG CCGTCCAATT TTAATCATTT TACTCTGGA AACAGAGAT 1020
GGGCAAGTCC TGGGCCGACG CTGCTTTGAG GCCCGGATCT GTGCTTGCCC AGGAAGAGAC 1080
AGGAAGGCGG ATGAAGATAG CATCAGAAAG CAGCAAGTTT CGGACAGTAC AAAGAAGCGT 1140
GATGGTACGA AGCGCCCGTT TCGTCAGAAC ACACATGCTA TCCAGATGAC ATCCATCAAG 1200
AAACGAAGAT CCCCAGATGA TGAACGTGTA TACTTACCG TGAGGGGCGG TGAGACTTAT 1260
GAAATGCTGT TGAAGATCAA AGAGTCCCTG GAACCTATGC AGTACCTTCC TCAGCACACA 1320
ATTGAAACGT ACAGGCAACA GCAACAGCAG CAGCACCAGC ACTTACTTCA GAAACATCTC 1380
CTTTGAGCTT GCTTCAGGAA TGAGCTTGTG GAGCCCCGGA GAGAACTCC AAAACATCTC 1440
GAGCTCTTCT TTAGACATTC CAAGCCCCCA AACCGATCAG TGTACCCATA GAGCCCTATC 1500
TCTATATTTT AAGTGTGRTT GTTGTATTTT CATGTGTATA TGTGAGTGTG TGTGTGTGTA 1560
TGTGTGTGCG TGTGTATCTA GCCCTCATAA ACAGGACTTG AAGACACTTT GGCTCAGAGA 1620
CCCACTGCTT CAAAGGCACA AAGCCACTAG TGAGAGAATC TTTTGAAGGG ACTCAAACTT 1680
TTACAAGAAA GGATGTTTTT TGCAATTTT GTATCCTTAG ACCGGCCATT GTTGGGTGAG 1740
GAACCACTGT GTTGTCTGTG GAGCTTCTGT TTGTTTCTGT GGAGGGAGGG GTCAGGTGGG 1800
GAAAGGGGCA TTAAGATGTT TATTGGAACC CTTTTCTGTC TTCTTCTGTT GTTTTCTAA 1860
AATTCACAGG GAAGCTTTTG AGCAGGTCTC AAACCTAAGA TGTCTTTTAA AGAAAGGAG 1920
AAAAAAGTTG TTATTGCTCTG TGCATAAGTA AGTTGTAGGT GACTGAGAGA CTCAGTCAGA 1980
CCCTTTTAAAT GCTGTGCTAG TAATAATATT GCAAGTAGTA AGAAACGAAAG GTGTCAAGTG 2040
TACTGCTGGG CAGCGAGGTG ATCAATACCA AAAGTAATCA ACTTTGTGGG TGGAGAGTTC 2100
TTTGTGAGAA TTTGCTATTAT TTTGTCTCTT CACTCATGTG TAGTAGAAGC ATTTCCTAAT 2160
GCTGTGTACC TGCTCTGCC ACTGTATGTT GGCATCTGTT ATGCTAAAGT TTTTCTTGTA 2220
CATGAACCC TGAAGACCTT ACTACAAAAA AACTGTTGTT TGGCCCCCAT AGCAGGTGAA 2280
CTCATTTTGT GCTTTTAATA GAAAGACAAA TCCACCCAG TAATATTGCC CTTAAGTAGT 2340
TGTTTACCAT TATTTAAAGC TCATAATAGA ATTTGAAGCC CTCTCAGAAA ATCTGTGATT 2400
AATTTGCTTA TATGAGCTTT CTATCCCTCA AGCCTACCTA CCATAAAACC AGCCATATTA 2460
CTGATAGCTT TCASTGCTAT TAGCCAGGAG ACTTACGTTT TGAGTAAGTG AGATCCAAGC 2520
AGAOGTGTTA AATCAGCAC TCCTGGACTG GAAATTAAGG ATTGAAGGG TAGACTACTT 2580

TTTCTTTTT TACTCAAAG TTTAGAGAAT CTCTGTTTCT TTCCATTTTA AAAACATATT 2640
 TTAAGATAAT AGCATAAAGA CTTTAAAAAT GTTCTCTCCC TCCATCTTCC CACACCCAGT 2700
 CACCACACT GTATTTTCTG TCACCAAGAC AATGATTTCT TGTATTGAG GCTGTGCTT 2760
 TTGTGATGT GTGATTTTAA TTTTCAATAA ACTTTTGCAAT CTGTGTTTAA AAGAAA

Seq ID NO: 22 Protein sequence:
Protein Accession #: NP_003713

1 11 21 31 41 51
 MSQSTQTNEF LSPEVQHIW DFLEQPICSV QPIDLNFVDE PSEDGATNKI EISMDCIRMQ 60
 DSDLSDPMWF QYTNLGLLNS MDQQIQNGSS STSPYNTDHA QNSVTAPSPY AQPSTTFDAL 120
 SPSPAIPSNIT DYRGPHSFDV SFQQSSTAKS ATWYTSTELK KLYCQIAKTC PIQIKVMTFP 180
 PQGAVIRAMP VYKKAHVTE VVKRCPNHEL SREFNEGQIA PPSHLIRVEG NSHAQYVEDP 240
 ITGRQSVLVP YEPPQVGTET TTVLYNFMCH SSCVGGMWRP PILIIVTLET RDGQVLGRRR 300
 FEARICACPG RDRKADSDSI RRQVSDSTK NGDGTKRPPR QNTHGIQMTS IKRRSPDDE 360
 LLYLVPVRGE TYEMLLKIKE SLELMQVLPQ HTIETRYQQQ QQHQHLLQK HLLSACFRNE 420
 LVEPRRETPK QSDVFPFRHSK PPNRSVYP

Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_001944.1
Coding sequence: 84-3083

1 11 21 31 41 51
 TTTTCTTAGA CATTAAGTGC AGACGGCTGG CAGGATAGAA GCAGCGGCTC ACTTGGAATT 60
 TTTCAACAGG GAAATCAGAG ACAATGATGG GCCTCTTCCC CAGAACTACA GGGGCTCTGG 120
 CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAATTGGG AATAGAGACT AAAGGTCAAT 180
 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAAAGAAG GCAAAAACGT GAATGGGTGA 240
 AATTTCGCAA ACCCTGCAGA GAAGGAGAAG ATAACTCAA AAGAAACCCA ATTGCCAAAGA 300
 TTACTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
 ATCAGCCGCC TTTTGGAAATC TTTGTTGTTG ACAAAAACAC TGGAGATATT AACATAACAG 420
 CTATAGTCGA CCGGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTGGGGCT CTAATATGCC 480
 AAGGACTAGA TTATGAGAAA CCACCTTATC TAACGGTTAA AATTTTGGAT ATTAATGATA 540
 ATCTCCAGT ATTTTCAACA CAAATTTTCA TGGGTGAAT TGAAGAAAT AGTGCCCTCA 600
 ACTCACTGGT GATGATAC TAATGCCACAG ATGCAGATGA ACCAAACCCAC TTGAATTCTA 660
 AAATTGCCCT CAAATTTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCTTAAGCA 720
 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTCCTCTGA COGAGAGCAA GCTAGCAGCT 780
 ATGCTCTGAT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT 840
 GTAATATTA AGTGAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900
 CAGCAGTAT TGAAGAAAT ATTTTAAGTT CTGAATTACT TCGATTTCAA GTAACAGATT 960
 TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGGAAATGAAG 1020
 GAAATTTGGT TGAATACAAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAAGTGGTGA 1080
 AGGCTCTAGA TTATGAGAAA CTACAAAGCG TGAAACTTAG TATTGCTGTC AAAAAACAAAG 1140
 CTGAATTTCA CCAATCAGTT ATCTCTGAT ACCGAGTTCA GTCAACCCCA GTCAAAATTC 1200
 AGGTAATAAA TGTAGAGAA GGAATTGCAT TCGTCTGTC TTCAAGACA TTTACTGTGC 1260
 AAAAAAGCAT AAGTAGCAAA AAATTGGTGG ATTATATCCT GGGAAACATAT CAAGCCATCG 1320
 ATGAGGACAC TAACAAGCT GCCTCAATG TCAATATATG CATGGGACGT AACGATGGTG 1380
 GATACCTAAT TGCCTGATCA AAAACTGCTG AAATCAAATT TGTCAAAAAT ATGAACCGAG 1440
 ATTCTACTTT CATAGTTAAT AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500
 CGGGTAAAAA TTCTACAGGC ACGGTATATG TTAGAGTACC CGATTTCAAT GACAATTGTC 1560
 CAACAGCTGT CCTGGAAGAA GATGCAATTT GCAGTTCTTC ACCTTCCGTC GTTGTCTCCG 1620
 CTAGAACACT GAATAATAGA TACACTGGCC CCTATACATT TGCACTGGAA GATCAACCTG 1680
 TAAAGTTGCC TCTGCTGTTG AGTATACAAA CCTCAATGC TACCTCGGCC CTCTCAGAG 1740
 CCCAGGAACA GATACCTCCT GGAGTATACC ACATCTCCCT GGACTTACA GACAGTCAGA 1800
 ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT CTGTCACTGT GACAACAGGG 1860
 GCATCTGTGG AACTTCTTAC CCAACCAAAA GCCCTGGGAC CAGGTATGGC AGGCGGCAGT 1920
 CAGGAGGGCT GGGGCTGCCC GCCATCGGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT 1980
 TGGCCCCCCT TCTGCTGTTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040
 GTGGTTTAT CCCAGTTCTC GATGGCTCAG AAGGAACAA TCACTAGTGG GGAATTGAAG 2100
 GAGCCCATCC TGAAGACAAG GAAATCACA ATATTTGTGT GCCTCCTGTA ACAGCCAATG 2160
 GAGCGGATTT CATGGAAGTT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2220
 TGGAAAGCAC TTTGAGAAAT GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 2280
 GTGCTGCAGG CTTTGCACAA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340
 CTGGAGTTGG CATCTGTTC TCAGGGCAGT CTGGAACCAT GAGAACAAAG CATTCCTACT 2400
 GAGGAACCAA TAAGGACTAC GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT 2460
 TTTCTCAGAA AGCATTGTCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520
 TGTGTATCTA TGATAATGAA GGCGCAGATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT 2580
 GTTGCACTTT TATGTCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640
 TTAATAAACT TGCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAGAA GTTCAGCCAC 2700
 CCTCTAAAGA CAGCGGTTAT GGGATTGAAT CCTGTGGCCA TCCATAGAA GTCCAGCAGA 2760
 CAGGATTGTG TAAGTGCCAG ACTTTGTGAG GAAGTCAAGG AGCTTCTGCT TTGTCGCGCT 2820
 CTGGGCTCTG CCAGCCAGCT GTTTCCATCC CTGACCCCTC GCAGCATGGT AACTATTAG 2880
 TAACGGAGAC TTACTCGGCT TCTGGTTCCC TCGTGCAAC TTCCAAGTGA GCTTTGATC 2940
 CACTTCTCAC ACAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCCAT TCCAGTGTTC 3000
 CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG 3060
 ATCCTTGCTC CGGTCTAAAT TGACCAAGAT GAGCTGGAAT ACCACACTGA CCAATCTG 3120
 ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAGGCTC ACTGTATTGG GCTAATAATT 3180
 TGGCACTTAT TAGCTTCTCT CATAAAGTGA TCAAGATTAT AAATTAAGT TTTGGGTCA 3240
 TACCCCAAAA GCAATATGTT GTCACTCCTA ATTCCTCAAGT ACTATTCAAA TTGTAGTAAA 3300
 TCTTAAAGTT TTTCAAAACC CTAAATCAT ATTCGC

Seq ID NO: 24 Protein sequence:
Protein Accession #: NP_001935.1

1 11 21 31 41 51

	MMGLFPRTTG	ALAFVIVVIL	VHGLRIETK	QGYDEEEMTM	QQAQRQRRE	WVKPAKPRE	60
	GEDNSKRNPI	AKITSDVQAT	QKITYRISGV	GIDQPPFGIF	VVDKNTGDIN	ITAIVDREET	120
	PSFLITCRAL	NAQLDLVEKP	LILTVKILDI	NDNPPVPSQQ	IFMGEIEENS	ASNLSVMILN	180
5	ATDADEPHHL	NSKIAFKIVS	QEPAGTPMFL	LSRNTGEVRT	LTNSLDREQA	SSYRLVVSQA	240
	DKDGEGLSTQ	CECNIKVKDV	NDNPFMRDSS	QYSARIEENI	LSSELLRFQV	TDLDEEYTDN	300
	HLAVYFPTSG	NEGNNFPIQT	DPRINEGILK	VVKALDYEQL	QSVKLSIAVK	NKAEFHQSVI	360
	SRVYQSTPV	TIQVINVREG	IAPRPASKTF	TVQKGISSEK	LVDYILGTQY	AIDEDTNKAA	420
	SNVYVNGRN	DGGVLMDSK	TAEIKFVKNM	NRDSTFIVNK	TI TAEVLAID	EYTGKTSTGT	480
10	VYVVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPTYFALED	QPVKLPVWS	540
	ITTLNATSAL	LRAQEQIPPG	VYHISLVLT	SQNNRCMPR	SLTLEVOQCD	NRGICGTSYP	600
	TTSPTTRYGR	PHSGRLGPA	IGLLLLGLLL	LLLAFLLLLT	CDOGAGSTGG	VTGGFIPVPD	660
	GSEGTIBQWG	IEGAHPDEKE	ITNICVPPVT	ANGADFMES	EVCINTYARG	TAVEGTSQME	720
	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	QSGTMRTRH	STGGTNKDYA	780
15	DGAI SMFID	SYFSQKAPAC	AEEDDGQEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDDSFILSLG	PKPKKLAEIS	LGVDGEGKEV	QPPSKDSGVG	IESCGHPIEV	QQTGFVKCQT	900
	LSSQSGASAL	SASGSVQPAV	SIPDPLQHG	YLVTETYSAS	GSLVQPSSTAG	FDPLLTQNV	960
	VTERVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLI			

20 Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

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25	AGTATCCCAG	GAGGAGCAAG	TGGCACGTCT	TCGGACCTAG	GCTGCCCTCG	CCGTCATGTC	60
	GCAAGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTGG	TAGTTTCTCC	120
	CATGTTTGAG	TCCACAGCTG	CAGATTGGGG	GTCTGTGGTA	CGCAAGAAC	TGCTATCAGA	180
	CTGCTCTGTC	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCATCTG	AGGCAGTAT	240
30	GGAGAAGGGT	AAAGTATATC	TGAGGGTTAG	GCCCTTGTTA	CCTTCAGAGT	TGGAAACGACA	300
	GGAAAGATCG	GGTTGTGTCC	GTATTGAGAA	TGTGGAGACC	CTTGTTCTAC	AAGCACCCAA	360
	GGACTCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGGTTTAC	420
	CTTTTCCCAG	ATCTTTGGGC	CAGAACTGGG	ACAGGCATCC	TTCTTCAACC	TAACTGTGAA	480
	GGAGATGGTA	AAGGATGTAC	TCAAAGGGCA	GAACTGGCTC	ATCTATACAT	ATGGAGTCAC	540
35	TAACTCAGGG	AAAACCCACA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAACTT	CATCCAACAC	CTGATCTGAA	660
	GCCCTGTGCT	TCCAATGAGG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAG	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGCTAA	ATGGAGGCCT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTGAA	780
40	GAGGAGTGTC	TACATCGAAA	GTCCGATAGG	TACCAGCACC	AGCTTCGACA	GTGGCATTGC	840
	TGGGCTCTCT	TCTATCAGTC	AGTGTACCAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
	ATGGGCACAG	CCAGCAGCTG	CCCCACTACC	TGTCCCGCCA	AACATTCGCT	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAACT	GCTTTATGAC	CTATTAGAAC	CGCCTAGCCA	1020
	ACAGCGCAAG	AGGCAGACTT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
	AGATCTCAAC	TGGATTTCAT	TGCAAGATGC	TGAGGAGGCC	TGGAAGCTCC	TAAAGTGGG	1140
45	TCGTAAAGAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACCA	AACTCCAGCG	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCC	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCT	CTCTGTGATC	TGGCTGGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAAAC	CTCTCTACAC	ACCCCTGGGC	GCTGTATTGC	1380
	TGCCCTTCCT	CAAAACCCAG	AGAACCGGTC	AAAGCAGAAC	CTGGTTCCTT	TCCGTGACAG	1440
50	CAAGTTGACT	CGAGTGTTC	AAGGTTTCTT	CACAGGCCGA	GGCGGTTCTT	GCATGATTGT	1500
	CAATGTGAAT	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGTAGC	CAGGTGACTT	GTGCATGCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTGTTTCAT	CAAGGAACAT	AGTCTTCAGG	TATCCCCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
	CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAG	1740
55	AGGAGCTCCT	ACAAGTTTGT	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GGAGATGCAT	CTCCGAGATG	AAATTGTCAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGGTGC	AGTGAACATT	TGGACACCCA	AAAGGAATA	TTGAGGAGAA	1920
	TGTATGAAGA	AAAACCTAAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTTCAC	CAAGAAGAGA	1980
	TTCAAGAGCG	GGATGAAAG	ATTGAAGAGC	TAGAAGCTCT	CTTGACAGGAA	GCCAGACAAC	2040
60	AGTCAGTGCC	CCATCAGCAA	TCAGGGTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAAG	2160
	CAGAGCTAAA	CTCTACCAC	GAAGAGTTGC	ATAAGTATCA	GAAATGTGTA	GAACACCAC	2220
	CCTCAGCCAA	GCCCTTCACC	ATTGATGTGG	ACAAGAAGTT	AGAAGAGGGC	CAGAAGAAAT	2280
	TAAGGCTGTT	GGGACAGAG	CTTCAGAAAC	TTGGTGAAGT	TCTCCAACTA	GCAGAGAGAG	2340
65	CTTGTGCTCA	CAGCACTGGG	GCAGGAAAAC	TTGGTCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCTTAATCAA	ACAGGACCA	ACTCTGGCTG	AACTGCGAG	CAACATGGTG	CTAGTGAATC	2460
	TGGACCTTGG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATCTGTG	TTGAACTCC	2520
	AAGGCCAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAATACAG	CAACCAACCC	2580
	AACAACCCAC	AGGGAAGAAA	CCATTCTCTC	GAAATTTACT	TCGCCGAACA	CCAACCTGCC	2640
70	AAAGCTCAAC	AGACTGCAGC	CCTTATGCC	GGATCCTAAG	CTCACGGCGT	TCCCTTTTAC	2700
	TCAAACTGCG	GCCTTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTGAGCT	ACTCTCTGTA	AGAAATAGGT	CTCTTTTATG	CTTTACCATA	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTTGTAT	2880
	TATAACCAAC	TATGTAACTC	CATGTTGTTG	TTTTTTTATA	TTTACTTATA	TGATTTCTAT	2940
75	GCACACAAA	ACAGTTATAT	TAAAGATAT	ATTGTTTACA	TTTTTTATTG	AATTCCAAAT	3000
	GTAGCAAAAT	CATTAAACAA	AATTATAAAA	GGGACAGAAA	AA		

80 Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

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85	MSQGISLPPA	GLLSDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSTSL	EDKQQVPSSE	60
	SMEKVKVYLR	VRPLLPELE	RQEDQGCVR	ENVETLVLOA	PKDSFALKSN	ERGIGQATHER	120
	PTPSQIFGPE	VQASFPNLT	VKEMVKDVLK	GQNLVIYTVG	VINSKTHITI	QGTIKDGGIL	180
	PRSLALIPNS	LQGLHPTPD	LKPLLSNEVI	WLDSKQIRQE	EMKKLSLLNG	GLQEEELSTS	240
	LKRSVYIESR	IGTSTSPDSG	IAGLSSISQC	TSSSQLDETS	HRNAQPDTPA	LPVPANIRFS	300

IWISFFBIYN ELLYDLLEPP SQQRKQTLR LCEQNGNPF VKDLNWIHVQ DAEBAWKLLK 360
 VGRNQSPAS THLNQSSRS HSIFSIIRLE LQGGDIPVK ISELSDCLA GSERCKDQKS 420
 GERLKEAGNI NTSLETLGR IALRQNNQN RSKQNLVPPR DSKLTRVFGQ FFTGRGRSQM 480
 IVNVNPCAST YDSTLEHVAKF SAIASQVTC CPTVATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 13-1424

10 1 11 21 31 41 51
 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
 CTTCOCCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGGG TGAAGGATAC 120
 TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 15 GGAACCTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTGGATGTGG AGTCCCGAT 300
 GTCCATCATT TCAGGGAAAT GCCAGGGGGG CCGGTATGGA GGAAACATTA TATCACTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGGAAA 420
 GCITTCCAAG TATGGAGTAA TGTTACCCCT TTGAAATTC ACAAAGTTAA CACAGGCATG 480
 20 GCTGACATT TGCTGGTTTT TGCCCGTGA GCTCATGGAG ACTTCCATGC TTTTGATGGC 540
 AAAGGTGGAA TCCTAGCCCA TGCTTTTGA CCTGGATCTG GCATTGGAGG GGAATGCACAT 600
 TTGATGAGG ACGAATCTCG GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT 660
 GTTCAGGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAAATG 720
 TTCCCCACCT ACAATATATG TGACATCAAC ACATTTGGCC TCTCTGCTGA TGACATACGT 780
 25 GGCATTACAT CCTGTATGG AGACCCAAA GAGAACCAC CTTTGCACAA TCCTGACAAAT 840
 TCAGAACCAAG CTCTCTGTGA CCCCAATTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTT TCTTCAAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960
 AGTGTAAAT TAATTTCTTC CTTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT 1020
 GAAATGAAG CCAGAAATCA AGTTTTTCTT TTTAAAGATG ACRAAATCTG GTTAATTAGC 1080
 30 AATTGAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGGTTTT TCCTAACTTT 1140
 GTGAAAAAAA TTGATGCAGC TGTTTTTAAC CCACGTTTT ATAGGACCTA CTTCTTTGTA 1200
 GATAACCACT ATTGGAGGAT TGATGAAAGG AGACAGATGA TGGACCCCTG TTATCCCAAA 1260
 CTGATTACCA AGAACTTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA 1320
 AACCAATACT ACTATTCTCT CCAAGGATCT AACCAATTG AATATGACTT CCTACTCCAA 1380
 35 CGTATCACCA AACCACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAATG GTGTAATTA 1440
 TGGTTTTGT TAGTTCACCT CAGCTTAATA AGTATTTAAT GCATATTGCT TATGCTCTCA 1500
 GTGTACCCT ACTTAGATAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560
 TTATATAAAA TACATAATAT TTTTCAATTT TGAAACTCT AATTGTCCAT TCTTGTCTGA 1620
 40 CTCTACTATT AAGTTTGAAA ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 CTCTGTAAGT TGCTTCTTAA CATCCTTGA CTGAGAAATT ATACTTACTT CTGGCATAAC 1740
 TAAATTAAG TATATATATT TTGCTCAA TAAATTTG

Seq ID NO: 28 Protein sequence:
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 MKFLILLIQ ATASGALPLN SSTSLERQNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
 KEKIQEMQHF LGLKVGTQLD TSTLEMHAF RCGVPDVHFF REMPGGPVWR KHYITYRINN 120
 50 YTFDMHREDV DYALRKAFQV WSNVPLKFS KINTGMADIL VVPARGAHGD PHAPDGKGGI 180
 LAHAFPGSG IGDGAHFDDE EFWITHSGGT NLPLTAVHEI GHSGLGHSS DPKAVMFPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPEKNQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIPF 300
 PKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAEIEA RNQVFLPKDD KYWLISNLRP 360
 55 EPNPKYSIHS FGPFNVFKKI DAAVFNPRFY RTYFPVDNQY WRYDERRQMM DPGVPKILITK 420
 NFQGIQFKID AVFYSENKYY YFPQGSNQPE YDFLLQRIITK TLKSNWPFGC

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_006115.1
 Coding sequence: 236..1765

60 1 11 21 31 41 51
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 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 65 ACTCTCTGAG GAAAAACCAT TTTGATTAT ACTCTCAGAC GTGGGTGGCA ACAAGTGACT 180
 GAGACCTAGA AATCCAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTGGCT TCAAAATGGA 240
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Seq ID NO: 30 Protein sequence:
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Seq ID NO: 34 Protein sequence:
 Protein Accession #: NP_077741.1

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 KTRHRETVL RRAKRNAPI PCSMQENSLG PFPLPLQVE SDAQNYTVF YSISGRGVDR 180
 EPLNLFYIER DTGNLFPCTR VDRREYDVED LIAYASTADG YSADLPLPLP IRVEDENDNH 240
 75 PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDTHMTRL KYSILQOTPR SPGLFSVHPS 300
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 80 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPEILQE YVVICPKFMG YTDILAVDPD 600
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Seq ID NO: 35 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 146-1273

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	GGATAACTGT	GACTCCAGGC	CCGCAATGGA	TGCCCTGCAA	CTAGCAAATT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACCTTG	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
10	TGAAATTGGA	CAGGTCTCTT	ATTTTGAAAA	TGTCAAAGAT	ATACCTTTTG	GATTTCAAAC	360
	AGTAACATCG	GATGTAAACA	AACTTAGTTC	CTTTTACTCA	CTGAACTAA	TCAAGCGGCT	420
	CTACGTAGAC	AAATCTCTGA	ATCTTCTTAC	AGAGTTTATC	AGCTCTACGA	AGAGACCCCTA	480
	TGCAAAAGGAA	TTGAAACTG	TTGACTTCAA	AGATAAATTG	GAAGAAAACG	AAGGTCAGAT	540
	CAACAACCTCA	ATTAAGGATC	TCACAGATGG	CCACTTTGAG	AACATTTTAG	CTGACACAG	600
15	TGTGAACGAC	CAGACCAAAA	TCCCTGTGGT	TAATGCTGCC	TACTTTGTGG	GCAAGTGGAT	660
	GAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
	CAAAACAGTG	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAAACA	TTGACAGTAT	780
	CAATTGTAGG	ATCATAGAGC	TTCTTTTCCA	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
	ACCCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGAGAGAG	ATTGAAAAAC	AACTCAACTC	900
20	AGAGTCACTG	TCACAGTGGA	CTAATCCCAG	CACCATGGCC	AATGCCAAGG	TCAAACTCTC	960
	CATTCCAAAA	CCTGAAGTGG	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAATCTAGG	1020
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	AGTGGCCCTA	TCAAATGTGA	TCCACAAAGT	GTGCTTAGAA	ATAACTGAAG	ATGGTGGGGA	1140
	TTCCATAGAG	GTGCCAGGAG	CACGGATCCT	GCAGCACAG	GATGAATTGA	ATGCTGACCA	1200
25	TCCTTTTATT	TACATCATCA	GGCACACAA	AACTCGAAAC	ATCATTTTCT	TTGGCAAATT	1260
	CTGTTCTCCT	TAAAGGGCAT	AGCCCATGTT	AAGTCTCTCC	TGACTTTTCT	GTGGATGCOG	1320
	ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTTCTAGAT	ACAATAAATT	GCTAATGTGG	1380
	CTGGATCAGG	AAGCCGCCAG	TACTTGTGAT	ATGTAGCCTT	CACACAGATA	GACCTTTTTT	1440
	TTTTTCCAAT	TCTATCTTTT	GTTTCCCTTT	TTCCCATAG	ACAATGACAT	ACGCTTTTAA	1500
30	TGAAAAGGAA	TCACGTTAGA	GGAAAAATAT	TTATTCAATTA	TTTGTCAAAT	TGTCGGGGGT	1560
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	CCTGAAGAC	TGAAGAAAGT	GTAGTGCAAT	GGACCAACGA	AACTGCCCTG	GCTCCAGTGA	1740
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40	AAATGCAAGA	CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACCTTC	ATTTTGTATA	2160
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	GCACAGGGAT	TCTCAATAA	GCCGATATCA	GAATTTGTGT	TGAAGGAAC	TGTCTCTTCA	2280
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45	AGATGGCAAG	CATGTAACCT	ATATTAATAG	TAAATTTGTA	AGTTGGGTGG	ATAAGCTATC	2460
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Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

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	FKDKLEETKG	QINNSIKDIT	DGHFENILAD	NSVNDQTKIL	VVNAAYFVGK	WMKRPPESET	180
	KECPFLINKT	DTKPVQMMNM	EATPCMENID	SINCKIIELP	PQNKHLSMFI	LLPKDVEDES	240
	TGLEKIEKQL	NGSELSQWTN	PSTMANAKVK	LSIPKPKVER	MIDPKACLEN	LGLKHIPSED	300
60	TSDFSGMSET	KGVALSNIH	KVCLEITEDG	GDSIEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
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Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

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	CCATGGCCCA	GTTTGGAGGC	CTGCCCCGTC	CCCTGGACCA	GACCCGCCCC	TTGAATGTGA	180
	ATCCAGCCCT	GCCTTTGAGT	CCCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
	ATGGCCCTGT	GTCGCGGGGC	CTGTGGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
75	TGAAGCCTGG	AGGAGGTACT	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGG	AAAGTGAAGT	360
	CAGTGATTCC	TGGCCTGAAC	AACATCATTG	ACATAAAGGT	CACTGACCCC	CAGCTGCTGG	420
	AACTTGGCCT	TGTGCAGAGC	CCTGATGGCC	ACCGTCTCTA	TGTCAACATC	CCTCTCGGCA	480
	TAAAGCTCCA	AGTGAATACG	CCCCTGGTGG	GTGCAAGTCT	GTTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGCAGAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGTGCC	600
	TTGGTACATG	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
80	CCCTCCCATC	TCAAGCTCTT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCTGCTGCT	720
	AGTTGGTTCA	GGGCAACGTC	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
	CCCTGTGTCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTG	ATCAAGGTCT	840
	AAGCCTTCCA	GGAGGGGGCT	GGCCTCTGCT	GAGCTGCTTC	CCAGTGCTCA	CAGATGGCTG	900
	GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCCTT	960
85	TCCCAACAGG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAAAAGGCT	CTTCTTCTGC	1020
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Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

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Seq ID NO: 39 DNA sequence
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Coding sequence: 115-2223

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TCTGACCTGT ACTCTTGAAT ACAGTTTCT GATACCACTG CACTGTCTGA GAAITTTCAA 2640
AACTTTAATG AACTAACTGA CAGCTTCATG AAACGTGTTA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760
TTCCAGATT TCAGGAAACT TTTTCTCTTT TAAGCTATCC ACTCTTACAG CAATTGATA 2820
AAATATACCT TTGTGAACAA AAATTGAGAC ATTTACATT TCTCCTATG TGGTCTGCTC 2880
AGACTTGGGA AACTATTCAT GAATATTTAT ATTTATGGT AATATAGTTA TTGCACAGT 2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA
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Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

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75 1 11 21 31 41 51
| | | | |
MESPSAPPHER WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLHNLPQ 60
HLFGYSWYK ERVDGNRII GYVIGTQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFI 120
TLHVIKSLDV NEBATQQRV YPELPKPSIS SNNSKPVEDK DAVAFCEPE TQDATYLMWV 180
NNQSLVSPR LQLSNGNRTL TLFNVTRNDT ASYKCBTQNP VSARRSDSVI LNVLYGPDAP 240
TISPLNTSYR SGENALSLCH AASNPAAQYS WFNVTGTFQS TQELFIPNIT VNNSGSYTOQ 300
AHNSDTGLNR TTTTITTYVA EPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLMWVNN 360
QSLFVSPRLQ LSNDRNRTL LSVTRNDVGP YECGIGNELS VDHSDPVILN VLYGPDFTI 420
SPSYTYTRFG VNLSLSCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
NSASGSRSTT VKTITVSAIL PKPSISENNS KPVEDKDAVA FTCEPEAQNT TYLWVNGQS 540
LPVSPRLQLS NGNRTLTFN VTRNDARAYV CGIGNSVSAN RSDPVTLDVL YGPDTPIIIS 600
PDSSYLSGAN LNLSCSASN PSPQYSWRIN GIPQOHTOVL FIARKITPNNN GTYACFVSNL 660
85 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI
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Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

5
10
15
20

1	11	21	31	41	51	
AATCCGAC	ATGGCGAAAG	ACAACCTCAAC	TGTTCTGTTGC	TTCCAGGCGCC	TGCTGATTTT	60
TGGAAATGTG	ATTATTTGGTT	GTTCGCGCAT	TGCCCTGACT	GCGGAGTGCA	TCTTCTTTGT	120
ATCTGACCAA	CACAGCCTCT	ACCCACTGCT	TGAAGCCACC	GACAACGATG	ACATCTATGG	180
GGCTGCGTGG	ATCGGCATAT	TTGTGGGCAT	CTGCCTCTTC	TGCTGTCTGT	TTCTAGGCAT	240
TGTAGGCATC	ATGAAGTCCA	GCAGGAAAT	TCTTCTGGCG	TATTTCAATC	TGATGTTTAT	300
AGTATATGCC	TTTGAAGTGG	CATCTGTAT	CACAGCAGCA	ACACAACGAG	ACTTTTTCAC	360
ACCCAACTCT	TTCTGAAGC	AGATGCTAGA	GAGGTACCAA	AACAACAGCC	CTCCAAACAA	420
TGATGACCAG	TGGAAAAACA	ATGGAGTCAC	CAAAACCTGG	GACAGGCTCA	TGCTCCAGGA	480
CAATGTCTGT	GGCGTAAATG	GTCCATCAGA	CTGGCAAAAA	TACACATCTG	CCTTCCGGAC	540
TGAGATAAAT	GATGCTGACT	ATCCCTGGCC	TGCTCAATGC	TGTGTTATGA	ACAATCTTAA	600
AGAACCTCTC	AACTCGGAGG	CTTGTAAACT	AGGCGTGCC	GGTTTTTATC	ACAATCAGGG	660
CTGCTATGAA	CTGATCTCTG	GTCCAAATGAA	CCGACACGCC	TGGGGGGTTG	CCTGGTTTGG	720
ATTTCGCATT	CTCTGCTGGA	CTTTTGGGT	TCTCTCTGGT	ACCATGTTCT	ACTGAGCAG	780
AATTGAATAT	TAAGAA					

Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

25
30

1	11	21	31	41	51	
MAKDNSTVRC	FQGLLIFGNV	IIGCCGIALT	AECIFFVSDQ	HSLYPLLEAT	DNDDIYGAAW	60
IGIFVVICLP	CLSVLIGIVI	MKSSRRILLA	YFILMPIVYA	FEVASCITAA	TQRDFPTPNL	120
FLKQMLERYQ	NNSPPNNDQ	WKNNGVTKTW	DRLMLQDNCC	GVNGPSDWQK	YTSAPRTENN	180
DADYFWPRQC	CVNNLKEPL	NLEACKLVFP	GFYHNQCYE	LISGPMNRHA	WGVANFGPAI	240
LCWTFWVLLG	TFMYSRIRBY					

35
Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

40
45
50
55
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75
80
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1	11	21	31	41	51	
GCGGACAGA	TCTGCGGCTA	TCCTGGAGCC	GGCCCACTTG	TGAAC TAGGA	GAGCTTTGGG	60
ACCTCTGTCC	CAAGCAAGAG	AGATGAATGG	AGAGTATAGA	GCCAGAGGAT	TTGGACGAGG	120
AAGATTTCAA	AGCTGGAAAA	GGGGAAGAGG	TGGTGGGAAC	TTCTCAGGAA	AATGGAGAGA	180
AAGAGAACAC	AGACCTGATC	TGAGTAAAC	CACAGGAAAA	CGTACTTCTG	AACAAACCCC	240
ACAGTTTTTG	CTTTCAACAA	AGACCCACAA	GTCAATGCAG	TCAACATTGG	ATCGATTCTAT	300
ACCATATAAA	GGCTGGAAGC	TTTATTCTCT	TGAAGTTTAC	AGCGATAGCT	CTCCTTTGAT	360
TGAGAAGATT	CAAGCATTTG	AAAAATTTT	CACAAGGCAT	ATTGATTTGT	ATGACAAGGA	420
TGAAATAGAA	AGAAAGGGAA	GTATTTTGGT	AGATTTTAAA	GAACAGCAG	AAGGTGGTGA	480
AGTAATCAAC	TTGATACCA	ATATAGCAAC	TGAAC TAGGA	GATGCACCTG	AGAAAACTT	540
GGCTTGCAAT	GGTTTGGCAA	TACATCAGGT	GTAACTAAG	GACCTTGAAA	GGCATGCAGC	600
TGAGTTACAA	GCCCGAGGAG	GATTGTCTAA	TGATGGAGAA	ACAATGGTAA	ATGTGCCACA	660
TATTCATGCA	AGGGTGTACA	ACTATGAGCC	TTTGACACAG	CTCAGAATG	TCAGAGCAAA	720
TTACTATGGA	AAATACATTG	CTCTAAGAGG	GACAGTGGTT	OGTGTGAGTA	ATATAAAGCC	780
TCCTTGCAAC	AAGATGGCTT	TTCTTTGTGC	TGCATGTGGA	GAAATTCAGA	GCCTTCTCT	840
TCAGATGGA	AAATACAGTC	TTCCCAACAA	GTGTCTGTG	CCGTGTGTG	GAGGCAGGTC	900
ATTACTGCT	CTCCGCACT	CTCCTCTCAC	AGTTACGATG	GACTGGCAGT	CAATCAAAAT	960
CCAGGAATTG	ATGCTGTATG	ATCAGAGAGA	AGCAGGTGGG	ATTCACGAA	CAATAGAAATG	1020
TGAGCTTGT	CATGATCTTG	TGGATAGCTG	TGTCCCGGGA	GACACAGTGA	CTATTACTGG	1080
AATTGTCAA	GTCTCAAAAT	CGGAAGAAGG	TTCTCGAAAT	AAGAATGACA	AGTGTATGTT	1140
CCTTTGTAT	ATTGAAGCAA	ATTCTATTAG	TAATAGCAAA	GGACAGAAAA	CAAAGAGTTC	1200
TGAGGATGGG	TGTAAGCATG	GAATGTTGAT	GGAGTTCTCA	CTTAAAGACC	TTTATGCCAT	1260
CCAAGAGATT	CAAGCTGAAG	AAAACCTGTT	TAAACTCATT	GTCAACTCGC	TTTGCCCTGT	1320
CATTTTGGT	CATGAACCTG	TTAAAGCAGG	TTTGGCAATTA	GCACCTCTTG	GAGGAAGCCA	1380
GAAATACGCA	GATGACAAAA	ACAGAATTCC	AAATCGGGGA	GACCCCAACA	TCCTTGTGTT	1440
TGGAGATCCA	GGCCTAGGAA	AAAGTCAAAAT	GCTACAGGCA	GCGTGCAATG	TTGCCCAAG	1500
TGGCGTGTAT	GTGTTGGTGA	ACACCAAGAC	CACCTCTGCT	CTGACGGTAA	CTCTTTCAAA	1560
AGATAGTTC	TCTGGAGATT	TTGCTTTGGA	AGCTGGTGCC	CTGGTACTTG	GTGATCAAGG	1620
TATTTGTGGA	ATCGATGAAT	TTGATAAGAT	GGGGAATCAA	CATCAAGCCT	TGTTGGAAGC	1680
CATGGAGCAG	CAAGTATTA	GTCTTGCTAA	GGCTGGTGTG	GTGTTAGTCC	TTCTCTCAAG	1740
AACCTCCATT	ATTGCTGTCTG	CAATCCAGT	TGGAGGACAT	TACAATAAAG	CCAAAACAGT	1800
TTCTGAGAAAT	TTAAAAATGG	GGAGTGCACT	ACTATCCAGA	TTTGATTTGG	TCCTTATCCT	1860
GTTAGATACT	CCAAATGAGC	ATCATGATCA	CTTACTCTCT	GAACATGTGA	TTGCAATAAG	1920
AGCTGGAAAG	CAGAGAACCA	TTAGCAGTGC	CACAGTAGCT	OGTATGAATA	GTCAAGATTG	1980
AAATACTTCC	GTACTTGAAG	TAGTTTCTGA	GAGGCCATT	TCAGAAAGAC	TAAAGGTGGT	2040
TCCTGGAGAA	ACATAGATC	CCATTCCCA	CCAGCTATTG	AGAAAGTACA	TTGGCTATGC	2100
TCGGCAGTAT	GTGTACCCAA	GGCTATCCAC	AGAAGCTGCT	OGAGTCTTTC	AAGATTTTAA	2160
CCTTGAGCTC	CGGAAACAGA	GCCAGAGGTT	AAATAGCTCA	CCAATCACTA	CCAGGCAGCT	2220
GGAACTCTTG	ATTCTGTCTGA	CAGAGGCACG	AGCAAGGTTG	GAATTGAGAG	AGGAAGCAAC	2280
CAAGAGAGAC	GCTGAGGATA	TAGTGGAAAT	TATGAATAT	AGCATGCTAG	GAACTTACTC	2340
TGATGAATTT	GGGAACCTAG	ATTTTGAGCG	ATCCAGCAT	GGTCTGGAA	TGAGCAACAG	2400
GTCAACAGCG	AAAGATTTTA	TTTCTGCTCT	CAACAACTGT	GCTGAAAGAA	CTTATAATAA	2460
TATATTTCAA	TTTCACTAAC	TTGCGCAGAT	TGCCAAAGAA	CTAAACATTG	AGGTTGCTGA	2520
TTTTGAAAT	TTTATGGAT	CACATAATGA	CCAGGGTTAC	CTCTTGAATA	AAGGCCCAAA	2580
AGTTTACCAG	CTTCAAACTA	TGTAAGAGGA	CTTCAOCCAG	TTAGGGCTCT	CTGGGTTTAT	2640
TGCAGATTAA	AGCCATCTCA	GTGAAGATAT	GCGTGACGCG	ACAGACAGAC	AGACACACAC	2700
ACACACACAC	ACACACACAC	ACACACAGTC	AAATACTGTT	CTCTGAAAAA		2760
TGATGTCCCA	AAAGTATTAT	AATAGGAAAA	AAGCATTAAA	TATAATAAAC	TAATTTAAGA	2820

AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAATC ACAGTGACTC AGGAGGCTGA 2880
 GGTGAGAGGA TTCTTGTAGG CCAGGGTTCC AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
 CATTTCTTAA AAAAAAATAA AAAAAATTTA AACTTAGCTG GGTATGGTGG CACATGCCTA 3000
 TAGTCTCAGC TACTTGTGAG GCTGAGGCAG GAGGATTCTT TGAGCCCGAG AGTTTGAGGT 3060
 TACAGTGAGC CACAATCACA CCAATCACTG CACTCCAGCC TGGCAATAA AGTAACTCTT 3120
 GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTTA AATAAATCTT 3180
 CCAAGGGCTT AAAAGTAAAT TACTTATAAA TTTTATTATG TTGTATTGTT GACCTGCCTT 3240
 TTATATGTAT GAATATTCCA TAGTTTGTCA TATCAGATGT AGGCATACAG ACAATATCAT 3300
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 ATTTGAATTT CATAAAATTT TCCCATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
 GCTATTAAAT AATAGGTCTC ATTTATTCCA CAGGCTGTAG TTGTAGTCTT TGCTTGAAAC 3480
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 AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCACCAATTT GTAAAAACAT 3600
 GCCTTAGAAT TGGACTAAGG AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
 AGAAAGTGCT GCTGCTCTCC TGCCCCACCT TTGCCACTTC TGCCAGCAGG ATAGGTAGAA 3720
 GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTC TGCTAGATAT GCCTCCCTAA 3780
 ATTGCTGAAT TCAAAAGAGA AGTTGCATAC AAAGCATCTT GATTGAAAAA GGGTATGTTA 3840
 TATGCCCTTT TCATAGGCTG CTAGGGAGTT TTCTGTGTTT TACTTTCAGG TGGTGGGATC 3900
 AATAAGACCA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTACAGG GTTGCCAGCC 3960
 AAACATATCA TCATGTATAA ATCCAACAAA CACTTTGTAA CATACAGAA CTCAGGAAAT 4020
 GTGAACCAAT GTTGAGGAAT CTACTAAAT ACAGCTTCCC GCACACGAAG ATGAATGGAA 4080
 AATGTAATAA AAAAGAACTG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
 GATGTGGAGA CTATTGCCAT AGACCACAAT GTAAATTTTT AAGTGAGGAA GGAATAATCA 4200
 GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATAA TCCAGAGCTT TTGGAGTTC 4260
 GAGGAGGAG GATCACTTGA AGCCAGTTTT GAGACAGGCC TATGCAACAC ATTGAGACCC 4320
 TATCTCTACA AAAAAATAGT TAGCTGGGCA CGGTGGTGCA TGCCATTGTT CCTACCTACT 4380
 GTGGAGGCTG AAGTAGGAAA TCACTTGAGC COGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
 TTATACCATT GCACTCCAGC CTGGGCAAGA GAGCAAGACC TTGTCTCTT

30 Seq ID NO: 44 Protein sequence:
 Protein Accession #: CAB55276.2

1 11 21 31 41 51
 35 MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK 60
 TPQSMQSTLD RPIFYKQWKL YFSEVYSDSS PLIEKIQAPE KFFTRHIDLY DKDEIERKGS 120
 ILVDFKELTE GGEVYNLIPD IATELRDAPE KTLACMGLAI HQVLTKDLER HAAELQAQEG 180
 LSNDGETMYN VPHIHARVYN YEPLTQLKNV RANYGYKYIA LRGTVVVRVSN IKPLCTKMAP 240
 40 LCAACGEIGS FPLPDGKYSL PTKCPVPVCR GRSPALRSSH PLTVTMDWQS IKIQELMSDD 300
 QREAGRIPRT IECLELVDLV DSCVPDGTVT ITGIVKVSNA BEGSRNKNDK CMPLLYIEAN 360
 SISNSKQKQT KSSSDGCKHG MLMEFSLKDL YAIQEIQAEE NLFLKLVNSL CPVIFGHELV 420
 KAGLALALPG GSQRYADDKN RIPIRGDPHI LVVGDPLGLK SMLQAACNV AFRGVYVCGN 480
 TTTTSLGLTV LSKDSSSGDF ALEAGALVIG DQIGCGIDEF DDMGNQHQAL LEAMEQQSIS 540
 LAKAGVVCSL PARTSIIAAA NFVGGHYNKA KTVSENLMKG SALLSRFDLV FILLDTPNEH 600
 45 HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVVPGETIDP 660
 IPBQLLRKYI GYARQVYVPR LSTEAAARVLQ DFYLELRKQS QRLNSSPITT RQLESILRLT 720
 BARARLELR EATKEDAEDI VEIMKYSMLG TYSDEFNLD FERSQHGSGM SNRSTAKRFI 780
 SALANVAERT YNNIFQPHQL RQIAKELNIQ VADPFENFIG LNDQGYLLKK GKPVYQLQTM

50 Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_005416.1
 Coding sequence: 149..658

1 11 21 31 41 51
 55 ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCTTGAGCAG 60
 CTGAAGACCA GAAAGGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
 AAAGAGTGTG TCCACGATCC TTGAAGCAT GAGTCTTAC CAGCAGAAGC AGACCTTTAC 180
 60 CCCACCACT CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
 AATATTGTTT CCCACAACCA AGGAGCCATG CCACTCAAGG GTTCCACAAC CTGGAACAC 300
 AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCTTGAGCCA GGCTGTACCA AGGTCCCTGA 360
 GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
 CAAGGTCCCT GAGCCAGGTT GTACCAAGGT CCTTGAGCCA GGCTACACCA AGGTCCCTGA 480
 65 ACCAGGCAGC ATCAAGGTCC CTGACCAAGG CTTTATCAAG TTTCTGAGC CAGGTGCCAT 540
 CAAAGTTCTT GAGCAAGGAT ACACCAAGT TCCTGTGCCA GGCTACACAA AGCTACACGA 600
 GCCATGTCTT TCAACGCTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAAAT 660
 TGGTGACACG ACAAGCCCTT GAGAAGCCAA CCAACAGATG CTGGACACCC TCTTCCCATC 720
 70 TGTTCTGTG TCTTAATGT CTGTAGACCT TGTAAATCAG ACATTGTGAC CCAAGCCAT 780
 AGTCTCTCTC TTATTGTAT CCTAAAAATA CGTACTATAA AGCTTTTGTG CACACACACT 840
 CTGAAGAATC CTGTAAAGCC CTGAATTAAG CAGAAAGTCT TCATGCTTTT TCTGCTCTTC 900
 GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAGAAGAA TGCATGTTTC CTGCTCTTCC 960
 CTCATTAAAT TGCTTTTAAT TCCA

75 Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_005407.1

1 11 21 31 41 51
 80 MSSYQKQKTF TFPFQLQQQQ VKQPSQPPPO ELPVPTTKEP CHSKVPQPGN TKIPEPGCTK 60
 VPEPGCTKVP EPDCTKVPPE GCTKVPPEPGC TKVPEPGCTK VPEPGYTKVP EPKSIKVPDQ 120
 GFIFPEPEGA IKVPEQGYTK VEVPGYTKLP EPCPSTVTPG PAQKQTKQK

85 Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 5 GCGTCGTGTG CAGGCGTCCG CGGCTGTG ATAAATTAGAC ACGTTCCTCC CTCATTGCC 60
 AAGGCTCGTT AGAATTCCGC CTAGAGCTGT ATCATGTATT TTCTTTCAAA TTAACCTTGC 120
 TTGCAATTAA GCTTAGGGAA CCAGCAACAA AAGCAAACCT GGCCCGAGGT CGTTCACCGC 180
 GAAAAATGAT TAGAGAAACT TCCTCCCGCA TTTAAGGGGA AAGATTCTGT CGGCCAGCGC 240
 TTTGGGGAAG GTGCCCGAC GCAGAGGGCG ACGACAGGGG AGCAGGAAGC TGCTCAGGCT 300
 AGTCGGCGTT GGCGGCAGCG GTGGCCTTCC TCATCTGGGC GATGTGGGCT CCTAGAAGAG 360
 TAAGGATAAC ATCTCGGAAA TGACTTCTGT ACGTCTTGTG CCAACTGCA CACTCATGAC 420
 10 TTGAGCTGCT CCTGTGGAGT TACAGTTTAC CAAACACATT CATGAACATA ATCTCATTTA 480
 CTAAAAACTT TGTGAGAAAT TTCTTTTACT AAAATTTTTT CTATTACAA A

Seq ID NO: 48 DNA sequence:
 Nucleic Acid Accession #: CAT cluster

15 1 11 21 31 41 51
 20 TTCCAAATTT TTTTTTTTGT AATAAGAAAA AATTTTAGTA AAAGAAAATT CTCACAAAGT 60
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 CTCCAAGTCA TGAGTGTGCA GTTGGGCTCA AACGCTACAG AAGTCATTTC CAGGATGTTA 180
 TCCTTACTCT TCTCGGAGCC CACATCGCCC AGATGAGGAA GGCCACCGCT GCCGCCAAGC 240
 CGGACTACCG TGAGCAGCTT CCTGCTCCCC TGTCTGCGCC TCTGCGGTGG GGGCACTTTC 300
 CCCAAGGCGC TGGCCGCGAG AATCTTTCCC CTAAATCGG GGAAGAAGTT TCTCTAATCC 360
 25 ATTTTGGGCG TGAACTGACT CGGGCCAAAT TTGCTTTTGT TGCTGGTTCC CTAAGCTTAA 420
 TTGCAAGCAA AGTTAATTTG AAAGAAAATA CATGATACAG CTCTAGGGCG AATTCTAAAG 480
 AGCCTTGGGC AATGAGGAAA GAACGTGTCT AGTTATCCAC AGCCCGGGGA CGCTGCACA 540
 CGACGCT

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: CAT cluster

30 1 11 21 31 41 51
 35 TCCTTCTTCT GCTGCTCGTT TGTCTCTCCT GTGCTCTTCT TCTTCTTTC CCTGCGCGCT 60
 CCTGCGCGAC TCTGTTGTCT CTCTCTGAT GGCGGGGGGC GGGAGAAAGCT GACCGGTGAG 120
 ACGTAGACCG CGAAACCAAT GGGTGTACCA AGCCGCTCGC CGGCTTTTTT GGGAGAACCC 180
 GACACATGCA GACCACTTTT CCTGGAACNG CATGACCATG TTATTACTAT GGGCCGCTTC 240
 40 CCCAACCAAA GTGTTTAAAA CTTTTATAGG CACCCCAAAA ATTTTTTTTT TTTTTTTTTT 300
 TTCAATTAAA AAACCTTAAT ATTTATATTA AATACAAAGA TACCCAAACC CTTTATGCTT 360
 CTCTCTCTGA TCTGTGTCTT TTTTCTTTGA CAGCATCTCC ATTTTTTTTC TGCTGCTTCA 420
 TCCTCTGAGC CATGGGAATC CGTTTCATTA TTATGGTAGC AATATGGAGT GCTGTATTCC 480
 TAAAGAACT GACACAGGAG AATCACTTGA ACTTGGGAGG CAGAGTTTGC AGTGAGCCGA 540
 GATTGAACCA GTGCCTTCCA GCCTTGGCAG CGGAGCAGAA TTCTGTCACT GTTCTGTAAG 600
 45 TGCTGTATC GTGCTGACG CCGATCCTCG GTTCCATTGC GCTGCCAGGC AGGGTGTCTGG 660
 GAGTGGGGA GAGCTGGTCT ATATATCCGG GTGAAGCTCA GCTGTGGCAC ACCTTGGATG 720
 CCGGGTCTCT CCGTGGCCCG GGGACCTAGT ATTTTGTCCA CAGTGTACA CCAACAAAG 780
 GAGACAGCAT CATTTATGAG CCTGCAGCAT CCACCCTACT GCTGTATCCA GTTTCATTG 840
 ACTG

Seq ID NO: 50 DNA sequence
 Nucleic Acid Accession #: L05187
 Coding sequence: 1991..2260

55 1 11 21 31 41 51
 CTGCAGGGAG GCAGGTAGAA AAGGCTTTTG GGTTTTCAGG TGGGGGGCAG TCTAGCCTGA 60
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 60 CAGAGAAGGG ATTAGCCCCC GAAAGTCCCT GAAGTAGGAG AAGGGTAAAG GTGTGGTTGG 180
 TGAAGGAAGG CAGGTTTTC CAGATTAGCA ACCAGTCAGG GGGAGGAAGG TGAGAGTGGG 240
 AGAGTCATAA GTAAATTATT CTGAATGTGT GTAGTTTAAT GGAATTGGGA AAAAGATGGG 300
 GGAATGGAT GGAAGGTCTT GGACTCTGAG ACAAGGGGTC TATAATCAGT CCAITTCATT 360
 ATTTCTAGCT TCCACCTTCA CCAAGGCAGA CAAGGAGGGC CCACCTCAGC TCCTCTGCTC 420
 65 CCCCTCCCTT TCCACCTAT TCATGTGTGC AAGAGTCCCC TGTCCACAG AACACGGGGA 480
 ACAACCATCT CAATGACRAG GACAGCAGGT GGCAGGCTC AACAGGACTC AGATGTCCCC 540
 CCAGGGTTAA CTATGAAAC CCTCCATGAA GCCTGCTGCT CACCCCTCCC TCAAGGCAG 600
 CCCTGCACCT GGGTCTGAGG ATGAGGGTGG CAGTGAATAT TAGGCCAGTG ACATCATTTT 660
 CAGCCAGCTA GTGCCAAAAA ATATCAGGTG GTGTTTATCA AATAAGCCGA GCCAACCGGT 720
 GATGAGGATG GTAGTGTGAG TCATGTGTGA CAGGTGAGGA ATGAAAACAG AGTGCOCGAG 780
 70 AGCTTCTATT TCCTTGAGGC AGGGCTCAIT CATCTTATAA AAGCCAGCTG GCCATTGCTT 840
 TCACACCAAA CCCAGGGGAC CACACAGCCC ATTCTGTCTC GTATACGAGG TAAGTCTCTG 900
 ATTGCAACAA ACTGGCAATT CTAGTGTACT TTTTCATTAT TAGAAATTAG CTAAGGGCAA 960
 ATATGTGTAA GCAGGTATAA CCAGGGTTTC AATGGGAGAT AGAGAATAGT GGAATATCTT 1020
 TATTTTAAGT TAAATACAG TCTGGATTG AAAGGACCTT AGAGATGGTT AGGGCTCCCA 1080
 75 CCTCAGTAGA TAGTCAITGA ACTGGGAGTC CTGGAGAAGA TTGTTCAAAT GCCCATGGGA 1140
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 TGACAGATA TTTATAGAAA TTTTAATTTA TTAGATGGAT CTCTACTGAG CATTTATTCC 1260
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 80 AGTAATTGGC ATGACGGAGA TGGGCAGAGA AGGGCTGTGC ACTTTTGGGA GACTTGCTCA 1440
 AGGAGACCTC TAGGGTGTCA AGTGATGTGA GCTATGATGG AGGGGTATTT GGACAGCAG 1500
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 GAGGCTTAGA TGAATATAAA GCCATCCTAT AAGTCACAGG CTCTCTACAT GGTACTAGGA 1620
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 85 GAAGCCAGCT TTAGTAGGCG ATTTTCCAG AACAGATATA AGGTGCGCTT GGTAGGAAGG 1740
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 TTCAAAGGSC CTGAAAAATTA TCCAAGCTTA TTTCAITTTT AAATGTAATG GGGGAGCTAA 1860

5 GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920
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CATTTGAAGC ATGAATTTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040
GCAGCAGCAG GTGAACAACAC CTTGCCAGCC TCACCCACAG GAACCATGCA TCCCCAAAC 2100
CAAGGAGCCC TGCCAACCCA AGGTGCCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160
CCAGCCCAAG ATTCAGAGGC CCTGCCAGCC CAAGGTGCCCT GAGCCTGCC CTTCACCGGT 2220
CACTCCAGCA CCAGCCACAG AGAAGACCAA GCAGAAGTAA TGTGTTCCAC AGCCATGCC 2280
TTGAGGAGCT GGCCACTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATTT 2340
GCCTATTGAC CCTGCAGTTA GCATGCTGTC AOCCTGAATC ATAATCGCTC CTTTGCACCT 2400
10 CTAAAAAGAT GTCCCTTACC CTCATTCTCG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460
GTCTCACTGA CTGAGCTAGT CTCTCTGTG CTCGGGTGCA TTTGAGGATG GATTTGGGGA 2520
AGGTCAAGTG ACCATCCCTA G

15 Seq ID NO: 51 Protein sequence:
Protein Accession #: AAC26838

20 1 11 21 31 41 51
MNSQQQKQPC TPPPPQPPQQ VKQPCQPPPP EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
IPEPCQPKVP EPCPSTVTPA PAQQRTEKQ

25 Seq ID NO: 52 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120-473

30 1 11 21 31 41 51
CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CGCCCTGGA GCCAGGCCAA 60
GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGCTTCTAG 180
AGGCAGCTGT CACGGAGATT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCTAT 240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAAGTAA AGGTCAAGAT AAAGTCAAAG 300
GGCAGAGAGC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
35 TCCGGTGGCC CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCACAGAA 420
TCAGAAGATG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC 480
CGGTCCCTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
TGCTGCCCTT CCCCCTCCCA CACTGTCCAT TCTTCTCTCC ATTCAAGATG CCCACGGCTG 600
40 GAGCTGCCCT TCTCATCCAC TTTCCAATAA A

Seq ID NO: 53 Protein sequence:
Protein Accession #: NP_002629.1

45 1 11 21 31 41 51
MRASSFLIVV VPLIAGTLVL EAAVTGVPVK GQDTVKGKRP FNGQDPVKGQ VSVKGQDKVK 60
AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCGSGSG MACFVPPQ

50 Seq ID NO: 54 DNA sequence
Nucleic Acid Accession #: NM_019618
Coding sequence: 75-584

55 1 11 21 31 41 51
GGCAGGAGCC ACGATTCACT CCCCTGGACT GTAGATAAAG ACCCTTTCTT GCCAGGTGCT 60
GAGACAACCA CACTATGAGA GGCACTCCAG GAGACGCTGA TGGTGGAGGA AGGGCCGCTCT 120
ATCAATCAAT GTGTAAACCT ATTACTGGGA CTATTATAGA TTTGAATCAG CAAGTGTGGA 180
CCCTTCAGGG TCAGAACTTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAGTCACTG 240
60 TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT 300
ATTTGGGAAT CCAGAAATCCA GAAATGTGTT TGTATTGTGA GAAGGTTGGA GAACAGCCCA 360
CATTGCAGCT AAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCGGTGAAC 420
CCCTCCCTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCCTTC 480
CGGACTGGTT CATGCTCTCC TCCAAGAGAG ACCAGCCCAT CATTCGACT TCAGAACTTG 540
GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAACCTAG CTAAGAGGTG 600
65 GCAGCTTGGT CTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTTCTCT ACATTTCCT 660
AGTGTCAATT TCACGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720
TAATGAAGAA GAAGCAATTA CTTCATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA 780
GGAGAGCTGG GTGGTATAAG GCTGTCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT 840
70 CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900
TGAAGATGCT TCAGAGCTCA TGCGCGTTAC CCAAGATGGC ATGACTAGCA CAGAGCTGAT 960
CTCTGTTTCT GTTTTGTCTT ATTCCCTCT GGGATGATAT CATCCAGTCT TTATATGTG 1020
CCAATATACC TCAATTGTGT TAATAGAACC TTCTTAGCAT TAAGACCTTG TAAACAAAA 1080
TAATTCCTGT GTTAAGTTAA ATCAATTTTG TCCTAATTGT AATGTGTAAT CTTAAAGTTA 1140
75 AATAAACTTT GTGTATTAT ATAATAAAAA AAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:
Protein Accession #: NP_062564

80 1 11 21 31 41 51
MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGG NLVAVPRSDS VTFVTVAVIT 60
CKYPEALBQG RGDPIYLGIQ MPENCLYCEK VGEQPTLQLK BQKIMDLYG PEPVKPLFLY 120
RAKTGTSTL ESWAFPDWPI ASSKRDQPII LTSELGKSYN TAFELNIND

85 Seq ID NO: 56 DNA sequence
Nucleic Acid Accession #: NM_003125
Coding sequence: 65-334

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1      11      21      31      41      51
AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGSACCA GCCACTGTGG 60
5 CAGCATGAGT TCCCAGCAGC AGAAGCAGCC CTGCATCCCA CCCCCTCAGC TTCAGCAGCA 120
GCAGGTGAAA CAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCACTCCCA AAACCAAGGA 180
GCCCTGCCAC CCCAAGGTGC CTGAGCCCTG CACCCCAAAA GTGCTGAGC CCTGCCAGCC 240
CAAGCTTCCA GAGCCATGCC ACCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC 300
AGCACAGGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG 360
10 AGCCGGCCAC CAGATGCTGA ATCCCTATC CCATTCTGTG TATGAGTCCC ATTTGCTTTG 420
CAATTAGCAT TCTGTCTCCC CCAAAAAAGA ATGTGCTATG AAGCTTTCTT TCCTACACAC 480
TCTGAGTCTC TGAATGAAGC TGAAGTCTT AGTACCAGAG CTAGTTTTCA GCTGCTCAGA 540
ATTCACTCGA AGAGAGACTT AAGATGAAAG CAAATGATTC AGCTCCCTTA TACCCCATTT 600
15 AAATTCACTT TCAATTCCA

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Seq ID NO: 57 Protein sequence:
Protein Accession #: NP_003116

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1      11      21      31      41      51
MSSQQQKQPC IPPPQLQQQQ VKQPCQPPFQ EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK 60
25 LPEPCHPKVP EPCPSIVTPA PAQKTKQK

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Seq ID NO: 58 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71-2560

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1      11      21      31      41      51
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCGGTGCG GGCAGCTGCT TCACCCCTCT 60
30 CTCTGCAGCC ATGGGGCTCC CTGCTGGACC TCTCGGTCTC CTCTCCTTC TCCAGGTTTG 120
CTGGCTGAGC TGCGCGGCTC CCGAGCGGTG CCGGGCGGTC TTGAGGGAGG CTGAAGTGAC 180
35 CTTGAGGCGG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAGG TATTTCATGGG 240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGSAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
40 ATCCAAAGCT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
TGAAAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCAOGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
45 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGTCTT TTGGCCACGC TGTGTGAGAG AATGGTGCTC CAGTGGAGGA 660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAAGT 780
45 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
CCATAGCCAA GAACCAAGG ACCACACGCA CCTCATGTTC ACCATTCAAC GGAGCACAGG 900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAGAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGACATGG ATGGGGAGCG CTCACACACC ACGGCAGTGG CAGTAGTGGA 1020
50 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
GGCTGAGAAAT GATGAGGCGG ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGGCCC 1140
CAACTACCCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCAATT 1200
TACCATCACC ACCCAACCTG AGAGCAACCA GGGCATCCTG ACAACCAAGA AGGGTTTGA 1260
55 TTTTGAGGCC AAAAACCAGC ACACCCCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGCTCCAC GTGGAGGATG TGAATGAGGC 1380
ACCTGTGTTT GTCCCAACCT CAAAGTCTGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
60 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGSAG AATCAAAGA TCAGTACCG 1500
CATCTTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
TGTGGGCACC CTGAGCGGTG AGGATGAGCA GTTTGTGAGG AACCAACTCT ATGAAGTCAT 1620
GTCTTGTGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGTAAAC 1680
ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
65 CCRAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGAACAG GACCTGTCTC CCCACACCTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAAAGA 1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCCT AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
70 GTGGAACCTG CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
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GAGAAAGAGG CGGAAGATCA AGGAGCCCTC CTTACTCCCA GAAGATGACA CCCGTGACAA 2160
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GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGAAG TGGCACCAAC 2280
75 CATCATCCCG ACACCCAGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CCGCTAACAC AGACCCACCA GCCCGCCCTC ACGACACCTT 2400
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80 GAAGCTGGCA GACATGACG GTGGCGGGGA GGACGACTAG GCGGCTGACC TGCAGGGCTG 2580
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GACTTCGGAG CTGTGAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
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85 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGTGTGA ACTTAATTTT 2940
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GCTGGGCCCA CTGGCCGTCC TGCAATTCTG GTTTCAGAC CCAATGCGT CCAATTGGGA 3060
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTT TATTTCCCT 3120
90 GTTGGTGTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAAACT TTTCCAGAAA AAAAA

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Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

1 11 21 31 41 51
5 MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTL EA GGAEQEPGQA LGKVPWGCPG 60
QEPALFSTDN DDPTVRNGET VQERRSLKER NPLKIFPSKR ILRREKRDWV VAPISVPENG 120
KGPPFPQRLNQ LKSNCKDRDTK IFYSITGPGA DSPPEGVFAV EKETGMLLLN KPLDREIAK 180
YELFGBHVS NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSISQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
10 TDMDGDSGTT TAVAVVEILD ANDNAPMFDP QKYEAVPEN AVGEHVQRLT VTDLDAPNSP 360
AMRATYLMG GDDGDHFTIT THPESNQGI L TTRKGLDFEA KNQHTLYEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGFCV VYTAEDFDKE NQKISYRILR 480
DPAGWLAMPD DSQVTAAGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLD 540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSFHTSPFO AQLTDDSDIY WTAENVBEGD 600
15 TVVLSLKKFL KQDYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILFVL 660
GAVLALLFL LVLLLLVLRK RKIKEPLLLP EDDTRDNVYF YGEBGGGEED QDYDITQLHR 720
GLEARFEVVL RNDVAPTIIP TFMYPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVP 780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEED

20 Seq ID NO: 60 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 162-428

1 11 21 31 41 51
25 GGGTTCGGT GGGCGCGGAT TCGAACGTTT GGAAGGAGGT TTTTCTGCCT GAAGAAGCGT 60
CATACGGACC GGATTTGTTT CGCTGGCCCA GTGTCCCGG AGCTTGTGTG CGATACAGAG 120
AGCACCTCGG AAGCTGAGGC AGCTGGTACT TGACAGAGAG GATGGCGCTG TCGACCATAG 180
TCTCCACAGG GAAGCAGATA AAGCGGAAG CTCCCGCTGG CTTTCTAAGG CGAGTCTTCA 240
30 AGCGAAAGAA GCCTCAACTT CGTCTGGAGA AAAGTGGTGA CTTATTGGTC CATCTGAAGT 300
GTTTACTGTT TGTTCATCGA TTAGCAGAAG AGTCCAGGAC AAACGCTTGT GCGAGTAAAT 360
GTAGAGTCAT TAACAAGGAG CATGTACTGG CCGCAGCAAA GGTAATTCTA AAGAAGAGCA 420
GAGGTTAGAA GTCAAGAAGC ATATTCTTGA AAGTTATGAT GCATTCTTTT GGGTGGTAAAC 480
AGATCATAAA GACATTTTTT ACACATCAGT TAATATGGGA TTATTAAATA TTGG

35 Seq ID NO: 61 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
40 MALSTIVSQR KQIKRKAPRG FLKRVFKRKK PQLRLEKSGD LLVHLNCLLF VRLABESRT 60
NACASKRCVI NKEHVLAAAK VILKKSRR

45 Seq ID NO: 62 DNA sequence
Nucleic Acid Accession #: NM_000094.2
Coding sequence: 99-8913

1 11 21 31 41 51
50 GGGCTGGAGG GGGCGTGGGC TCGGACCTGC CAAGGCCACC GCAGGGGGGA GCAAGGGACA 60
GAGGCGGGGG TCCTAGCTGA CGGCTTTTAC TGCCTAGGAT GACGCTGCGG CTTCTGGTGG 120
CGCGCTCTG CGCGCGGATC CTGGCAGAGG CGCCCCAGT GCGAGCCGAC CACAGGGAGA 180
GAGTGACCTG CAGCGGCTTT TACGCGCTGC ACATTGTGTT CTTACTGGAT GGCTCCTCAT 240
CCATTGGCGG CAGCAATTTT CGCGAGTCC GCGAGCTTCT CGAAGGGCTG GTGCTGGCCT 300
55 TCTCTGGAGC AGCCAGTGCA CAGGGTGTGC GCTTTGCCAC AGTGCGATAC AGCGATGACC 360
CAGCGACAGA GTTCGGCTG GATGCACTTG GCTCTGGGGG TGATGTGATC CGCGCCATCC 420
GTGAGCTTAG CTACAAGGGG GSCAACACTC GCACAGGGGC TGCAATTCTC CATGTGGCTG 480
ACCATGTCTT CCTGCCCGAC CTGGCCGAGC CTGGTGTGCC CAAGGTCTGC ATCCTGATCA 540
CAGACGGGAA CTCACAGGAC CTGGTGGACA CAGCTGCCCA AAGGCTGAAG GGGCAGGGGG 600
60 TCAAGCTATT TGTGTGGGGG ATCAAGAATG CTGACCCCTG GAGGCTGAAG CGAGTTGCCCT 660
CACAGCAAC CTCCGACTTC TTCTTCTTGG TCAATGACTT CAGCATCTTG AGGACACTAC 720
TGCCCCCTGT TTCCCGGAGA GTGTGCAAGA CTGCTGGTGG CGTGCTGTG ACCCGACCTC 780
CGGATGACTC GACCTCTGCT CCAAGAGACC TGGTGTCTGC TGAGCCAGGC AGCCAACTCT 840
TGAGAGTACA GTGGACAGCG GCCAGTGGCC CTGTGACTGG CTACAAGGTC CAGTACACTC 900
65 CTCTGACGGG GCTGGGACAG CCACTGCCGA GTGAGCGGCA GGAGGTGAAC GTCCAGCTG 960
GTGAGACCAG TGTGCGGCTG CGGGTCTCC GGCCACTGAC CGAGTACCAA GTGACTGTGA 1020
TTGCCCTCTA CGCCAACAGC ATCGGGGAGG CTGTGAGCGG GACAGCTCGG ACCACTGCCC 1080
TAGAAGGGCC GGAAGTGAAC ATCCAGAATA CCACAGCCCA CAGCCTCCTG GTGGCCTGGC 1140
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70 CACAGCAGCA GGAGCTGGCG CTTGGGCAAG GTTCAGTGTG GCTGCGTGAC TTGGAGCCTG 1260
GCACGAGCTA TGAGGTGACC GTGAGCAACC TATTGTGCGG CAGTGTGGGG CCGGCCACTT 1320
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75 GCTACCAATT GAGTGGGCTG CAGCCGGGCA CTGAGTACCG CCTCACACTC TACACTCTGC 1560
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80 GCCTTAGCTA CACTGTGGGG GTGTCTGCTC GAGTGGGTCC CGGTGAGGGC AGTCCAGT 1860
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TGTCAGATGC AAGCGAGTGG AGGGTGGCCT GGGGACCGGT CCCTGGAGCC AGTGGATTTT 1980
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85 TGCGAGGAG AGAGGAGGGC CTTGCTGCAG TCATGTGGC TCGAACGGAC CCACTGGGCC 2160
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GGTTCCTGG CGCCACAGGA TACAGGGTTT CCTGGCACTC AGCCCAAGGC CCAGAGAAAT 2280

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CCCAGTTGGT TTCTGGGGAG GCCACGGTGG CTGAGCTGGA TGGACTGGAG CCAGATACTG 2340
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 GGGACCTGG AGAAGACGG AGGAAGGGAG AGAAAGGAGA TTCAGGCGCC TCTGGGAGAG 5700
 AAGGTCTGTA TGGCCCCAAG GGTGAGCGTG GAGCTCTTGG TATCCTTGA CCCCAGGGGC 5760
 CTCACGGCTT CCAAGGGCCA GTGGGCCCTC CTGGCCAGGG TTTTCTGTGT GTTCCAGGAG 5820
 GCAAGGGCCC CAGGGGTGAC GTGGGGGAGA CTGGATCCAA AGGGGAGCAG GGCCTCCCTG 5880
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	GTGATGTTGG	GAGTGCAGGA	CTAAGGGGTG	ACAAGGGAGA	CTCAGCTGTG	ATCTGGGGGC	7680
5	CTCCAGGGCC	ACGGGGTGCC	AAGGGGGACA	TGGGTGAACG	AGGGCTCGGG	GGCTTGATG	7740
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	AACCTGGTGC	AGCAGGGTGC	CCTGGTGACC	CGGGATCCCC	AGGAAAGGAT	GGAGTGCCCTG	7920
	GTATCCGAGG	AGAAAAAGGA	GATGTTGGCT	TCATGGGTCC	COGGGGCTCT	AAGGGTGAAC	7980
10	GGGGAGTGAA	GGGAGCCTGT	GGCCTTGATG	GAGAGAAGGG	AGACAAGGGA	GAAGCTGGTC	8040
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	CCGGAGAGAG	AGTGGTGGGG	GCTCCTGGGG	TCCCTGGAGC	TCCTGGCGAG	AGAGGGGAGC	8400
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	ATGACATCCG	GGGCTTTGTG	GGCCAAGAGA	TGAGTCAGCA	CTGTGCGCTG	CAGGGCCAGT	8520
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20	TCCATGCTGT	GCCTGTGCTC	CGCTCTCTC	ATGCAGAGGA	GGAAGAGCGG	GTAACCCCTG	8640
	AGGATGATGA	GTACTCTGAA	TACTCCGAGT	ATTCTGTGGA	GGAGTACCAG	GACCCCTGAG	8700
	CTCCTTGGGA	TAGTGATGAC	CCCTGTTCCC	TGCCACTGGA	TGAGGGCTCC	TGCACTGCCT	8760
	ACACCCCTGG	CTGTGATACC	CGGGCTGTGA	CAGGCAGCAC	AGAGGCGCTG	CACCCCTTTG	8820
	TCTATGTGTG	CTGTGGAGGG	AATGCCAACC	GTTTGGGAC	CGGTGAGGCC	TGCGAGCGCC	8880
25	GCTGCCACCC	CCGGGTGGTC	CAGAGCCAGG	GGACAGGTAC	TGCCCAAGAC	TGAGGCCCCAG	8940
	ATAATGAGCT	GAGATTGAGC	ATCCCTGGGA	GGAGTCGGGG	TCTCAGCAGA	ACCCCACTGT	9000
	CCCTCCCTTT	GGTGCTAGAG	GCTTGTGTGC	ACGTGAGCGT	GCGAGTGAC	GTCCGTATT	9060
	TCAGTGACTG	TGTCCTGGTG	GTCTAGCCTT	CCCCCTGTG	GACAAACCCC	CATTGTGGCT	9120
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Seq ID NO: 63 Protein sequence:
Protein Accession #: NP_000085.1

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40	AILLHVADHV	FLPLQARPGV	PKVCILITDG	KSQDLVDTA	QRLKGQGVKL	FAVGKKNADP	180
	EELKRVASQP	TSDFFFPVND	FSILRTLPL	VSRVCTTAG	GVFVTRPPDD	STSAFRLDLV	240
	SEPSQSLRV	QWTAAGSPVT	GKVKQYTPLT	GLGQPLPSE	QEVNVPAGET	SVRLRGLRPL	300
	TEQVTVIAL	YANSIGRAVS	GTARTALEG	PELTQNTTA	HSLLVANRVS	PGATGYRVTV	360
	RVLSSGPTQQ	QELPGQGSV	LLRDLEPGTD	YEVTVSTLFG	RSVGPATSLM	ARTDASVEQT	420
45	LRPVILGPTS	ILLSNLWVPE	ARGYRLWRR	ETGLEPPQKV	VLPSPDVTRYQ	LDGLQPGTGY	480
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	VRSTQGVERT	LVLPGSQATF	DLDDVQAGLS	YTVRVSAVVG	PREGSASVLT	VRRPEFETPLA	600
	VPGLRVVSD	ATRVRVWAGP	VPASGFRIS	WSTGSGPESS	QTLPPDSTAT	DITGLQPGTT	660
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	SVRVLTALVD	REGTFVSIIV	TTPPEAPPAL	GTLHVVRQGE	HSLRLRWEPV	PRAQGFLLHW	900
	QPBGGQQRSR	VLGPELSSVH	LDGLEPATQY	RVLRSVLGPA	GEGPSAEVTA	RTESFVRPSI	960
	ELRVVDTSID	SVTLAWTFVS	RASSYILSWR	PLRGPGQEV	GSPQTLPGIS	SSQRTVGLPE	1020
55	GVSYIFSLPT	VLDDVRGPEA	SVTQTFVCP	GLADVVLPH	ATQDNHRAE	ATRRVLERLV	1080
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	AHRYMLAPDA	PGRRQHVPGV	MVLLVDEFLR	GDIFSPIREA	QASGLNVVML	GMAGADPEQL	1200
	RRLAPGMDSV	QTFFAVDDGP	SLDQAVSGLA	TALCQASFTT	QPRPEPCFVY	CPKQKQKPG	1260
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	PGKKGKGDG	EDGAPGLPGQ	PGSPGEGQPR	GPPGAIGPKG	DRGFPGLGE	AGEKGERGPP	1500
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70	KGEQGLPGER	GLRGEPGSPV	NVDRLLETAG	IKASALREIV	ETWDESSGTF	LPVPERRRGP	1980
	KGDSGEGQFP	KGEPIGFPFG	ERGLKGRDGD	PGPQCPPLGA	LGERGPPGPF	GLAGEPKKPG	2040
	IPGLPGRAGG	VGEAGRPERG	GERGEKGERG	EQGRDGPPLG	PGTGPPGPP	GPXVSVDEPG	2100
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85	ADTAGSQLEA	VPVLRVSHA	EEERVPPEDD	EYSEYSEYSV	EYQDPEAPW	DSDDPCSLPL	2880
	DEGSCATYTL	RNYHRAVTGS	TEACHPFVYG	GCGGNANRFG	TREACERRCP	PRVVQSQGTG	2940
	TAQD						

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	CCCGCTGTAT	CGAGTCTCTG	GAGAACAAAG	TTCTGAGGCT	GTCTGGGGGA	CTGTGAGGTG	1320
	GAGGGGCGCT	CAACTGGGAG	GTACCGCTTT	GTCTGTGGCG	CTGTGGGTGT	CTGTCTACT	1380
	TCTGTGTCTG	GAAAGGGGTC	AAATCCACGG	GAAAGAGTGT	GTACTCTACT	GCTCATCTCC	1440
	CTACGTTGGT	CTGGTGGGTC	GTCTGGTGGC	GTGGAGTGTG	GCTGCTTGGC	CGCTGTGATG	1500
	GCATCATTTA	CTATCTCAAG	CCTGACTGGT	CAAAGCTGGG	GTCCCCCTAG	GTGTGGATAG	1560
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60	CCCTCTGTGT	TGGCCTCTGC	TGTCTCATOG	ATCTCTCCAT	GGTGACTGAT	GGCGGGATGT	2040
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5

Seq ID NO: 67 Protein sequence:
 Protein Accession #: NP_005620.1

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 65 GAATCTCGA GGCTCAAGCC CCCAGCCAAA GTAGGGGAGC TGGATTTCAG CCAAGTACAA 2100
 ACCTCCAGG GTGCTCTGA CCCCTTGCTT GACCCCTGCG GGCTGATGGA TCTCAGCACC 2160
 ACTCCCTTGC AAAGTGTCC CCCCTTGAA TCACCGCAA GGCTCCTCAG TTCAGAACCC 2220
 TTAGACCTCA TCTCGTCCC CTTTGGCAAC TCTTCTCCT CAGATATAGA CGTCCCCAAG 2280
 CCAGGCTCCC CGGAGCCACA GGTTCCTGCG CTTGCAGCCA ATGTTCTCT GACAGAGGCC 2340
 70 CTGGTCTCGG ACACAATGAA TGACAGCCTC AGCAAGATCC TGCTGGACAT CAGCTTCTCT 2400
 GGCTCGAGG AGGAGCCACT GGGCCCTGAC AACATCAACT GGTCCAGTT TATTCTGAG 2460
 CTACAGTAGA GCCTGCGCTT TGCCCTGTG CTCAAGCTGT CCACCATCCC GGGCACTCCA 2520
 AGGCTCAGTG CACCCCAAGC CTCTGAGTGA GGACAGCAGG CAGGGACTGT TCTGCTCCTC 2580
 ATAGCTCCCT GTGCCCTGAT TATGCAAAAG TAGCAGTCA ACCTAGCCA CTGCTGGGAC 2640
 75 CTTGTGTTCC CCAAGAGTAT CTGATTCTCT TGCTGTCCCT GCCAGGAGCT GAAGGGTGGG 2700
 AACAAACAAAG CCAATGGTGA AAAGAGATTA GGAACCCCCC AGCCTGTTTC CATCTCTGC 2760
 CCAGCAGTCT CTACCTTCC CTGATCTTTG CAGGGTGGTC CGTGTAAATA GTATAAATTC 2820
 TCCAAATAT CTCTAATTA TAAATGTAAG CTTATTCTCT TAGATCATT TCCAGAGACT 2880
 GCCAGAGGT GTGTAGGATG ACCTGGGGTT TCAATTGACT TCTGTTCCTT GCTTTTAGTT 2940
 80 TTGATAGAG GGAAGACCTG CAGTGCAAGG TTTCTTCCAG GCTGAGGTAC CTGGATCTTG 3000
 GGTCTCTCAC TGCAGGACCC CAGACAAAGT GATCTGCTTG CCAGAGTCTT TTTTGCCCT 3060
 CCTGCCCAC TCCCGTGTG TCCAAGTCAG CTTTCTCTGA AGAAGAAATC CTGTTAAAA 3120
 AAGTCTTTTG TATTTGGTCA GGAGTTGAAT TTGGGGTGGG AGGATGGATG CAACTGAAGC 3180
 AGAGTGTGGG TGCCAGATG TGGCTATTA GATGTTTCTC TGATAATGTC CCAATCATA 3240
 85 CCAGGGAGAC TGGCATTCAG GAGAACTCAG GTGGAGGCTT GAGAAGGCCG AAAGGGCCCC 3300
 TGACCTGCTT GCCTTCTTGA CTTTGGCCCT CAGCTTTGCA AAGAGCCACC CTAGGCCCCA 3360
 GCTGACCGCA TGGGTGTGAG CCAGCTTGAG AACACTAAT ACTCAATAAA AGCGAAGGTG 3420
 GACCNAAAAA AAAAAAAAAA AAAA

Seq ID NO: 69 Protein sequence:
Protein Accession #: NP_068772.1

5	1	11	21	31	41	51	
	MKASPRRLI	LKRRRLPLPV	QNAPSETSEE	EPKRSAPAQBE	SNQAEASKEV	AESNSCKCPA	60
	GIKIIINHPTM	PNTQVVAIFN	NANIHSIITA	LTAKGKESGS	SGPNKIFILIS	CGGAPTQPPG	120
	LRPQTQTSVD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	BQKRETCADG	EAAGCTINNS	180
10	LSNIQWLRLM	SSDGLGSRSI	KQEMEKEKNC	HLBQRQVKVE	EPSPRSASWQ	NSVSRPPYS	240
	YMAMIQFAIN	STERKRMRLK	DIYTWIEDHF	PYFKHIAKPG	WKNSIRHNLS	LHDMFVRETS	300
	ANGKVSFWTL	HPSANRYLTL	DQVFKPLDPG	SPQLPEHLES	QOKRPNFELR	RNMTIRTELP	360
	LGARRKMKPL	LPRVSSYLVF	IQFPVNQSLV	LQPSVKVPLP	LAASLMSEEL	ARHSKRVRIA	420
	PKVLLAEBGI	APLSSAGPGK	EELKLFGEFP	SPLLFVQTIK	EEZIQGEEM	PHLARPIKVE	480
15	SPPLEWPSFP	APSPKEESSH	SWEDSSQSPT	PRPKKSYSGI	RSPTRCVSEM	LVIQHRERRE	540
	RSRSRRKQHL	LPPCVDEPEL	LPSEGPSTSR	WAAELPPPAD	SSDPASQLSY	SQEVGGPFKT	600
	PIKETLPISS	TPSKSVLPRT	PESWRLTPPA	KVGGLDPSPV	QTSQASDPL	PDPLGLMDLS	660
	TTPLQSAFPL	ESQRLLSSE	PLDLISVPPG	NSSPSDIDVP	KPGSPPEQVS	GLAANRSLTE	720
20	GLVLDTWMS	LSKILLDISF	PGLDEDPLGP	DNINWSQFIP	ELQ		

Seq ID NO: 70 DNA sequence
Nucleic Acid Accession #: BC006529.1
Coding sequence: 178-2424

25	1	11	21	31	41	51	
	GGCAOGAGGG	GGACCCGGCC	GGTCCGGGCG	GAGCCCCCGT	CGGGGGCCCT	GGCTCGGCC	60
	CCAGGTGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGGG	GCGGCGACTG	120
30	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAAAACGAG	ATTCATAATG	180
	AAAACCTAGC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCC	TCCTGTTCAA	240
	AATGCCCAAA	CGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCCGCCCCA	ACAGGAGTCT	300
	AATCAAGCAG	AGGCTCTCAA	GGAAAGTGCA	GAGTCCAAC	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATT	TTAAACACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAA	420
35	GCTAAATATC	ACAGCACTAT	CACAGCACTG	ACTGCCAAGG	GAAAGAGAGG	TGGCAGTAGT	480
	GGGCCCAACA	AAATCATCTC	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
	CGGCTCTCAA	CCCAACACAG	CTATGATGCC	AAAAGGACAG	AAGTGACCTC	GGAGACCTTG	600
	GGACCAAAAC	CTGCAGTAG	GGATGTGAAT	CTTCCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
40	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACATATCA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGGAAAAGGA	GAATTGTAC	CTGGAGCAGC	GACAGGTAA	GGTTAGGAGG	840
	CCTTCGAGAC	CATCAGGTCT	CTGGCAGAAC	TCTGTGTCTG	AGCGGCCACC	CTACTCTTAC	900
	ATGGCCATGA	TACAATTCGC	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAGAC	960
45	ATCTATAGCT	GGATTGAGGA	CCACTTTCCT	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCCGCCACAA	CCCTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGCTGTCC	1080
	AATGGCAGGG	TCTCTCTCTG	GACCATTCAC	CCCAGTGCCA	ACCGCTACTT	GACATGGGAC	1140
	CAGGTGTITA	AGCAGCAGAA	ACGACCGAAT	CCAGAGCTCC	GCCGGAACAT	GACCATCAAA	1200
	ACCGAACTCC	CCCTGGGGCG	ACGGCGGAAG	ATGAAGCCAC	TGCTACCAAG	GGTCAGCTCA	1260
50	TACCTGGTAT	CTATCCAGTT	CCCGGTGAAC	CAGTCACTGG	TGTTGCAGCC	CTCGGTGAAG	1320
	GTGCCATTGC	CCCTGGGGCG	TTCCCTCATG	AGCTCAGAGC	TTGCCCGCCA	TAGCAAGCGA	1380
	GTCGCGATTG	CCCCCAAGGT	GCTGCTAGCT	GAGGAGGGGA	TAGCTCCTCT	TTCTTCTGCA	1440
	GGACCAAGGA	AAGAGGAGAA	ACTCCTGTTT	GGAGAAGGGT	TTTCTCCTTT	GCTTCCAGTT	1500
	CAGACTATCA	AGAGGAGGAA	AATCCAGCCT	GGGGAGGAAA	TGCCACACTT	AGCGAGACCC	1560
55	ATCAAGATGG	AGAGCCCTCC	CTTGGAAAGG	TGGCCCTCCC	CGGCCCCATC	TTTCAAGAGG	1620
	GAATCATCTC	ACTCTCTGGA	GGATTCTGCC	CAATCTCCCA	CCCCAAGACC	CAAGAAGTCC	1680
	TACAGTGGGC	TTAGTCTCCC	AACCGGTGT	GTCTCGGAAA	TGCTTGTGAT	TCAACACAGG	1740
	GAGAGGAGGG	AGAGGAGCCG	GTCTCGGAGG	AAACAGCATC	TACTGCTCTC	CTGTGTGGAT	1800
	GAGCCGGAGC	TGCTCTTCTC	AGAGGGGGCC	AGTACTTCCC	GCTGGGCGCG	AGAGCTCCCG	1860
60	TTCCAGCAG	ACTCTCTTGA	CCCTGCCTCC	CAGCTCAGCT	ACTCCAGGGA	AGTGGGAGGA	1920
	CCTTTTAAGA	CACCCATTAA	GGAAACGCTG	CCCATCTCCT	CCACCCCGAG	CAAACTCTGT	1980
	CTCCCCAGAA	CCCTCGAATC	CTGGAGGCTC	ACGCCCCCAG	CCAAAGTAGG	GGGACTGGAT	2040
	TTCCAGCCAG	TACAAACCCC	CCAGGGTGCC	TCTGACCCCT	TGCCTGACCC	CCTGGGGCTG	2100
	ATGGATCTCA	GCACCACTCC	CTTGCAAAAT	GCTCCCCCCC	TTGAATCACC	GCAAGGCTC	2160
65	CTCAGTTCAG	AACCCCTTGA	CCTCATCTCC	GTCCCTTTTG	GCAACTCTTC	TCCCTCAGAT	2220
	ATAGACGTCC	CCAAGCCAGG	CTCCCGGAG	CCACAGGTTT	CTGGCCTTGC	AGCCAATCGT	2280
	TCTCTGACAG	AAGGCTCTGT	CCTGGACACA	ATGAATGACA	GCCTCAGCAA	GATCCTGCTG	2340
	GACATCAGCT	TTCTGGCCTT	GGACGAGGAC	CCACTGGGCC	CTGACAACAT	CAACTGGTCC	2400
	CAGTTTATTC	CTGAGCTACA	GTAGAGCCCT	GCCCTTGCCC	CTGTGCTCAA	GCTGTCCACC	2460
70	ATCCCGGGCA	CTCCAGGCTT	CAGTGCAACC	CAAGCCTCTG	AGTGAGGACA	GCAGGCGAGG	2520
	ACTGTTCTGC	TCCTCATAGC	TCCTGCTGCG	CTGATTATGC	AAAAGTAGCA	GTCAACCCCT	2580
	AGCCACTGCT	GGGACCTTGT	GTTCGCCAAG	AGTATCTGAT	TCCTCTGCTG	TCCCTGCCAG	2640
	GAGCTGAAGG	GTGGGAACAA	CAAGGCAAT	GGTGAAAAGA	GATTAGGAAC	CCCCCGCCT	2700
	GTTTCCATTC	TCTGCCACAG	AGTCTCTTAC	CTTCCCTGAT	CTTTGCAGGG	TGGTCCGTGT	2760
75	AAATAGTATA	AAATCTCCAA	ATTATCTCTT	AAATATAAAT	GTAAGCTTAT	TTCTCTAGAT	2820
	CATTATCCAG	AGACTGCCAG	AAGTGGGTA	GGATGACCTG	GGGTTTCAAT	TGACTTCTGT	2880
	TCCTTGCTTT	TAGTTTGTAT	AGAAGGGAAG	ACCTGCAGTG	CACGGTTTCT	TCCAGGCTGA	2940
	GGTACCTGGA	TCTTGGGTTT	TTCACTGCAG	GGACCCAGAC	AAGTGGATCT	GCTTGCAGAG	3000
	GTCTTTTGTG	CCCTCCCTCG	CCACCTCCCG	GTGTTTCCAA	GTCACTTTTC	CTGCAAGAAG	3060
80	AAATCCTGGT	TAAAAAAGTC	TTTTGTATTG	GGTCAGGAGT	TGAATTGGGG	GTGGGAGGAT	3120
	GGATGCAACT	GAAGCAGACT	GTGGGTGCC	AGATGTGGCC	TATTAGATGT	TTCTCTGATA	3180
	ATGTCCCAAA	TCATACCAGG	GAGACTGGCA	TTGACGAGAA	CTCAGGTGGA	GGCTTGAGAA	3240
	GGCGGAAGGG	GCCCCGTACC	TGCTTGCTTT	CCTTAGCTTG	CCCCCTCAGT	TTGCAAGAGG	3300
	CCACCTAGG	CCCCAGCTGA	CCGCAATGGT	GTGAGCCAGC	TTGAGAACAC	TAACTACTCA	3360
85	ATAAAGCGCA	AGGTGGAATA	AAAAAATAAA	AAAAAATAAA			

Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

	1	11	21	31	41	51	
5	MKTSPPRPLI	LKRRRLPLPV	QNAFSETSEE	EPKRSPAQQE	SNQAEASKEV	AESNSCKFFA	60
	GIKIINHPTM	PNTQVVAIPN	NANIEHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
	LRPQTQTSYD	AKRTEVTLET	LGPKPAARDV	NLFRPPGALC	BQKRETCADG	BAAGCTINNS	180
	LSNIQWLIRM	SSDGLGSRSI	KQEMEKEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSRPPYS	240
	YMAIQFALN	STERKMTLK	DIYTWIEDHF	PYFKHIAKPG	WKNISIRENLS	LHDMFVRETS	300
10	ANGKVSFWTI	HPSANRYLTL	DQVFQKQKRP	NPELRNMTI	KTELPLGARR	KMKPLLPRVS	360
	SYLVPIQPFV	NQSLVLQPSV	KVPLPLAASL	MSSELAHRSK	RVRILAPKVL	AEEGIAPLSS	420
	AGPGKEEKLL	FGESFSPLLP	VQTIKEEETQ	PGEEMPHLAR	PIKVESPPLE	EWSPSPSPFK	480
	EESHSWEDS	SQSFTPRPKK	SYSGLRSPTR	CVSEMLVIQH	RERRERSRSR	RKQHLPLPCV	540
	DEPELLFSEG	PSTRMAAEL	PFPAOSSDPA	SQLSYSQSEVG	GPFTPIKET	LPISSTPSKS	600
15	VLPRTPESNR	LTPPAKVGGL	DFSPVQTFQG	ASDPLPDLG	LMDLSTTFLQ	SAPPLESPQR	660
	LLSSEPLDLI	SVPPGNSSPS	DIDVPKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSLKIL	720
	LDISFPGLE	DPLGPDNINM	SQPIPELQ				

Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

	1	11	21	31	41	51	
25	GGCACGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCC	60
	CCAGGTGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAAGCGCAG	ATTCTATAATG	180
	AAAACTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCTT	TCCTGTTCAA	240
30	AATGCCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCCTGCCCA	ACAGGAGTCT	300
	AATCAAGCAG	AGGCCTCCAA	GGAAAGTGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATT	TTAAACACCC	CACCATGCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAT	420
	GCTAATATT	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTTCATCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
35	CGGCCTCAAA	CCCAACACAG	CTATGATGCC	AAAAGGACAG	AAGTGACCTT	GGAGACCTTG	600
	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCTTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGGAAAAGGA	GAATTGTCTC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
40	CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGTCTG	AGCGGCCACC	CTACTCTTAC	900
	ATGGCCATCG	TACAATTCAC	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAGAC	960
	ATCTATAGCT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCGCGCACAA	CCTTTCCCTG	CAAGACATGT	TTGTCCGGGA	GACGTCTGCC	1080
	AATGGCAAGG	TCTCCTTCTG	GACCATTCTC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
45	CAGGTGTTTA	AGCCACTGGA	CCCAGGCTCT	CCACAATTGC	COGAGCACTT	GGAACTCACAG	1200
	CAGAAACGAG	CGAATCCAGA	GCTCCGCGCG	AACATGACCA	TCAAAACCGA	ACTCCCGCTG	1260
	GGCGCAACGG	GGAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCOCGG	TGAACAGCTG	ACTGGTGTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCGCTG	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCOG	CATTGCCCCC	1440
50	AAGGTTTTTG	GGGAACAGGT	GGTGTGTGGT	TACATGAGTA	AGTTCTTTAG	TGGGATCTGTG	1500
	CGAGATTTTG	GTACACCCAT	CACCAGCTTG	TTTAATTCTA	TCTTTCTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCTG	GACCAGGGAA	AGAGGAGAAA	1620
	CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGCATATCAA	GGAGGAAGAA	1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
55	TTGGAAAGAT	GGCCCTCCCC	GGCCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
	GATTGCTCCC	AATCTCCAC	CCCAAGACCC	AAGAAGTCTT	ACAGTGGGCT	TAGTCCOCCA	1860
	ACCCGCTGTG	TCTCGGAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
	TCTCGGAGGA	AACAGCATCT	ACTGCCCTCC	TGTGTGGATG	AGCCGGAGCT	GCTCTCTCTCA	1980
	GAGGGGCCCC	GTACTTCCCG	CTGGGCGCGA	GAGCTCCCGT	TCCAGCAGCA	CTCCTCTGAC	2040
60	CCTGCTCCCC	AGCTCAGCTA	CTCCAGGAA	GTGGGAGGAC	CTTTTAAGAC	ACCCATTAGG	2100
	GAAAGCTGCG	CCATCTCCTC	CACCCGAGC	AAATCTGTCC	TCCCGAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CGCCCCAGC	CAAAGTAGGG	GGACTGGATT	TCAGCCCATG	ACAACTCTCC	2220
	CAGGGTGCTT	CTGACCCCTT	GCCTGACCCC	CTGGGCTGTA	TGGATCTCAG	CACCACTCCC	2280
	TTGCAAAAGT	CTCCCCCTCT	TGAATCACCG	CAAAGGCTCC	TCAGTTTACA	ACCTTAGAGC	2340
65	CTCATCTCCG	TCCCCCTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
	TCCCGGAGC	CACAGGTTTC	TGGCCTTGCA	GCCAATCGTT	CTCTGACAGA	AGGCTTGCTC	2460
	CTGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGCTGG	ACATCAGCTT	TCCTGGCCTG	2520
	GACGAGGACC	CACTGGGCCC	TGACAAATC	AATGGTCCCC	AGTTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
70	AGTGACCCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTTCTGCT	CCTCATAGCT	2700
	CCCTGCTGCC	TGATTATGAC	AAAGTAGCAG	TCACACCCCTA	GCCACTGCTG	GGACCTTGTG	2760
	TTCCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAC	2820
	AAAGGCAATG	GTGAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGCA	2880
	GTCTCTTACC	TTCCCTGATC	TTTGAGGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
75	TTATCTCTTA	ATTATAAATG	TAAGCTTATT	TCCTTAGATC	ATTATCCAGA	GACTGCCAGA	3000
	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCTTGCTTTT	AGTTTGTATA	3060
	GAAGGGAAGA	CCTGAGTGC	ACGGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
	TCAGTGCAGG	GACCCAGACA	AGTGGATCTG	CTTGCCAGAG	TCTTTTTCG	CCCTCCCTGC	3180
	CACCTCCCCG	TGTTTCCAG	TCAGCTTCC	TGCAAGAGA	AATCCTGTTT	AAAAAAGTCT	3240
80	TTTGATTAGG	GTGAGGAGTT	GAATTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
	TGGGTGCCCA	GATGTGCCCT	ATTAGATGTT	TCTCTGATAA	TGCCCCCAAT	CATACGAGGG	3360
	AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCTTGACCT	3420
	GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAGAGAG	CACCTAGGCC	CCAGCTGAC	3480
85	CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACCTACTCA	TAAAAGCGAA	GGTGGACAAA	3540
	AAAAAAAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1

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1      11      21      31      41      51
5      |      |      |      |      |
      MKTSPPRLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNOAEASKEV AESNSCKFPA 60
      GIKRIINHPTM PNTQVVAIPN MANIHSIITA LTAKGKESGS SGPNNKFILIS CGGAPTQPPG 120
      LRPTQTSTYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
      LSNIQWLRIM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPVYS 240
      YMAIQTAFIN STERKMTLK DIYTWIEDHF PYFKHIAKPG WKNISIRHNS LHMDFVRETS 300
      ANGKVSFWTI HPSANRYLTL DOVFVKPLDPG SPQLPEHLES QQRFPNPELR RNMTIKTEL 360
10     LGARRRMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASIMSSEL ARHSKRVRIA 420
      PKVFGQVVF GYMSKFSSGD LEDFGTPITS LFNFIPLCLS VLLAEEGIAP LSSAGPGKEE 480
      KLLFGBGFPF LLPVQTIKEE EIQPGGEEMPH LARPIKVESP PLEWPSAP SPKEESSHW 540
      EDSSQSPTFR PKKSYSGLR SPTCVSEMLV IQHRRRERS RSRRQHLLP PCVDEPELLP 600
      SEGPSTSRWA AELPFPADSS DPASQLSYSQ EVGGPFKTP I KETLPISSPT SKSVLPRTPE 660
15     SWRLTPPARV GGLDFSPVQT SQGASDPLPD FLGLMDLSTT PLQSAPPLES PQRLLSSEPL 720
      DLISVPFGNS SPSPIDVFKP GSPEPQVSGL AANRSLTEGL VLDTMNDSLS KILLDISFPG 780
      LDEDPLGPDN INWSQIPEL Q

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20 Seq ID NO: 74 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

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25     1      11      21      31      41      51
      |      |      |      |      |
      GGGAGAGCC AGGCTGAGCC TTATAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
      TCATCCTTCT ACTCGTGAGC CTTCCAGCT CTGGCTTTT GAAAGCAAAG ATGAGCAACA 120
      CTCAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGT TCACAAATAC ACCGAGCGTG 180
      ATGACAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
      TTAGTGCTCT TGACAAAAG GGCACAAAT ACCTCGCGA TGTCTTTGAG AAAAAGGACA 300
30     AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTGCTGGGA GACATAGCCA 360
      CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCCTGTT CCGGGGCAGC CAGTGAOCCA 420
      GCCCCACCAA TGGGCTTCCA GAGACCCAG GAACAATAA ATGTCTTCTC CCACCAGA

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35 Seq ID NO: 75 Protein sequence:
Protein Accession #: Eos sequence

```

40     1      11      21      31      41      51
      |      |      |      |      |
      MSNTQAERSI IGMIDMFHYK TRDDKIEKP SLLTMKENF PNFLSACDKK GTNYLADVFE 60
      KDKKNEDKKI DFSEPLSLLG DIAADYHKQS HGAAPCSGGS Q

```

45 Seq ID NO: 76 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

```

50     1      11      21      31      41      51
      |      |      |      |      |
      GGGAGAGCC AGGCTGAGCC TTATAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
      TCATCCTTCT ACTCGTGACA CTTCCAGTT CTGGCTTTT GAAAGCAAAG ATGAGCAACA 120
      CTCAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGT TCACAAATAC ACCGAGCGTG 180
      ATGGCAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
      TCAGTGCTCT TGACAAAAG GGCATACATT ACCTCGCCAC TGTCTTTGAG AAAAAGGACA 300
      AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTGCTGGGA GACATAGCGG 360
55     CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCCTGTT TGGGGGAAGC CAGTGAATCCA 420
      GCCCCACCAA GGGGCTTCCA GAGACCCAG GAACAATAAG TGTCTCTCTC CACCAGA

```

60 Seq ID NO: 77 Protein sequence:
Protein Accession #: XP_048124.1

```

65     1      11      21      31      41      51
      |      |      |      |      |
      MSNTQAERSI IGMIDMFHYK TGRDGKIEKP SLLTMKENF PNFLSACDKK GIHYLATVFE 60
      KDKKNEDKKI DFSEPLSLLG DIAADYHKQS HGAAPCSGGS Q

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70 Seq ID NO: 78 DNA sequence
Nucleic Acid Accession #: Z73678.1
Coding sequence: 251-2433

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75     1      11      21      31      41      51
      |      |      |      |      |
      GGGGTGTCG AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TCGCCAGTGC 60
      CAGAGAGGGA CGAACCAGGG TGGAAAGGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
      CCTGCACTC TATGGCCGTA GGGAGCGGCT GAGAGCGAGA AGAGCAAGCT CTGCGCGGCC 180
      CGCTGCACCG CACCTGCGCT CGCCTCTCTG CTCTCTTAGG CCGCGGCGCG GCGCCACCGG 240
      CCTCCGCGCA CCATGAACCA CTCGCGGCTC AAGACCGCT TGGCGTACGA ATGCTTCCAG 300
      GACCAGGACA ACTCCAGGTT GGCTTTGCGG TCGGACCAAA AGATGAATAA AGGCAGTCT 360
      GGCAAGGAGC GCGTGAGGA GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAGTCT 420
80     TCCAGTGTG CCACCTGAG CCACTCCAAT CGAGGTTCCT TGTATGATGG CTTGGCTGAC 480
      AATTACACT ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCT GGCAGGGAAT 540
      GGCTCATGGG GATATCGAT CTACAAATGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
      TTCAGCTCTT ACAGCCAGAT GGAGAACTGG AGCGGCACT ACCCGCGGG CAGCTGTAA 660
      ACCACGCGCG CAGGCAGGCA CATCTGCTTC ATGCAGAAAA TCAAGGCGAG CCGCAGTGA 720
85     CCGACCTCT ACTGTGACCC ACGGGGCACC CTGGGCAAGG GCAAGCTGGG CAGCAAGGGC 780
      CAGAAGACCA CCGAGAACCG CTACAGCTTT TACAGCACT GCAAGTGTCA GAAGGCCATA 840
      AAGAAGTGCC CTGTGCGGCC GCCCTCTGT GCCTCCAAGC AGGACCTGT GTATATCCG 900

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	CCCATCTCCT	GCAACAAGGA	CCTGTCCTTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
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	CAGGATGAGA	AGTACCAAGC	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACCAGAACGT	CCAGCAGGCC	GCGGCAGGGG	OCCTGCGCAA	CCTGGTGTTC	1200
	AGGAGCAGCA	CCACAAAGCT	GGAGACCCGG	AGGCAGAAATG	GGATCCGCGA	GGCAGTCAGC	1260
	CTCCTGAGGA	GAACCGGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTGTCTTCCA	CTGACGAGCT	GAAGGAGGAA	CTCATTTGCG	ACGCCCTGCC	TGTTCTGGCC	1380
	GACCGGTCGA	TCAITTCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
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	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GAAGACAAGT	CTGTGGAAAA	CTGCATGTGT	1620
	GTCTCTGCAC	ACCTCTCTCA	CGCCTGGGAC	GCGCAGGTGC	CCACCCGCTA	CGCCAGCTCG	1680
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	AAGGGCAGCG	GCTGTTTGTG	CCATTTCAGT	GGCATTCGCA	CCTACCTGAA	CCTCATGGGC	1860
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	AGCAAGGGGC	TGATGTCCAG	TGGCATGAGC	CAGTTGATTG	GGCTGAAGGA	AAAGGGCCTG	1980
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20	CTCCTGAGCA	ACATGTCCCG	CCACCCCTCT	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTT	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCGCCAC	ACTGGCAATA	CCAGCAACTC	CGAAGACATC	2160
	TTGTCTCGG	CTGTCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAA	2220
	CAGTACTTCT	CCAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCGGAAG	CAGTGCTCTA	2280
	CCCAAGGCGG	CAGAAGCTGC	CCGGCTCTCT	CTGTCTGACA	TGTGGTCCAG	CAAGGAACCT	2340
25	CAGGGTGTTC	TGAGCAGCA	AGGTTTGGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACTTCA	CTCCGATTC	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCCAG	CTCAGGCCCT	GCTGGATGGG	GTTTCTGTGC	2520	
	CATCCTGTGC	AGTATTGTGG	AAAGTTCA	AGAAACTGAG	AAGAAACCTA	AAACTGTGG	2580
	ATAGTGGAAA	GATTTTGTAG	TTTTTTTTTT	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
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	GCGTGCAAGT	GTTGTGTGTG	GAGTGTCTTA	AAGCATAACC	ACAACTGCA	AAAAGCTAGG	2820
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	AGTGGTCTCC	AAGGGTGCAG	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	GCCTTCCAGT	AAGGGAGGTC	TGTTGTATCT	CATGGGAGAA	TCTGGGGTGT	CTGTAGTGTG	3120
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40	AGGACACTCT	CGCATCTTTT	GCCAAATGAG	GCCTGTCTAG	AGGAGTAGGA	GCTGAAAGAT	3240
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	TGCATTGAGA	GGTCTGTGTA	TCTACTTGT	GCGAGAGAAA	GAAGGTAAAA	AATGATTTTT	3360
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45	GTGGATGGA	GTGCGGGTAT	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGTCTGT	3540
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	AGGAAGGGA	AGTGCCATAT	CAGGGTACCG	GTACCGGCAA	GCTCACATCT	CAGCCAGGGG	3660
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	TCTCTAGAAG	AATATAAGAT	GCTCCTCCTC	CTCACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCCTCTTCTG	CACCACCCCC	GAGTCCAAAC	CCACCTCTTG	CCCCAGCAAT	CAGGCTGGAA	4080
55	AACACTGATG	TGGAGCTACT	ATGACAACTG	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCTCCGGA	GAGGTGTCCC	CGGCTGTTAG	CCAGCTGTGC	TGTGGTCTGT	TGGGTCTGTC	4200
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65	CCCTGCCCCG	GGAAACAGGC	AGCCTTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
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	ATTGGCCTCA	CATAGCCCTA	GGCCAATGCC	CAAAATAAGG	AGTTCCAAAT	TGGGGCCAAA	4980
70	TGAGGAAGGA	CACAGACTCT	GCCCTGGGAT	CTCCTGTGCT	AGCGGCCAAT	GACAAATCCA	5040
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	ACTGGCTGGG	AGGACCAAGA	CTGGGGCTGG	GSTGGGCAGG	GAAGGGAGGC	CGGGGGCTGC	5220
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Protein Accession #: CAA98022.1

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85	QNRYSFYTC	SGQKAIKCP	VRPPSCASKQ	DPVYIPFISC	NKDLSPGHSR	ASSKICSEDI	240
	ECSGLTIPKA	VQYLSSQDEK	YQAIGAYYIQ	HTCFQDESAK	QVYQLGGIC	KLVDLLRSPN	300
	QNVQAAAGA	LRNLVPRSTT	NKLETRRONG	IREAVSLRR	TGNAEIQRL	TGLLWNLSTT	360

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RNAYTEKST GCFPNKSKDM MNNDYDCPLP EEBTNPKGSG WLYHSDAIRT YLNLWKGSKK 540
DATLEACAGA LQNLTASKGL MSSGMSQLIG LKEKGLPQIA RLQSGNSDV VRSGALLSN 600
MSRHPLLHRV MGNQVFPBVT RLLTSHTGNT SNSEDILSSA CYTVRNLMAS QPQLAKQYFS 660
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65 Seq ID NO: 81 Protein sequence:
Protein Accession #: NP_006507.1

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	CNLEGGPPINS	SVFKEYAGSM	GESCGGLWLA	ILLLLASIAA	GLSL		

Seq ID NO: 84 DNA sequence
Nucleic Acid Accession #: NM_022893.1
Coding sequence: 229-2726

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	TTTTCTCTGG	AGTCTCTCTC	TTTCTAACCC	GGCTCTCCCG	ATGTGAACCG	AGCCGTCTGT	180
	CGCCGCGCGC	CGCGCGCGCC	GCGCGCGCGC	CCCGCCCGCG	AGCCCAACAT	GTCTGCGCGC	240
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	GATGAGCCCA	GGAACAATG	ATGTACAAC	TGCAAAACAG	CATTACCCAG	TGATGGTTT	780
	CTCTTGCAAC	AGCAACAGAA	CATCATGGA	TTAAGAACT	ACTTAGAAAG	CGAACACGGA	840
	AGTCCCTTGA	CCCGCGGGT	TGGTATCCCT	TCAGGACTAG	GTGCAGAAAT	TCCTTCCAG	900
55	CCACCTCTCC	ATGGGATTTA	TATTGACAG	AATAACCCCT	TTAACTGTCT	AAGAATACCA	960
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	GAAGAAATGG	CCCTGGCCAC	CCATCACCGG	AGTGCCTTTG	ACAGGGTGCT	GCGGTGAAT	1140
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	TCGGTGGTGG	CCAAGTTCAA	GAGCGAGAAC	GACCCCAACC	TGATCCCGGA	GAACGGGGAC	1680
	GAGGAGGAGG	AGGAGGACGA	CGAGGAAGAG	GAAGAAAGAG	AGGAAGAGGA	GGAGGAGGAG	1740
	CTGACGGAGA	GCGAGAGGGT	GGACTACGGC	TTGGGGCTGA	GCCTGGAGGC	GGGCGGCCAC	1800
	CACGAGAACA	GCTCGCGGGG	CGCGTGGTGG	GGCGTGGGGG	ACGAGAGCCG	CGCCCTGCC	1860
70	GACGTATGCG	AGGGCATGGT	GCTCAGCTCC	ATGCAGCACT	TCAGCGAGGC	CTTCCACAG	1920
	GTCTTGGGGG	AGAAGCATAA	GCGCGGCCAC	CTGGCGGAGG	CCGAGGGGCA	CAGGGACACT	1980
	TGCGACGAAG	ACTCGGTGGC	CGCGAGTTCG	GACCGCATAG	ACGATGGCAC	TGTTAATGGC	2040
	CGCGGCTGCT	CCCGGGGCGA	GTGGGCTCTG	GGGGGCTCTG	CCAAAAGCT	GCTGCTGGGC	2100
75	AGCCCGACCT	CGCTGAGCCC	CTTCTCTAAG	CGCATCAAGC	TCGAGAAGGA	GTTGACCTTG	2160
	CCCGCGGCCA	CGATGCCCAA	CACGGAGAAC	GTGTACTGCG	AGTGGCTGCG	CGGCTACGCG	2220
	GCTCCAGGAG	AGCTCAAGCA	TCCCTTCTTT	AGCTTGGGAG	ACTCCAGACA	ATCGCTTTT	2280
	GCCTCTCTGT	CGGAGCACTC	CTGGGAGAAC	GGGAGCTTGC	GCTTCTCCAC	ACCGCCCGGG	2340
	GAGCTGGAGC	GAGGGATCTC	GGGGCGCAGC	GGCACGGGAA	GTGGAGGGAG	CAOCCCCCAT	2400
80	ATTAGTGGTC	CGGGCAGGGG	CAGGCCACGG	TCAAAAGAGG	GCAGACGCGC	CGACACTTGT	2460
	GAGTACTGTG	GGAAAGTCTT	CAAGAACTGT	AGCAATCTCA	CTGTCCACAG	GAGAAGCCAC	2520
	ACGGGCGAAA	GGCCTTATAA	ATGCGAGCTG	TGCAACTATG	CCTGTGCCCA	GAGTAGCAAG	2580
	CTCACACAGC	ACATGAAAC	GCATGGCCAG	GTGGGGAAGG	ACGTTTACAA	ATGTGAAATT	2640
	TGTAGATGTC	CTTTTAGCGT	GTACAGTACC	CTGGAGAAAC	ACATGAAAAA	ATGGCACAGT	2700
85	GATCGAGTGT	TGAATAATGA	TATAAAAACT	GAATAGAGGT	ATATTAAATC	CCCTCCCTCA	2760
	CTCCCACTGT	ACACCCCTTT	TTTCAACACT	CCCTTTCCCT	ATCGCCCTCC	AGCCCACTC	2820
	CTGTAGAGAT	TTTTTCTTAG	TCCCATGTGA	TTTAAACAAA	CAACAAACAA	AACAGAAGTA	2880
	ACGAAGCTAA	GAATATGAGA	GTGCTTGTCA	CCAGCACACC	TGTTTTTTTT	CTTTTCTTTT	2940
	TTCTTTTCTT	TTTTTCTTTT	TTTTTTTTTT	TCCTTTATGT	TCTCACCGTT	TGAATGCATG	3000

	ATCTGTATGG	GGCAATACFA	TTGCATTTTA	GGCAAACTTT	GAGCCTTTCT	CTTGTGCAAT	3060
	AATTACATG	TTGTGTATGT	TTTTTTTAA	ACITAGACAG	CATGTATGGT	ATGTTATGGC	3120
	TATTTTAAAT	TGTCCTTAAT	TCGTTGCTGA	GCAAAACATGT	TGCTGTTTCC	AGTTCGGTTC	3180
5	TGAGAGAAA	AGAGAGAGAG	AGAGAAAAAG	ACCATGCTGC	ATACATTCTG	TAATACATAT	3240
	CATGTACAGT	TTTATTTTAT	AACGTGAGGA	GGAAAAACAG	TCTTTGGAIT	AACCCCTCTAT	3300
	AGACAGAATA	GATAGCACTG	AAAAAAATC	TCTATGAGCT	AAATGTCTGT	CTCTAAAGGS	3360
	TTAAATGTAT	CAATTGGAAA	GGAGAAAAAA	AGGCCTTGAA	TTGACAAATT	AACAGAAAAA	3420
	CAGAACAGT	TTATTCATAT	ATTGGGTTT	AAAAATATGAG	TGCGTTGGAT	CTATTAAAC	3480
	CACATGATG	GTTCTTCTAT	CTTGTATATA	ACTTGTAGCT	TAATTCAGCA	TTGGGTGAGS	3540
10	TAATAAACCT	TAGGAACCTAG	CATATAATTC	TATATTGTAT	TTCTCACAA	AATGGCTACC	3600
	TAAAAAGATG	ACCCATTATG	TCCTAGTTAA	TCATCATTTT	TCCTTTAGTT	TAATTTTATA	3660
	AACAAAACCTG	ATTATACCA	TATAAAGCT	ACTTTGCTCC	TGGTGAGAGC	TAAAAAGAAA	3720
	TGGGCTGTTT	TGCCAAAGT	TTTATTTTT	TTAAACAATG	ATTAAATTGA	ATGTGTAATG	3780
	TGCAAAAGCC	CTGGAACCA	ATTAAATACA	CTAGTAAGGA	GTTTCAITTTA	TGAAGATATT	3840
15	TGCTTTAATA	ATGTCTTTTT	AAAAAATCTG	GCACCAAAAG	AAATAGATCC	AGATCTACTT	3900
	GTTTGTCAAG	TGGACAATCA	AATGATAAAC	TTTAAGACCT	TGTATACCAT	ATTGAAAGGA	3960
	AGAGGCTGAC	AATAAGGTTT	GACAGAGGGG	AACAGAAAG	AATAATATGA	TTTATTAGCA	4020
	CAAGCTGGTA	CTATTTGCCA	TTTAAACTA	GAACAGGTAT	ATAAGCTAAT	ATTGATACAA	4080
	TGATGATTAA	CTATGAATTC	TAAAGACTTG	CATTTAAATG	TGACATTCTT	AAAAAAGAA	4140
20	GAGAAAGAA	TTTAAGAGTA	GCAGTATATA	TGCTGTGTCT	CCCTAAAGT	TGTACTTCAT	4200
	TTCTTTTCCA	TACACTGTGT	GCTATTGTG	TAAACATGGA	AGAGGATTCA	TGTGTTTTAT	4260
	TTTTATTTTT	TTAATTTTT	CTTTTTTAT	AAGCTAGCAT	CTGCCCCAGT	TGGTGTTC	4320
	ATAGCACTTG	ACTCTGCTG	TGATATCTGT	ATCTTTTCTC	TAATCAGAGA	TACAGAGGTT	4380
25	GAGTATAAAA	TAAACCTGCT	CAGATAGGAC	AATTAAGTGC	ACTGTACAAT	TTTCCAGTT	4440
	TACAGTCTA	TACTTAAGGG	AAAAGTTGCA	AGAAATGCTGA	AAAAAAATG	AACACAATCT	4500
	CATTGAGGAG	CATTTTTTAA	AACTAAAAA	AAAAAAACT	TTGCCAGCCA	TTTACTTGAC	4560
	TATTGAGCTT	AATTACTTGG	ACGCAACAT	GCAAGCGCTG	TGAATGGAAA	CAGAATACAC	4620
	TTAACATAGA	AATGAATGAT	TGCTTTCTGCT	TCTACAGTGC	AAGGATTTTT	TTGTACAAA	4680
30	CTTTTTTAAA	TATAAATGTT	AAGAAAAAT	TTTTTTTAAA	AACACTTCAT	TATGTTTAGG	4740
	GGGGAACCTG	ATTTTAGGGT	TCCATTGCT	TGGTGGTGT	ACAAGACTGT	TTATCCATT	4800
	AAAAATGGTA	GTGGAAATTC	TATGCCCTGG	ATACACACCG	CTCTTCAGGT	TGTAAAAAAA	4860
	AAAAACATAC	ATTGGGGAAA	GGTTTAAGAT	TATATAGTAC	TAAATATAG	GAAAAATGCAC	4920
	ACTCATGTTG	ATTCCATATG	TAAATACAT	TTATGGTCTT	TTTTCTGTAT	TTCTAGAATG	4980
35	GTATTTGAAT	TAAATGTTCA	TCTAGTGTTA	GGCACTATAG	TATTTATATT	GAAGCTTGTA	5040
	TTTTTAACTG	TTCTGTGTT	TCCTTAAAGS	TATCAATGTA	CCCTTTTGG	TAGTGGAAAA	5100
	AAAAAAGACA	GGCTGCCACA	GTATATTTTT	TAAATTTGGC	AGGATAATAT	AGTGCAAAAT	5160
	ATTTGTATGC	TTCAAAAAA	AAAAAAGAG	AGAAACAAA	AAGTGTGACA	TTACAGATGA	5220
	GAAGCCATAT	AATGGCGGTT	TGGGGGAGCC	TGCTAGAATG	TCACATGGAT	GGCTGTCTATA	5280
40	GGGGTGTATC	ATATCTCTTT	TTGTTCTCTT	TTCTGCTGTC	CATCTGTAT	GCAGTACTGC	5340
	AAGCTAATAA	CGTTGTTTGG	TTATGTAGTG	TGCTTTTGT	CCCTTTCTCT	CTATCACCCCT	5400
	ACATTCACGC	ATCTTACCTT	CATATGCGAT	AAAGAAAGA	AAGAAAAAAA	AAGGAAAAAA	5460
	AAAAAAAAC	CAATGTTTGG	CAGTTTTTTT	CATTGCCAAA	AACTAAATGG	TGCTTTATAT	5520
	TTAGATTGGA	AAGAATTTCA	TATGCAAGC	ATATTAAAGA	GAAAGCCCGC	TTTAGTCAAT	5580
45	ACTTTTTTGT	AAATGGCAAT	GCAGAATATT	TTGTTATTGG	CCTTTTCTAT	TCCTGTAATG	5640
	AAAGCTGTTT	GTCTGAACCT	GAAATTTTAT	CTTTTACTAT	GGGAGTCACT	ATTTATTATT	5700
	GCTTATGTGC	CCTGTTCAAA	ACAGAGGCAC	TAAATTTGAT	CTTTTATTTT	TCCTTGTGTT	5760
	TATTTTTTTT	TTTATTTAGA	TGACCAAAGS	TCATTACAAC	CTGGCTTTTT	ATTGTATTG	5820
	TTTCTGCTCT	TTGTTAAGTT	CTATTGGA	AACCACTGTC	TGTGTTTTTT	TGGCAGTTGT	5880
50	CTGCATTAA	CTGTTTATAC	ACCCATTTTG	TCCCTTTTAT	GAAAAAATAA	AAAAAATTAA	5940

Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

55	1	11	21	31	41	51	
	MSRRKQKGPQ	HLKREPSPE	PLEAILTDDE	PDHGPLGAPE	GDRLLLTCGQ	QMNFFPLGDI	60
	LIFIEKRKQ	CNGSLCLBKA	VDKPPSPSP	EMKKAENPVE	VGIQVTPEDD	DCLSTSSRI	120
60	CPKQELIADK	LLHWRGLSSP	RSAGHALIPT	PGMSAEYAPQ	GICKEPSSY	TCTTCRQFFT	180
	SAWFLIQAQ	NTHGLRIYLE	SEHGSPLTPR	VGIPSLGLAE	CPSQPLHGI	HIADNPFNL	240
	LRIFGVSRE	ASGLAEGRFP	PTPPLFSPPP	RHHLDPHRIE	RLGAEEMLA	THHPSAFDRV	300
	LRLNPMAMEP	PAMDFSRRLR	ELAGNTSSPP	LSPGRPSFMQ	RLQLPFPQGS	KPPFLATPPL	360
	PPLQSAPPSS	QPPVKSKECE	FCGKTFKQFS	NLVVHRRSHT	GEKPYKCNLC	DHACTQASKL	420
65	KRMKTHMHK	SSPMTVKSDD	GLSTASSPEP	GTSDLVGSAS	SALKSVVAKF	KSENDPNLIP	480
	ENGDEEEEEE	DEEEEEE	EEBELTESER	VDYGFGLSLE	AAREHENSRR	GAVVGVGDES	540
	RALPDMVQM	VLSSMQHFSE	APHQVLGEKH	KRGHLAEAG	HRDTCDEDSV	AGESDRIDDG	600
	TVNRRGCSFG	ESASGGLSKK	LLLGSPSSLS	PFSKRIKLEK	EPDLPPATMP	NTENVYSQWL	660
	AGYAAARQLK	DPFLSPGDSR	QSPFASSEH	SENGSLRFS	TPPGELDGGI	SGRSGTSGSG	720
70	STPHISGPGT	GRPSSKEGRR	SDTCEYCGKV	FKNCSNLTVA	RRSHTGERPY	KCELCLNYACA	780
	QSSKLTRMK	THGQVGKDVY	KCEICKMPFS	VYSTLEKHMK	KWHSRVLNAN	DIKTE	

Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53-1576

75	1	11	21	31	41	51	
	GCTCGCTGGG	CCGCGGCTCC	CGGGTGTCCC	AGGCCCGGCC	GGTGCAGAGA	GCATGGCGGG	60
80	TGCGGGCCCG	AAGCGGCGCG	CGCTAGCGGC	GCGGCGGGCC	GAGGAGAAAG	AAGAGGCGCG	120
	GGAGAAGATG	CTGGCGCGCA	AGAGCGCGGA	CGGCTCGCGG	CCGCGAGGCG	AGGGCGAGGG	180
	CGTGACCTTG	CAGCGGAACA	TCACTGTGCT	CAACGGCGTG	GCCATCATCG	TGGGGACCAT	240
	TATCGGCTCG	GGCATCTTGG	TGACGCCAC	GGGCGTGCTC	AAGGAGGCGG	GCTCGCGGGG	300
	GCTGGCGCTG	GTGGTGTGGG	CGCGTGCGGG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
85	CGCGGAGCTC	GGACACCA	TCTCCAAATC	GGGCGGCGAC	TACGCTACCA	TGCTGGAGGT	420
	CTACGCTCG	CTGCGCGCTC	TCTCTAAGCT	CTGATCGAG	CTGCTCATCA	TCCGCGCTTC	480
	ATCGCAGTAC	ATCGTGGCCC	TGGTCTTCCG	CACCTACCTG	CTCAAGCGCG	TCTTCCCCAC	540

CTGCCCGGTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGGGTGC TGCTGCTCAC 600
GGCCGTGAAC TGCTACAGCG TGAAGGCGCG CACCGGGTGC CAGGATGCCT TTGCCGCGCG 660
CAAGCTCTCTG GCCCTGGGCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAATCGGATG TGGGGAACAT 780
TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTTCTG 840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
CATCGTGACG CTGCTGTACG TGCTGACCAA CTTGGCCTAC TTCACCAACC TGTCCACCGA 960
GCAGATGCTG TCGTCCGAGG CCGTGGCGGT GGAATTCCGG AACTATCACC TGGCGCTCAT 1020
GTCTTGGATC ATCCCGCTCT TCGTGGCGCT GTCTGTCTTC GGCTCGGTCA ATGGGTCCCT 1080
GTTACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTCG CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGGCGTCC CTGTGTCTCA CGTGTGTGAT 1200
GACGCTGCTC TACGCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TCGTGGGCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGA CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
CCTCTTCTC ATGCGCGTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCTCT AGCGGGCTGC CGGTCTACTT CTTGGGGTGC TGGTGGAAA ACAAGCCCAA 1500
GTGGCTCTCT CAGGGCATCT TCTCCAGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGCT 1560
CCCCAGAGG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 87 Protein sequence:
Protein Accession #: XP_035292.2

1 11 21 31 41 51
MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTILQRNI TLLNGVAIIV 60
GTIIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
LKVYGLSLPAF LKWLLELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLV 180
LLTAVNCYSV KAARTVQDAF AAKLLALAL IILLGPVQIG KGDVSNLDFN PSFEGTKLDV 240
GNIVLALYSY LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSEEA VAVDPGNVHL GVMWSIIPVF VGLSCPGSVN GSLFTSSRLF FVGSREGHLP 360
SILSMIHPLQ LTFVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCLVAL AIIGMIWLHR 420
RKPELERPIK VNLALPVFFI LACLPLIAYS FWKTPVECGI GPTIILSGLP VYFPGVWWRN 480
KPKWLLQGI STTVLCQKLM QVVPQBT

Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168-989

1 11 21 31 41 51
TAAAAAGCAA AAGAATTGCG GGCCCGGTG ACACGGGCTT CCCCAGAAAC CTTCCCCGCT 60
TCTGGATATG AAAITCAAGC TGCTTGCTGA GTCTATTGCG CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
CTTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGCTCTGAGT CTTCTCTTC CGGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGSACTTC GACTGCAATA CTGCGCAGCC CGGCTGCTCC AAGCTGTGCT 360
TTGATGAGTT TTTCCCTGTG TCCATGTGCG GCGCTGCGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTCT ACTGCTGCTG GTGATGACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CGTGGGAGG AACAGTGGGC GCGCTTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT 600
TTCTCTAGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC 660
ACGAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAAC 720
TTTTCACCTT CTTCTGCTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTGCTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCTCG CAAACAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTCTG GGTCTCAGCA GTCATCTCTC TCTCTTACCA GACCGCCCC 960
GAGACCAATG GAAGAAAACC ATCTTGTGAG GGGCTGCTCG GACTGTGCTG GCAGGTGGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GAGAGCTAAGC 1080
CATGAGGTAG GGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

Seq ID NO: 89 Protein sequence:
Protein Accession #: NP_005259.1

1 11 21 31 41 51
MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVT A ERVNSDDHDK FDCNTRQPGC 60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKHREAHG ENSGRLYLNP 120
GKKRGGLWWT YVCSLVFKAS VDLAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHCLAAAR KAAQAMCTGHH PHGTTSSCKQ 240
DDLSSGDLIF LGSDSHPLL PDRPRDHVK TIL

Seq ID NO: 90 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26-457

1 11 21 31 41 51
CGGGCGAAGC AGCGCGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCTCTCT 60
CGCCCTGCTG GCGCTCACT CCGCGTCTGC CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGAGC GAGTGCCTG AGTGGGCTCG GGGGCGCTCG ACCCCAGCA GCAAGGATTG 180
CGGCGTGGT TTCCGCGAGG GCACCTGCGG GGCCAGACC CAGCGCATCC GGTGCGAGGT 240
GCCCTGCAAC TGGAGAGAG AGTTTGAGAG CGACTGCAAG TACAGTTTGG AGAACTGGGG 300
TGCCTGTGAT GGGGCGACAG GCACCAAGT CCGCAAGGC ACCCTGAAGA AGCGCGCTA 360

5

CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCCA AGACCAAAAGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGSAAG GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCOCCCTGGT TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
 CACCAAGTGC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCTCTCT 600
 ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAAATTC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCTCC CAATAAAAGC TCTTCTTTTT 780
 TAATAT

10

Seq ID NO: 91 Protein sequence:
 Protein Accession #: NP_002382.1

15

1 11 21 31 41 51
 | | | | |
 MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60
 CGAQTQIRIC RVPWNKKKEP GADCKYKFEN NGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
 RVTKPCPKT KAKAKAKKKK GKD

20

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_005130.1
 Coding sequence: 98-802

25

1 11 21 31 41 51
 | | | | |
 CTCTAOCCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCCTGGGATC 60
 CGTGTGCTCA GAACAAGGTG AACGCCACGC TGCAAGCCATG AAGATCTGTA GCCTCACCCCT 120
 GCTCTCCTTC CTCTACTGGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAAGTGAA 180
 GAATGGACTT CACAGCAAGG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240
 TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTG ACCAAAGACC AAGCCAACTG 300
 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCATCAATT 360
 GGACCATGAA TTTTCTGTGT TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 420
 TGAGAGAGTC TATTGGAAAC AAGTTGCCCG GAATCTGGCG TCACAGAAAG ACATCTGTAG 480
 ATATTCAGAG ACAGCTGTGA AAACCCAGAG GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540
 TAAGCTAGTC AGCTCCACTC TATTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600
 GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCC TCTAGCCTAG CAGTGACCCA 660
 GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
 GACTGCCCTG GAGTCTGTG GAGAGACTTG GAGCTCTCTC TGCACTTCTT TCCTCAGCAT 780
 AGTGACAGGAC ACCTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840
 TGTGTAAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACCTT 900
 TGTGCTTAGT GAGTGCAAGC AAATATTTAA ACAAGTTTGT TATTTTGTGC TTTTGTGTTT 960
 TGGAAITTGC CTATATTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCTCG CAGCATGTAT 1020
 TTCCATGGCC CACACAGCTA TGTGTTTGAG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
 GAGTGATAAT TTCAGTGCAA CGAACCTTCT GCTGAATTAA TGGTAATAAA ACTCTGSGTG 1140
 TTTTCAAAA AAAAAAAAAA AAA

45

Seq ID NO: 93 Protein sequence:
 Protein Accession #: NP_005121.1

50

1 11 21 31 41 51
 | | | | |
 MKICSLTLLS FLIIAAQVLL VEGKKIKVNG LHSKVVSEKQ DTLGNTQIKQ KSRPGNKGKP 60
 VTKDQANCRW AATEQEISIS LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 RSQDKICRYS KTAVKTRVCR KDFPESLKL VSSTLFGNTK PRKEKTEMSR REHIKGRETT 180
 PSSLAVTQMT ATKAPCEVED PDMANQRKTA LEPCGETWSS LCTFFLSIVQ DTSC

55

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: NM_012101
 Coding sequence: 125-1891

60

1 11 21 31 41 51
 | | | | |
 CTCTCAGAGC GTGTGTCTCT AGTCCCTGCT GTTGCTGCTC CCACTCCCTG CCGAGAGCGC 60
 TGCCAGAAAG GTCACTATTC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120
 TGGATGGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTG AGCCAGAAAG CCAAGGATGC 180
 CCGGAGCCCG TCGGGCCCCA GTGGCAGCCT GGAGAAATGC ACCAAGGCTG ACGGCAAGGA 240
 TGCCAAAGAC ACCAACGGGC ACGGCGGGGA GGCAGCTGAG GGCAGAGACC TGGGAGCGCG 300
 CCTGAAGCCA GGGGAAGGTA GGAGCGCCCT GTTCGCGGGC AATGAGTGGC GCGAGCCCAT 360
 CATCCAGTTT TCGAGTCCCG GGGACGACAA GAACTCCAAC TACTTCAGCA TGGACTCTAT 420
 GGAAGGCAAG AGGTGCGCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCGT 480
 TACCTTTGCC GAAAAGGGCG ACGTGCGCAA GTCCATTTTC TCGGAGTCCC GGAAGCCAC 540
 GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCGCGG CCGACACCGG 600
 CCTTTTTCCT CGGTCCAAGT CCGGCTCCGA GGAGGTGCTG TGCGACTCTT GCATCGGCAA 660
 CAAGCAGAAAG GCGGTCAAGT CCTGCCTGGT GTGCCAGGCC TCCTTCGCGC AGCTGCATCT 720
 CAAGCCCCAC CTGGAGGGCG CCGCTTCCG AGACACCCAG CTGCTCGAGC CCATCCGGGA 780
 CTTTGAGGCG CGCAAGTGTG CCGTGCAATG CAAGACGATG GAGCTCTTCT GCCAGACCGA 840
 CCAGACCTGC ATCTGCTACC TTTGCAATGT CCAGGAGCAC AAGAATCATA GCACCGTGAC 900
 AGTGAAGGAG GCCGAGGCG AGAAGGAGAC GAGCTGTGCA CTGCAAAAGG AGCAGCTGCA 960
 GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT 1020
 CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCGGAGCAG AACTTCCGGG ACCTGGTGCG 1080
 GGACCTGGAG AAGCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC 1140
 TGTGAGCAAA GTGAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGCTGCATGA 1200
 GAGCAAGCAG ACCCGGAGC AGCTGCATAG CATCAGCGAC TCTGTGTGT TCTGCGAGGA 1260
 ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCCACTC ATCATGTCTC 1320
 GCTGAGGCGG GAGGGCCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380
 ATGCATGGCG CACGTTGAGA AGATGTGCAA GCGGACCTTG AGCCGTAATC TCATTGAGAG 1440
 GAACCACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACAGA ACAGCTTCGG 1500

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 10
 15
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Protein Accession #: NP_036233.1

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	CCTGCTGAGC	TGCTGCCCAA	GCGAGTCCGT	GGGAAGGCC	GCTCCCTTCC	TGATGTCTCT	8820
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	GTAGATGGTG	AGCCACAGA	AGCCGAGAAG	GATTTTGGG	AACCTGCTATC	CCTTACTGCT	9060

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	GAGAAACCCCC	CAGACCTAAA	TAAATCTGG	AGTGAACCAT	TTTATCAGGA	AACATATCTA	9180
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	TACAGTCAAG	AGCTGAGTCT	GCTTTACCTC	CTGCAAGATG	ATGTTGACAG	AGCCAAATAT	9360
	TACATTCAAA	ATGGCATTTA	GAGTTTTATG	CAGAATTATT	CTAGTATTGA	TGTCTCTTTA	9420
	CACCAAGATA	GACTCAACCA	ATTGCAGTCT	GTACAGGCTT	TAACAGAAAT	TCAGGAGTTC	9480
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	GAAGATAATA	GTATGAATGT	GGATCAAGAT	GGAGACCCCA	GTGACAGGAT	GGAAAGTGAA	9720
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	AACTGTCTTC	GATGTGCTTT	TAGCTTTTGG	TGTTTTTTTT	TTTTCTCTCT	AACACTTGTA	13440
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Protein Accession #: NP_008835.5

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	LGEVHPSEMI	NNAENLPRAP	LGELKTQMTS	AVREPKLPLV	AGCLKGLSSL	LCNFTKSMEE	240
	DPQTSREIFN	FVLKAIRPQI	DLKRYAVPSA	GLRLPALHAS	QFSTCLLDNY	VSLFEVLLKW	300
	CANTNVELKK	AALSALSF	KQVSNMVAKN	AEHKNKLQY	FMEQFYGIIR	NVDSNNKELS	360

	IAIRGYGLFA	GPKCVINAKD	VDFMYVELIQ	RCKQMPLTQT	DTGDDRVYQM	PSFLQSVASV	420
	LLVLDTVPEV	YTPVLEHLVV	MQIDSFPQYS	PRMQLVCCRA	IVKVFLALAA	KGPVLRNCIS	480
	TVVHQGLIRI	CSKFPVLPKG	PESESEDEHA	SGEVRTGKWK	VPTYKYVDL	FRHLLSSDQM	540
	MDSLADEAF	FSVNSSSESL	NHLLYDEFVK	SVLKIVEKLD	LTLEIQTVGE	QENGDEAPGV	600
5	WMIPTSDPAA	NLHPAKPKDF	SAFINLVEFC	REILPERQAE	FFEPWVYSFS	YELILQSTRL	660
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	DRHVMOFPYK	DILECLDGYL	KTSALSDETK	NNWEVSALSR	AAQKGFNKVV	LKHLKKTENL	840
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	VDSTLRDFCG	RCIREFLKNS	IKQITPQQOE	KSPVNTKSLF	KRLYSLALHP	NAFKRLGASL	1080
	APNNIYREFR	EEESLVEQFV	FEALVIYMES	LALAHADEKS	LGTIQCCDA	IDHLCRIIEK	1140
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	RTSPQEGECL	NYSKCTVVVR	IMEFTTLLN	TSPEGWKLLK	KDLNTHLMR	VLVQTLCEPA	1380
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	LKMKQDAQVV	LYRSYRHGDL	FDIQIKESL	ITPLQVAQR	DPILAKQLFS	SLFSGILKEM	2820
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45	GIFTSEIGTK	QITQSALLAE	ARSDYSEAAK	QYDEALNKQD	WVDGEPTAE	KDFWELASLD	3000
	CYNHLAEWKS	LEYCSTASID	SENPPDLNKI	WSEFFYQETY	LPYMIRSKLK	LLQGEADQS	3060
	LLTFIDKAME	GELQKALBEL	HYSQELSLLY	LLQDDVDRAK	YYIQNGIQSF	MQNYSSIDVL	3120
	LHQSRILTQI	SVQALTEIQE	FISFISKQGN	LSSQVPLKRL	LATWNTNRYD	AKMDPMNIWD	3180
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	FRLTRQPINL	MLPMKETGLM	YSIMVHALRA	FRSDPGLLTN	TMDVVFKEPS	FDWQNFQKM	4020
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Nucleic Acid Accession #: NM_000673
Coding sequence: 101-1225

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GAAVKTGKVK PGSTCVVFLG GGVGLSVIMG CKSAGASRII GIDLKDKFE KAMAVGATEC 240
ISPKDSTKPI SEVLSEMTGN NVGYTFEIVG HLETMIDALA SCHPMYGTST VVGVPSSAKM 300
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Nucleic Acid Accession #: NM_006783.1
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ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTCTC CACCAGCATC 60
GGGAAGGTGT GGATCAGAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCTGTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTTCCCG GTGTCCACA TCCGGCTGTG GGCCCTCCAG 240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAGAAAGC ACAAGGTTTG GATAGAGGGG TCGCTGTGGT GGAAGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCITT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGTACTGC 540
TTTATTTCTA GGCCAAACAGA GAAGACCGTG TTACCATTT TTATGATTTC TGCGTCTGTG 600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
AGATCAAGAG GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

Seq ID NO: 103 Protein sequence:
Protein Accession #: NP_006774.1

1 11 21 31 41 51
MDWGLHTFI GGVNKHSTSI GKVIWITVIFI FRVMILVVAA QSVWGDQED FVCNTLQPGC 60
KNVCYDHFFP VSHIRLWALQ LIPVSTPALL VAMHVAYYRH ETTRKFRRG KRNDFKDIED 120
IKKHKVRIBG SLNWTYTTSS FFRILFEAAP MYVFYFLYNG YHLPWVLKQ IDPCPNLVDC 180
FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLLLKVCPR RSKRAQTQKN HPNHALKESK 240
QNEQNELISD SQNAITGPP S

Seq ID NO: 104 DNA sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86-526

1 11 21 31 41 51
GGACCTGGGA AGGAGCATAG GACAGGGCAA GCGGGGATAA GGAGGGGCAC CACAGCCCTT 60
AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GGCATGTTC 120
ACTGGGGGTC TTCCCATCGG CCCCTTGGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC 180
GGCGACTCGG GTCCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACAAG GCGGACACAC 240
ACAAACACAG AACACACAG CCAGTCCAG GAGCCAGTA ATGGAGAGCC CCAAAAAGAA 300
GAACGAGCAG CTGAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
ACAGCTGAGA TCCAGTGGCG CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
ACCGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAGAGGGA 480
ACACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG 540
AAACAAACGA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG 600
CAGCTTTCAC CAAAAAATA AAAAAA

Seq ID NO: 105 Protein sequence:
Protein Accession #: NP_065144.1

1 11 21 31 41 51

MLLMCPQCA CSLGVFPSP SPVWGTRRSC EPATRVPEVM ILSPLLREHG HTQTQNTAS 60
PRSPVMESPK KKNQQLKVG I LHLGSRQKKI RIQLRSQCAT WRVICKSCIS QTPGINLDLG 120
SGVKVKIIPK EEHCKMPEAG EBQPVQ

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: J04129
Coding sequence: 99-587

1 11 21 31 41 51
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCCTCTGC 60
TCACCCCTGGG OGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
15 ACATCTCCCT CATGGCGACA CTGAAGGCCCT CTCTGAGGGT CCACATCACC TCACTGTTCG 240
CCACCCCGGA GGACAACTGT GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTC 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAAGCA GGCCACGCTG CTGGATACCT ACTACGACAA TTCTCTGTTT CTCTGCCTAC 420
AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCGTGGTG 480
20 AGGACGATGA GATCATGCAG GGATTTCATCA GGGCTTTTCC GCGCCCTGCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCGGTGCCG TTCTTAGCTC ACCTCGGCTC 600
CCAGGAAGAC CAGCTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCT 660
TTTCAAAGAA TAAACACAGC TCAGAAGACG ATGAAGTGGT CATCTGTGTC GCCATCCCTC 720
25 TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

Seq ID NO: 107 Protein sequence:
Protein Accession #: AAA60147

1 11 21 31 41 51
MDIPQTKQDL ELPLKAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPPT EDNLEIVLHR 60
WENNSCVERR VLGEKGTGNPK KFKINYTVAN EATLLDLYDD NFLFLCLQDT TTFIQSMQ 120
35 YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPK RF

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 48-794

1 11 21 31 41 51
TCCAGGCGAG CAGTTAGCCC GCGGCCCGCC TGTGTGTCCC CAGAGCCATG GAGAGAGCCA 60
GTCTGATCCA GAAGGCCAAG CTGGCAGAGC AGGCGGAAGC CTATGAGGAC ATGGCAGGCT 120
45 TCATGAAGAG CGCGTGGAG AAGGGCGAGG AGCTCTCCTG OGAAGAGCGA AACCTGCTCT 180
CAGTAGCCTA TAAGAACGTG GTGGGCGGCC AGAGGGCTGC CTGGAGGGTG CTGTCCAGTA 240
TTGAGCAGAA AAGCAACGAG GAGGGCTCGG AGGAGAAGGG GCCCGAGGTG CGTGAGTACC 300
GGGAGAAGGT GGAGACTGAG CTCCAGGGCG TGTGCGACAC CGTGTGGGSC CTGTGTGACA 360
GCCACCTCAT CAAGGAGGCC GGGGACGCGG AGAGCCGGGT CTCTACCTG AAGATGAAGG 420
50 GTGACTACTA CGCTACCTG GCCGAGGTGG CCACCGGTGA CGACAAGAAG CGCATCATTG 480
ACTCAGCCCG GTACGCTTAC CAGGAGGCCA TGGACATCAG CAGAAGGAG ATGCCGCCCA 540
CCAAACCCAT CGGCTGGGC CTGGCCCTGA ACTTTCCGT CTTCACCTAC GAGATCGCCA 600
ACAGCCCGGA GGAGGCCATC TCTCTGGCCA AGACCACTTT CGACGAGGCC ATGGCTGATC 660
TGACACCCCT CAGCGAGGAC TCCTACAAAG ACAGCACCTT CATCATGCAG CTGCTGCGAG 720
55 ACAACCTGAC ACTGTGGAGC GCGGACAAAG CCGGGGAAGA GGGGGGCGAG GCTCCCGAGG 780
AGCCCCAGAG CTGAGTGTGG CCGGCCACCG CCGCGCCCTG CCGCTCCAG TCCCCACCC 840
TGCCGAGAGG ACTAGTATGG GGTGGGAGGC CCCACCTTC TCCCTAGGC GCTGTCTTGG 900
CTCCAAAGGG CTCCGTGGAG AGGGACTGGC AGAGCTGAGG CCACCTGGGG CTGGGGATCC 960
CACTCTTCTT GCAGCTGTGT AGCGCACCTA ACCACTGTGT ATGCCCTCAC CCCTGCTCTC 1020
60 CGCACCCGCT TCCTCCGAG CCCAGGACCA GGCTACTTCT CCGCTCCTCT TGCTCCCTC 1080
CTGCCCTGCG TGCTCTGAT CGTAGGAATT GAGGAGTGTG CCGCTTGTG GCTGAGAACT 1140
GGACAGTGGC AGGGCTGGA GATGGGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 1200
CGCGCGCGCC AGTGCAGAC CGAGATTGAG GGAAAGCATG TGTGTGTGGT GTGACCATGT 1260
65 TTCTCTCAA TAAAGTCCC CTGTGACACT C

Seq ID NO: 109 Protein sequence:
Protein Accession #: NP_006133.1

1 11 21 31 41 51
MERASLIQKA KLAQEAERYE DMAAFMKGAV EKGEELSCEE RNLLSVAYKN VVGQRAAWR 60
VLSSIEQKSN EHGSEKQPE VREYREKQET ELQGVCDTVL GLDLSHLIKE AGDABSRVVF 120
LKMKGYYRY LAEVATGDDK KRIIDSARSA YQEMDISKK EMPPTNPIRL GLALNFSVPH 180
75 YEIANSPEEA ISLAKTTFDE AMADLHTLSE DSYKDSLIM QLLRDNLTLW TADNAGEBGG 240
EAPQSPQS

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: NM_000695
Coding sequence: 407-1564

1 11 21 31 41 51
CACGAGTTGG TTTGGGAGCT GCCAGTCTCC TGGGAGGATC GCAGTCAGCA GAGCAGGGCT 60
GAGGCCTGGG GGTAGGAGCA GAGCCTGCGC ATCTGGAGGC AGCATGTCCA AGAAAGGGAG 120
85 TGGAGGTGCA GGAAGGACCC CAGGGGCGAG GCCACGCTG GGGATGACCC CCTTGGAGGA 180
CACACTGCGG CGGCTGCGTG AGGCCCTTCA CTGAGGGGCG ACAGGGCGCG CCGAGTTCGG 240
GGCTGCGCAG CTCACGGGCC TGGGCCACTT CTTTCAAGAA AACAAAGCAGC TTCTGCGCGA 300

	CGTGTGGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTTGACT	ACGCTCTCAA	GAACCTTCAG	GCCTGGATGA	AGGATGAACC	420
	ACGGTCCACG	AACCTGTTC	TGAAGCTGGA	CTCGGTCTTC	ATCTGGAAGG	AAACCTTTGG	480
	OCTGGTCTCT	ATCATGCGAC	OCTGGAACTA	CCATTGAAC	CTGACCTGG	TGCTCTGGT	540
5	GGGCAACCTC	CCCCCAGGGA	ATTGGGTGGT	GCTGAAGCCG	TCAGAAATCA	GCCAGGGCAC	600
	AGAGAAGTCT	CTGGCTGAGG	TGCTGCCCA	GTACCTGGAC	CAGAGCTGCT	TTGCGGTGGT	660
	GCTGGGGGGA	CCCCAGGAGA	CAGGGCAGCT	GCTAGAGCAC	AAGTTGGACT	ACATCTTCTT	720
	CACAGGGAGC	CCTCGTGTGG	GCAAGATTGT	CATGACTGCT	GCCACCAAGC	ACCTGACGCC	780
	TGTCACTCTG	GAGCTGGGGG	GCAAGAACCC	CTGCTAGTGG	GACGACAACT	GCGACCCCA	840
10	GACCGTGGCC	AACCGGTGG	CCTGGTCTCG	CTACTTCAAT	GCGGCCGAGA	CCTGGGTGGC	900
	CCCTGACTAC	GTCTGTGCA	GCCCCGAGAT	GCAGGAGAGG	CTGCTGCCCG	CCCTGCAGAG	960
	CACCATCAAC	CGTTTCTATG	GCGACGACCC	CCAGAGCTCC	CCAAACCTGG	GCGCATCAT	1020
	CAACCAGAAA	CAGTTCACG	GGCTGCGGGC	ATTGCTGGGC	TGCGGCCGCG	TGGCCATTGG	1080
	GGGCCAGAGC	AACGAGAGCG	ATCGCTACAT	CGCCCCCACG	GTGCTGGTGG	ACGTGCAGGA	1140
15	GACGGAGCCT	GTGATGCAGG	AGGAGATCTT	CGGGCCCATC	CTGCCCATCG	TGAAGTGCA	1200
	GAGCGTGGAC	GAGGCCATCA	AGTTTATCAA	CCGGCAGGAG	AAGCCCTTGG	CCCTGTAGCG	1260
	CTTCTCCAAC	AGCAGACAGG	TTGTGAACCA	GATGCTGGAG	CGGACGAGCA	GCGGCAGCTT	1320
	TGGAGGCAAT	GAGGGCTTCA	CCTACATATC	TCTGCTGTCC	GTGCCATTGG	GGGAGTGGG	1380
	CCACAGTGGG	ATGGGCGCGT	ACCAAGGCAA	GTTTACCTTC	GACACCTTCT	CCCACACCG	1440
20	CACCTGTGCT	CTCGCCCCCT	CGGGCTGGA	GAAATTAAGG	GAGATCCGCT	ATCCACCTTA	1500
	TACCGACTGG	AACGAGCAGC	TGTTACGCTG	GGGCATGGGC	TCCAGAGCT	GCAACCTCCT	1560
	GTGAGCGTCC	CACCGGCTC	CAACGGGTCA	CACAGAGAAA	CTGAGTCTA	GCCATGAGGG	1620
	GCTTATGCTC	CCAACCTACA	TTGTTCTTCC	AGACCGCAGG	CTCCCCAGC	CTCAGGTTCG	1680
	TGGAGCTGTC	ACATGACTGC	ATCCTGCCCTG	CCAGGGCTGC	AAAGCAAGGT	CTTGCTTCTA	1740
25	TCTGGGGGAG	GCTGCTCGAG	AGAGGCGGAG	AGGCGGCGAG	ACATGCCAGG	TGTTCTCACT	1800
	CACCCCAACC	TGCCCAATTC	CAGGCGCTTG	CCCTCTCGGT	CAGGGTTGGC	CAGGCCAGCT	1860
	CACAGGGGCA	GTGTCAACCT	GGAAATATA	GTGCCCTGCC	TTCTTAGGGG	CATCAGCCCT	1920
	GAACGGTTGA	GAGCGTGGAG	CCCTCCAGGC	CITTTGCTCT	CCCTTAGGGC	ACAAGCGCAC	1980
	TTCCACCTCT	GCCCATCCCC	AACCTGCACA	GCATGCCCTC	CCCGAGGGAT	CCTCTCATAT	2040
30	CCCACTACTG	TCTCTGCAAC	ACCCCTCTGG	TTCAACCGCG	ACCTGCACT	CACCCACAGC	2100
	AGCTCCATCC	ACTGGGAAAA	CTGGGGTTTG	CATCACTCCA	CTGCACAGTG	TTAGTGGGAG	2160
	CTGGGGGCA	GTCCCTTGAC	TTCTCTGAGC	CTCAGTTTCC	TTATGTGAAA	GTTGCTGGAA	2220
	CCAAATGGGA	GTCACTTATG	CCAAACTCTA	ATAAAATGGA	GTGCGGGGGG	CACATAGAAG	2280
	CCCTCACACA	CATATGCCCC	TAAACAGGAT	TATCACCAAG	ACACGCTTGC	ATGTAAGACC	2340
35	AGACACAGGG	CGATGTGAAA	AGCAAGTCTC	CAAGAGCTGT	AGTATTCCAG	ATGAGCTGCA	2400
	GATGCTTACC	TACCAAGGCC	GTCTCCACCA	GAAACCATC	GCCAACTCCT	GCGATCAGCT	2460
	TGTGACTTAC	AAACCTGTGT	TAAAGCTGTC	TTACATGGAC	TTCTGTCTCT	TAAACGTTTC	2520
	CCCTTGGCTG	TGGCCCTCTG	TGTATGCCCTG	GGATCCTTCC	AAGCACTCAT	AGCCACAGATA	2580
40	GGAACTCCTCT	GCTCTCCCA	AATAAATTCA	TCTGTTTC			

Seq ID NO: 111 Protein sequence:
Protein Accession #: NP_000686

45	1	11	21	31	41	51	
	MDDEPRSTNL	FMKLDSPVFIW	KEPPGLVLII	APWNYPLNLT	LVLIVGTLP	GNCVVLKPS	60
	ISQGTKEVLA	EVLPLQYLDQS	CPAVVLGGPQ	ETGQLLEHLK	DYIFFTGSPR	VGRIVMTAAT	120
	KHLTPVTLLE	GGKNPCYVDD	NCDPQTVANR	VAMFCYFNAG	QTCVAPDYL	CSPEMQERLL	180
50	PALQSTITRF	YGDDEPSSFP	LGRIINQKQF	QRLRALLGCG	RVAIGGQSN	SDRYIAPTVL	240
	VDVQETPEVM	QSEIIPGPIPL	IVNVQSVDEA	IKFINRQEPK	LALYAFNSNR	QVNVQMLERT	300
	SSGSPGGNEG	FTYISLLSVP	PGGVGHSGMG	RYHGKPTFDT	FSHRTCLLA	PSGLEKLKEI	360
	RYPPYTDWQ	QLLRWGMGSQ	SCTL				

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58-2298

60	1	11	21	31	41	51	
	GAATTCGCGG	CGACGCGCGG	GAACAACCGG	AGTCGCGCGG	CGGGACGAAG	AATAATCATG	60
	GGCCAGACTG	GGAGAAATTC	TGAGAAGGGA	CCAGTTTGTG	GGCGAAGCG	TGTAATATCA	120
	GAGTACATGC	GACTGAGACA	GCTCAAGAGG	TTCAAGCAGG	CTGATGAAGT	AAAGAGTATG	180
65	TTTAGTTCCT	ATCGTCAGAA	AATTTTGGAA	AGAACGGA	TCTTAAACCA	AGAAATGGA	240
	CAGCGAAGGA	TACAGCCTGT	GCACATCCTG	ACTTCTGTGA	GCTCATTTGG	CGGGACTAGG	300
	GAGTGTTCGG	TGACCACTGA	CTTGGATTCT	CCAACAAG	TCAATCCATT	AAAGACTCTG	360
	AATGCAGTTG	CTTCAGTACC	CATAATGTAT	TCTTGGTCTC	CCCTACAGCA	GAATTTTATG	420
	GTGGAAGATG	AAACTGTTTT	ACATAACATT	CTTATATG	GAGATGAAGT	TTTAGATCAG	480
	GATGGTACTT	TCAATGAAGA	ACTAATAAAA	AATTATGATG	GGAAAGTACA	CGGGATAGA	540
70	GAATGTGGGT	TTATAATGA	TGAAATTTTT	GTGGAGTTGG	TGAATGCCCT	TGGTCAATAT	600
	AATGATGATG	ACGATGATGA	TGATGGAGAC	GATCCTGAAG	AAAGAGAAGA	AAAGCAGAAA	660
	GATCTGGAGG	ATCACCGAGA	TGATAAAGAA	AGCCGCCAC	CTCGGAAATT	TCCTTCTGAT	720
	AAAAATTTGG	AGGCCATTTC	CTCAATGTTT	CCAGATAAGG	GCACAGCAGA	AGAACTTAAAG	780
75	GAAAAATATA	AAGAACTCAC	CGAACAGCAG	CTCCAGGGCG	CACCTCTCTC	TGAATGTACC	840
	CCCAACATAG	ATGGACCAAA	TGCTAAATCT	GTTCAAGAGG	AGCAAGCTT	ACACTCTTTT	900
	CATACGCTTT	TCTGTAGGCG	ATGTTTTTAA	TATGACTGCT	TCCTACATCC	TTTTCATGCA	960
	ACACCCACCA	CTTATAGGCG	GAAGAACACA	GAAACAGCTC	TAGACAACAA	ACCTTGTGGA	1020
	CCACAGTGTG	ACCGCATTTT	GGAGGGAGCA	AAGGAGTTTG	CTGCTGCTCT	CACCGCTGAG	1080
80	CGGATAAAGA	CCCCACCAAA	ACGTCCAGGA	GGCCGCGAG	GAGGACGGCT	TCCCAATAAC	1140
	AGTAGCAGGC	CCAGCACCCC	CACCATTAAT	GTGCTGGAA	CAAAGGATAC	AGACAGTGAT	1200
	AGGGAAGCAG	GGACTGAAC	GGGGGGAGAG	AACAATGATA	AAGAAGAAGA	AGAGAAGAAA	1260
	GATGAACACT	CGAGCTCTCT	TGAAGCAAA	TCTCGTGTCT	AAACACCAAT	AAAGATGAAG	1320
	CACAAATATT	AACCTCTCTG	GAATGTGGAG	TGGAGTGGTG	CTGAAGCCTC	AATGTTTGA	1380
	GTCCCTCATG	GCATCTACTA	TGACAATTTT	TGTGCCATTG	CTAGGTTAAT	TGGGACCAAA	1440
85	ACATGTAGAC	AGGTGTATGA	GTTTAGAGTC	AAAGAATCTA	GCATCATAGC	TCCAGCTCCC	1500
	GCTGAGGATG	TGGATACTCC	TCCAAGGAAA	AAGAAGAGGA	AACACCGGTT	GTGGGCTGCA	1560
	CATGCGAGAA	AGATACAGCT	GAAAAGGAC	GGCTCCTCTA	ACCATGTTTA	CAACTATCAA	1620

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CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAAAAT 1680
TTTTGTGAAA AGTTTGTGCA ATGTAGTICA GAGTGTCAAA ACOGCTTTCC GSGATGCCGC 1740
TGCAAAGCAC AGTGCACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC 1800
CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCAATTGG ACAGTAAAAA TGTGTCTGTC 1860
AAGAACTGCA GTATTTCAGCG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920
GCAGGCTGGG GGATTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
TGTGGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTA TGATAAATAC 2040
ATGTGCAGCT TTCTGTTCAA CTGGAACAAT GATTTGTGG TGGATGCAAC CCGCAAGGGT 2100
AACAAAAATC GTTTTGCAAA TCATTGCGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCAGAGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCG CATCGAAGAA 2280
GAAATGGAAG TCCCTTGACA TCTGCTACCT CCTCCCCCTC CTCTGAAACA GCTGCCTTAG 2340
CTTCAGGAAC CTCGAGTAGT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
AAITTGCAAA GTACTGTAAG AATAATTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCCTTCTCAC CAGCTGCAAA GTGTTTTGTA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTGAA AAAAAAAAAA AAAAAA
  
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20
 Seq ID NO: 113 Protein sequence:
 Protein Accession #: NP_004447

25
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 35

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1 11 21 31 41 51
| | | | |
MGQTGKKSEK GPVCRKRVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL ERTEILNQEW 60
KQRIQPVHI LTSVSLRGT RECSVTSDDL FFTQVPLKT LNAVASVPIM YWSPLQQNF 120
MVDEDTVLHN IPYMGDEVLQ QDGTFFIEELI KNYDGKVGHD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDPEEREKQ KDLEDHRDDK ESRPPRKFPK DKILEAIISSM FDKGTAEEL 240
KEKYKELTBQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRCP KYDCFLHPPH 300
ATPNTYKRN TETALDNKPC GPQCYQHLEQ AKSPAAALTA ERIKTPPKRP GRRRRGRLPN 360
NSSRPTPTI NVLESKDTDS DREAGTETGG ENNDKEEEER KDETSSSSEA NSRCQTPIM 420
KPNIEPPENV EWSGABASHF RVLIGTYIDN FCAIARLIGT KTCRQVYEFK VKESSIIAPA 480
PAEDVDTPPR KKKRKHRLNA AHCRKIQLKK DGSSNHVYNY QPCDHPROPK DSSCPCVIAQ 540
NPKCKPCQCS SECNRFPQGC RCKAQCNTRQ CPCYLAVREC DPDLCLTCGA ADHWDSKNVS 600
CKNCSIQRGS KKHLLAPSD VAGWGIPIKD PVQKNEPISE YCGEIIISQDE ADRRGKVYDK 660
YMCSPFLNIN NDFVVDATRK GNKIRPANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
ELFVDVRYSQ ADALKVYGI REMEIP
  
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40
 Seq ID NO: 114 DNA sequence
 Nucleic Acid Accession #: NM_001827
 Coding sequence: 96-335

45
 50
 55

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1 11 21 31 41 51
| | | | |
AGTCTCOGCG GAGTGTGTC CTGGGCTGGA CGTGGTTTGG TCTGCTGCGC COGCTCTTCG 60
CGCTCTOGTT TCATTTTCTG CAGCGCGCCA CGAGGATGGC CCACAAGCAG ATCTACTACT 120
GGGACAAGTA CTTCGACGAA CACTACGAGT ACCGGCATGT TATGTTACCC AGAGAACTTT 180
CCAAACAAGT ACCTAAACT CTCTGATGT CTGAAGAGGA GTGGAGGAGA CTTGGTGTCC 240
AACAGAGTCT AGGCTGGGTT CATTACATGA TTCATGAGCC AGAACCACAT ATCTCTCTCT 300
TTAGAGCACC TCTTCCAAAA GATCAACAAA AATGAAGTTT ATCTGGGGAT CGTCAAAATCT 360
TTTTCAAAAT TAATGTATAT GTGTATATAA GGTAGTATTC AGTGAATACT TGAGAAATGT 420
ACAAATCTTT CATCATACC TGTGCATGAG CTGTATTCTT CACAGCAACA GAGCTCAGTT 480
AAATGCAACT GCAAGTAGGT TACTGTAAGA TGTTTAAGAT AAAAGTTCTT CCAGTCAGTT 540
TTTCTCTTAA GTGCTGTGTT GAGTTTACTG AAACAGTTTA CTTTGTGTCA ATAAAGTTTG 600
TATGTTGCAT TTAATAAAAA AAAAAA
  
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Seq ID NO: 115 Protein sequence:
 Protein Accession #: NP_001818

60

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1 11 21 31 41 51
| | | | |
MAHKQIYSD KYFDEHYEYR HVMLPRELSK QVPKTHLMSE BEWRLGVQQ SLGWVHYMIH 60
EPEPHILLER RPLPKDQK
  
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65
 Seq ID NO: 116 DNA sequence
 Nucleic Acid Accession #: CAT cluster

70
 75
 80
 85

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1 11 21 31 41 51
| | | | |
TCAGACCTCA TGAGTCACTT GGACTCTTGA GCCACCTCTG GGGGTGGAGT CTCTCTCCTG 60
GCATCTGGAC CTTTGGTGCT ATCGACGAAG CTTGGGTGGG GCTCTTAGCT GCTATGTGCA 120
AGAGGTGTGT TCCAGGGAAG GCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC 180
GCAGCCAAAC GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGGCTCTGT GGAGGATGGG 240
AAGGACTGAT CCACATTCCC ACCAGGAAGT TTAGCAGAAC CCGCGCTGTC CAACTGGACC 300
CCTTGGAAAG ACCTGGCTCA GGCTGGACCA CCTCTTGAGA GGGAGGAGCT CTGGATTGTA 360
TCAAGAAATC TTTGCTGAGC ATGGTGCTTC ATGCTATATA TACCAACACT TTGGGAGGCC 420
AGTGTGGGAG GATCTCTTGA GCCCAGGAGT TCAAGACTAG CCTGGGCAAC ACAGAGAGAA 480
CCCATCTCTA AAATAATAAT AATAATAAAA TAAAAAATTA GCAGGGCATG GTGGCATGTG 540
CCTGTAGTTC CAGCTACCCA GGAGGCTGAG GCAAGAGGAT GGCTGGAGCC TGGGATGTTG 600
AGGCTGCAAT GAACTGTGAT TACCCCACTG CACTCCAGCC TGGGCAAAAG AGCGAGAGAA 660
CCTGTCTCAA ATAATAATAA TAATAATAAT CTTATTTTGG AGAATAAAGA GACCTCTGGA 720
TTTGAGGTGC CATTTGGGTA GAAAGAAAAG ACGTTTACAC CGAGAAATAG TCTGTGTTGC 780
CCTGAAGGAG CAGAGGGATG CATGCTGGA GGTGACCTAC AGTTGAAGAA GACTCATTAT 840
GACAGACCTT GTCTTCTTC CTGTGGAAA GTGTTCCTC TGTGCTACT GCTCATGAGA 900
CTCTTCCCCC TCCTGTCTCC AGGGAACCAA AGGGCTTTCT ACCACACCTT TCTTGTCCCC 960
CGGCTCCCA TGTCTGCTGT GCCTTTGTAC TCAGCAATTC TTGTTTGCTC CATTATCTTC 1020
CAGCCGGATA CAGAGTGAAT AGTTAACCACT ACTTAGGTCA AATAGGATCT AAATTTTGT 1080
TCTGCTCCG TGTAAAGAGG CCAGTGTGTT TGTGTGCAA GCAGCCTTGG AATAGTAAC 1140
  
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PCT/US02/12476

	CTTCTCATTT	GTTTGGGATC	TGGCCACCAA	GTTCCAGAAT	GATACACGGA	TCAGTGCAGA	1200
	AGTTCCATCG	GCTCTCGGAC	CTTAGGCGTG	TTCCAGGAAG	CTTCAGCAGC	AGAACTGATG	1260
	GTGAAGGCTC	GTGTTCTCCA	TCTTCAACTT	TCTTGTGCTT	GATCATACAC	AAGAATACAT	1320
	TTGGAAGGGC	AAAAAATGAA	CACGTGCGTT	CATTGCAGCC	GTGTTTGTGG	ACACAGATGC	1380
	ACAGTCTGCT	GTTGAAGACCT	TCTCTCAAGT	GGCATTTGGG	AGTCCATGCC	AGCATCATGT	1440
	GCTTCATGAG	AGACTGCACG	CTATCAGGGG	TTGTGGCACT	TAGTGAGGAC	TCTCTCTCCC	1500
	CAGTGTGTGC	TGATGACACA	TACACACCTC	ACAAAGCTTT	GAGTCTTCTC	TGTTCTTTT	1560
	ACTCTGTAGC	CACACATACA	ATGATTAAAA	AATATCTATC	ATGTTGTCAT	1620	
	CTTGTCCAAA	TGCAGAGTCA	GAGCTATTGT	TACTTCATTA	TTATTTCCAA	GGCGAATAGT	1680
	TGGCTTTCTT	TTTGCAAAAA	TAAATTAAAGT	TTTGTATGTG	TGCAAAAAAA	AAAAAAAAAA	1740
	AAACAAAAAA						

	TCATCTTCGG	TGTGGGCCAG	GGCCAGGGCC	AGAGCGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCCTCCA	GGACAGAGGG	GCTACTCTGG	COCTGACTCA	AGTCAACCCC	CAAGACGAGC	360
	GCATCTTCTT	GTGCCAGGGC	AAGGCGCCCT	GSTCCAGGGA	GTACCGCATC	CAGCTCCGCG	420
5	TCTACAAAGC	TCCGGAGGGG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAGGAGGCG	TGAGGAGGTC	GCTACCTGTG	TAGGAGGAGAA	CGGGTACCCC	ATTCTCTAAG	540
	TCATCTGGTA	CAAGAAATGC	CGGCTCTGTA	AGGAGGAGAA	GAACCGGGTC	CACATTCACT	600
	CGTCCAGAGC	TGTGGAGTCG	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAGATG	GCCGAGTTTT	ACTGTGAGCT	CAACTACCGG	CTGCCAGTGT	720
10	GGAAACACAT	GAAGGAGTCC	AGGGAAGTCA	COGTCCCTGT	TTTCTACCCG	ACAGAAAAAG	780
	TGTGGCTGGA	AGTGGAGCCC	GTGGGAATGC	TGAAGGAAGG	GGACCGCGTG	GAAATCAGGT	840
	GTTTGGCTGA	TGGCAACCCCT	CCACCACTCA	TCAGCATCAG	CAAGCAGAAC	CCCAGCACCA	900
	GGGAGGCAGA	GGAAAGAGCA	ACCAACGACA	ACGGGGTCTT	GSTGCTGGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAATGTGAGG	CCTGGAACCT	GGACACCATG	ATATCGCTGC	1020
15	TGAGTGAACT	ACAGGAAGTCA	CTGGTGAAGT	ATGTGTCTGA	CGTCCGAGTG	AGTCCCGCAG	1080
	CCCTCTGAGAG	ACAGGAAGGC	AGCAGCCTCA	COCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
	ACCTCGAGTT	CCAGTGGCTG	AGAGAAGAGA	CAGACCAGGT	GCTGGAAGG	GGGCGCTGTC	1200
	TTCACTTGCA	TGACCTTGAA	CGGAGGCGTA	TGCTGCGGTG	GCGTCTGTGC	1260	
	CCAGCATACC	CGGCTGGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTTT	GGCCCGCCCTT	1320
20	GGATGGCATT	CAGGAGAGTG	AAGGTGTGGG	TGAAGAGAGAA	TATGGTGTGT	AATCTGTCTT	1380
	GTGAAGGCTC	AGGGCAACCC	CGGCCACCA	TCTCTTGAA	CGTCAACGGC	AGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCTCTG	GCACCTTGAA	TGTCTCTGTG	ACCCCGGAGC	1500
	TGTTGAGGAC	AGGTGTGTGA	TGCACGGCTT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCTTCTGAGA	GCTGGTCAAT	TAAACCAACC	TCACACACAG	CTCCAAACAC	ACCACTGGCC	1620
25	TCAGCACTTC	CAGTGGAGTG	CCTCATACCA	GAGCCAAACG	CACCTCCACA	GAGAGAAAGC	1680
	TGCGGAGGCC	GGAGAGCCCG	GGCGTGGTCA	TGCTGGCTGT	GATTTGTGTG	ATCTCTGTGC	1740
	TGGCGTGTCT	GGGCGCTGTC	CTCTATTTC	TCTATAAGAA	GGGCAAGCTG	CCGTGACAGC	1800
	GCTCAGGAG	GCAGGAGATG	ACGCTGCCCC	CGTCTGTGTA	GACCGAAGCT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAAAGCTCCCA	GAAGAGATGG	GCCTCCTGCA	GGGCGAGCAG	GSTGACAAAG	1920
30	GGGCTCCGGT	AGAGCAAGGA	GAGAAATACA	TGGATCTGAG	GCAATTAGCC	CGAATCACTT	1980
	CAGCTCCCTT	CCCTGCTGCG	ACCAATCCCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCTTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TGGGCCCTGC	AAGCGCTTTT	TCAGGGACCA	2160
	GTCCACACCC	ATCTCTCCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
35	CCGAGCGGGT	AGGAGAGTTT	CTTGCAAGAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
	AAATACCTGG	CTCTTGCCAG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
	CAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CAGTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GCTGTCTCAT	GTGGAAGTGC	GCTGTTTACA	CCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTTCG	TGCCACCAAC	CTCTGCTCG	CCTCTTCAAA	GTCTCTGTG	2520
40	ACATTTTTTC	TTTGGTCAAG	AGCCAGGAAC	TGTTGTCAAT	CCTTAAAGAA	TACGTGCGCG	2580
	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGGACGAGAG	CATCTCTGCT	AACCGTGTGA	AACCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTCCTAG	CGGTAGTGGT	TGGCAACCTAT	AGTCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAATGGTAT	GAATCCAGGA	GSTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
45	CAGTGCACCT	CAGCCTGGGC	AACACAGCGA	GACTCCGCTC	CGAGGAAAAA	AAAAGAAAAA	2880
	ACGGGTACCT	GGGAGGAGGA	AGCTGGGGCG	TGTTTTCGAG	TTTCTGTTGA	TTAGCCTCAA	2940
	TCGCCGTGT	CAGTGTCTCC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGAGC	3000
	GGGAGCAGCA	CAAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCAAC	CCTAGAAAGG	CCCAATAGAG	3120
50	AGAATGGTAT	TTAGGAGTGG	AAAACGGGGC	CTGCGTAGAG	CTTCCGGTGT	GTGTGTCTGT	3180
	CTGTGTGAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
	TGTTTCTCTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCCGAAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	TATCCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACGTTTTCC	AGTTGGCAGC	3420
55	AGAGATCAGG	GGTACCTCTT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
	CTACCTACT	TTTACGAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTCATCG	TTTCCGTCCA	CTT		

Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

	1	11	21	31	41	51	
65	MGLPRLVCAF	LLAACCCCPR	VAGVPGEABQ	PAPELVEVEV	GSTALLKQGL	SQSQGNLSHV	60
	DMFSVEKEKR	TLIFRVRQGG	QSEPGYEYEQ	RLSLQDRGAT	LALTQVTPQD	ERIFLQGGKR	120
	PRSQEYRIQL	RVYKAPBEPN	IQVNPLGIPV	NSKEPEEVAT	CVGRNGYPIP	QVIWYKNGRP	180
	LKBEKNRVHI	QSSQTVESSG	LYTLQSLILKA	QLVKEDKDAQ	FYCELNYRLP	SGNHMKESRE	240
70	VTVPVPYPTE	KVWLEVEPVG	MLKEGDRVRI	RCLADGNPPP	HFSISKQNPS	TREAEZETTN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPQELLV	NYVSDVRVSP	AAPERQEGSS	360
	LTLTCEASSS	QDLFPQWLRB	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
	QLVKLAIFGP	PWMAFKERKV	WVKENMVLNL	SCEASGHPRP	TI SWNVNGTA	SEQDDPQVR	480
	LSTLNLVLT	ELLETGVECT	ASNDLGRNTS	ILFLLELVNLT	TLTPDSNTTT	GLSTSTASPH	540
75	TRANSTSTER	KLPEPBRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLP	RRSGKQBITL	600
	PPSRKTELVV	EVKSDKLPEE	MGLLQSSSGD	KRAPGDQGER	YIDLRL		

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

	1	11	21	31	41	51	
80	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAAGCCA	60
	TGGAGACTTC	AGCATCTCC	TCCCAGCCTC	AGGACAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTCC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAAC	ATATGAGAGA	AACAAGTCTT	CTTCTCTCTC	CTTCTCTTCC	TCCTCATCCT	240
	CCTCATCTTC	TTTCTCTCTC	TCTCTCTCAG	GTCTCTGGCA	TGGGAGCCT	GAGCTTTTGA	300

5	AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCCTCT GGGGAATCAG 360
	GACTCCGAG GAGAGGCTCT GACCCAGCAA GTGGAGAAGT GGAGGCTCT CAGTTAAGAA 420
	GACTGAATAT AAAGAAAGAT GATGAGTTT TCCATTTCGT CTCTCTGTGC TTTGCCATCG 480
	GGGCTCTGCT GGTGTGTTAT CACTATTACG CAGACTGGTT CATGTCTCTT GGGGTGGGCC 540
	TGCTCACCTT CGCCTCCCTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
	ACAGCGTCT CCAAGGCTTC ATCCCTCTCT TCCAGAAGTT TAGGCTGACA GGGTTCAGGA 660
	AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCAGTGT GACCACCACT 720
	GGGACCCCTG AGCCCAACAAG GGCAGAGCAG CATTCTGAGA GACGCACAGG AGACCAAGCC 780
10	AGACCAATAA ACAGAACACT TTTCCTTCCA TGTGGTCTGA ATGTTGGCAC CAGCCCGGGC 840
	AGGGGCATCT CATTTGGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
	GGTGGGTGTG GGGCTGAGG CTTACAGTA CCTGACCAAG CAGGAAGATT CTGGGAGGTC 960
	ACTGCTCTCA GAGGACAGCA AGGACCCCTG AGCTCTGCAA GCTGTGATCT GTCTGGGTTT 1020
	ATGGTTTTTC TCAATTCCTA GGCTATCTGC ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
15	GGGAGAGATG GATGGTCCAC TGCTTTGAGG CAGGGAGCCA TCGGCTGGG GCCCTTGGT 1140
	GAACTCTAAT CAGGTAAGAT GCTGAGGACT AAAACCATTT TTTTTCACCC CAAAAAATAA 1200
	GGCAGGAAAT TGATCTCAG AAACATAATG GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
	TCCTGCACT TTGGGAGGCT CAGGCTAAGG GTCGCTTGAA GCTGAGAGTT CAAGACCAAC 1320
	CTGGCAACA TAGTGAGACC CCCATCTCTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
20	TACATACCTG TACATACCTG CGGTTCCAGC TACTCAAGAG GCTGAGGCAG GAGGACTGCT 1440
	TGAGCCACAG AGTTCAGGGC TGCACTGAGG TACGATCAAG CCACCTGACT CCAGCCTGGG 1500
	CGACAGAGCA AGATCGTTTT TCTAAAAATT

25 Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_060776

30	1 11 21 31 41 51
	METSASSSQP QDNSQVHRET EDVDYGETDF HKQDGKAGLF SQEQYERNKS SSSSFSSSSS 60
	SSSSSSSSSS GPGHGEPPVL KDEQLYQDA PGEVVPSEGS GLRRRGSDPA SGEVEASQLR 120
	RLNIKKDDFF FHFVLLCPAI GALLVCYHY ADWPFMSLGVG LLTFASLETV GIYFLGVYRI 180
	HSVLQGFPL FQKFRLLTGR KTD

35 Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 243..896

40	1 11 21 31 41 51
	ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
	CCTTCTCTGG TCCGACCTCG GCCCGCGCGG CCCCTCTCGG CGCTCCGCTC TCOCGGCTCC 120
	TGGCGGCTCG GGTGGCGCGG GTTGGGCGCG CGCCTTGGCT GCTCCTCGGG GCGCGGACGG 180
	GGCTCAGCGG CGGCGCGCGC ACGGCTTCA CGCGCGCGCG CTCTGACGCC GGCATAAGGG 240
	CCATGTGTTC TGAATTTATT TTGAGGCAAG AAGTTTGAAG AGATGGTTTC CACAGAGACC 300
45	TTTTAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
	TTAAACAGGA CATTCTCTCA GGACTTTATG TGATTCGGTA TGAGTTGGCT TCATTACGAG 420
	AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAATTT TGATATAGAG GCCCTTAATC 480
	ATTTGTCCAA GGAGTCTGAA GTTCTCATTT ATGCCAGACG AGATTCACAG TGCAATGACT 540
50	GTTTTCAAGC CTTTTTGCTT GTGCACTGCC GCTATCATCG GCGCACAGT GAAGATGGAG 600
	AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTGTATGTT TTGTGACCAA GAGTTCCCGA 660
	TTTTGAAATG CTGGGCTCAC TCAGAAAGTG CAGCCCTTGG TGCTTTGGAT AATGAGGATA 720
	TATGCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
	CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGTCT ATTACAATCC 840
55	TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAAATATG CCATTTTTTC CTATAAGTTT 900
	TATGTAGTTA AATGCTCTCT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
	TTCTCTAAGA ATTAATTAAT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
	TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT 1080
60	CCTGGTAAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTTCTG TAAATTAATG 1140
	TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGCTAG AAAAATTAAT TCTTTATGTA 1200
	GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCAATT TAAGCTACAA ATTGAGAAAA 1260
	CGGTATATAA TAAGAAATAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCAGCAC 1320
	TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
	ACCTGTCTCT TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGCA TCTGTAGTCC 1440
65	CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
	GAGCCAAGAT CGCACCCTG CACTACAGCC TGGGCGACAG AACGAGACCC TGCTCCAAA 1560
	GGAAAAACAA AAAAGAGGAA TAAAAATAAT TGATGAAAA TCATGTTTAT TTAATAGTA 1620
	ATGTCAAGAG ACTATTAAAG ATGTGCCAGA GTTCAATGA AAATCATTAA AGTAGGACAG 1680
	CTAAGAAATT AATATTAAATA TAAAAATTAT TGATAATCTT AAATTATGTA TTATCTCTTA 1740
70	ACGCACCTCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
	GGACTTGATG AAACCTGAGT CTAAGATTGT GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860
	TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAAAAA AAAAAA

75 Seq ID NO: 124 Protein sequence:
Protein Accession #: AAH22542

80	1 11 21 31 41 51
	MCSBIILRQE VLKDGPHRDL LIKVKFGESI EDLHTRLLI KQDIPAGLYV DPYELASLRE 60
	RNITEAVMVS ENFDIEAPNY LSKESEVLIY ARDSQCIDC FQAPLPVHCR YHRPHSEDE 120
	ASIVVNFPL LMFCDQAGSR RMIRPRFDSF DKTIIEFPLK CWAHSEVAAP CALENEDICQ 180
	WNRKMYKSVY RNVILQVPVG LTVETSLVCS VTLLITILCS KKKKK

85 Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

1 11 21 31 41 51
AGACACCTCT GGCCTCACC TGAGCCTCTG GCAGCCCTG GTCTGGTGC TCCTGGTGT 60
GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTGTGCTCT TCCTGGAGA 120
5 CACTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180
CACTCGGGTG GCAGAGATGC GTGGAGATGC GAAATCTCTG GGGCTGCGC TGCTGCTTCT 240
CCAGAAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300
GCGAACCCCA CCGTGCGGGG TCCACAGACT GGGCAGATTG CAAACCTTTG AGGGCGACCT 360
CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGGCCGG 420
10 GCGGTGATT GACGAGCCT TTTCCCGCGC CTTCGCACTG TGGAGCGCGG TGAOCCGCT 480
CACTTCACT CGGTGTACA GCGGAGAGC AGACATGCTC ATCCAGTTTG GTGTGCGGA 540
GCAOAGGAG GGGTATCCCT TCGACGGGAA GGAOAGGCTC CTGGCACAGC CCTTTCCTCC 600
TGGCCCCGGC ATTCAGGGAG AGCCCCATT CGACGATGAC GAGTTGTGGT CCTTGGGCAA 660
GGCGTGTGT GTTCAACTC GGTTTGAAA CGCAGATGGC GGGCCCTGCC ACTTCCCTTT 720
15 CATCTTCGAG GGCCTCTCT ACTCTGCTC CACCAACGAC GGTGCTCGC AGGCTTGCC 780
CTGGTGCAGT ACCAAGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCAGCGA 840
GAGACTCTAC ACCCGGAGCG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCTCTT 900
CCAAGGCCAA TCTACTCCG CCTGCACAC GGAOGTGGC TCGACGGCT ACCTCTGGTG 960
20 CGCCACCAC GTCCTACTAG ACCGGGACAA GCTCTTCGGC TTCTGCGCGA CCGAGCTGA 1020
CTCGACGGTG ATGGGGGCA ACTCGCGGGG GAGCTGTGTC GTCTTCCCTT TCACTTCTCT 1080
GGGTAAAGAG TACTGCAGCT GTACCAAGCA GGGCCCGCGA GATGGGCGCC TCTGGTGGC 1140
TACCACCTTC AACCTTTGACA GCGACAAGAA GTGGGCTTC TGCCCGGACC AAGGATACAG 1200
TTTGTTCCTC GTGGGGGCGC ATGAGTTCCG CCAOCCGCTG GGTTAGATC ATTCTCTAGT 1260
GCGGAGGCG CTCTGTACT CTATGTACCG CTCTACTGAG GGGCCCCCTT TGCATAAGGA 1320
25 CGACGTGAAT GGCATCCGCG ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCTCC 1380
AACCACACAC ACACCGAGC CCACGGCTCC CCGACGGTC TGCCCCACCG GACCCCCAC 1440
TGTCCACTAC TCAGAGCGCG CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500
AGGTCCCCC ACTCTGCGCC CTCTACCGC CACTACTGTG CCTTGTAGTC CGGTGGACGA 1560
30 TGCTGCAAC GTCAACTACT TCGACGCCAT CGCGGAGATT GGGAAACGAG TGTATTGTT 1620
CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGG AGCGCGCGC AGGGCCCCCT 1680
CCTTATCGCC GACAGTGGC CGCGCTGCC CCGCAGCTG GACTCGTCT TTAGGAGGCC 1740
GCTCTCCAG AAGCTTTTCT TCTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCTG 1800
GGTGTGGGG CCGAGGGGTC TGGACAAGCT GGGCCTGGGA GCGACGTTG CCCAGGTGAC 1860
35 CGGGGCCCTC CGGAGTGGCA GGGGAAGAT GCTGCTGTT AGCGGGCGGC GCCTCTGAG 1920
GTTGAGCTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTG ACCGATGTT 1980
CCCCGGGGTG CCTTTGGACA CGCACGAGT CTTCAGTAC CGAGAGAAAG CCTATTCTG 2040
CCAGGACCGC TTCTACTGCA GCGTGAATTC CCGAGTGAAG TTGAACAGG TGAACCAAG 2100
GGGCTACGTC ACCTATGACA TCTGCAATG CCCTGAGGAC TAGGGCTCCC GTCTCTCTT 2160
40 CGAGTGCAT GTAAATCCCC ACTGGACCA ACCCTGGGA AGGAGCCAGT TTGCGGATA 2220
CAAACTGTA TTCTGTTCTG GAGGAAAGG AGGAGTGGAG GTGGGCTGG CCCTCTCTTC 2280
TCACCTTGT TTTTGTGTG AGTGTTTCTA ATAACTTGG ATTCTCTAAC CTTT

Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_004985.1

1 11 21 31 41 51
MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRLNLT DRQLAEYLY RYGYTRVAM 60
RGESKSLGPA LLLIQKQLSL PETGELDSAT LKAMRTPRCS VPDLRFTQF EGDLEKWHEN 120
50 ITYWIQYSE DLPRVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDDYP 180
FDGKDLGALL AFPPGPGIQG DAHPDDDELW SLGKGVVVPF RFGNADGAAC HPPFIFEGRS 240
YSACTTCCAG DGLPWCSTTA NYDTDDRFGP CPSERLYTRD GNADGKPCQF PPIFQGSYS 300
ACTTDRSDG YRWCAATTANY DRDKLFGPCP TRADSTVMGG NSAGELCVFP TFLGKEYST 360
55 CTSEGRGDGR LWCATTSNFD SDKKGWPCPD QGYSLPLVAA HEPHALGLD HSSVPEALMY 420
PMYRFTGEP LHRDDVNGIR HLYGPRPEPE PRPFTTTPQ PTAPPTVCP TGPPTVHPSE 480
PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDLAIBIGNQ LYLFDKGYW 540
RFSGRGRSP QGFLLADKV PALPRKLDV FEEPLSKLFP FFSGRQVWVY TGA SVLGPFR 600
LDKLGADGV AQVTGALRSR RGMMLFSGR RLNRFDVKAQ MVDPRSASEV DRMPGVPPLD 660
THDVQYREK AYFCQDRPYW RVSSRSELMQ VDQVGVVYTD ILQCPED

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_004181
Coding sequence: 32-670

1 11 21 31 41 51
GCAGAAATAG CTAAGGAGA TCAACCCCGA GATGCTGAAC AAAGTGTCTG CCGGCTGGG 60
GGTCCCGGCG CAGTGGCGCT TCGTGGACGT GCTGGGGCTG GAAGAGGAGT CTCTGGGCTC 120
70 GGTGCCAGCG CCGCTGCGC CGCTGCTGCT GCTGTTTCCC CTCACGGCCC AGCATGAGAA 180
CTTCAGGAAA AAGCAGATTG AAGAGCTGAA GGGACAAGAA GTTAGTCTTA AAGTGTACTT 240
CATGAAGCAG ACCATTGGGA ATTCTGTGG CACAATCGGA CTTATTCAAG CAGTGCCCAA 300
TAATCAAGAC AAACGGGAT TTAGGATGG ATCAGTTCTG AAACAGTTTC TTTCTGAAC 360
AGAGAAAATG TCCCTGAAG ACAGAGCAA ATGCTTTGAA AAGATGAGG CCATACAGGC 420
75 AGCCCATGAT GCGTGGCAC AGGAAGGCCA ATGTCGGGTA GATGACAAGG TGAATTTCCA 480
TTTTATTCTG TTTAACAACG TGGATGGCCA CCTCTATGAA CTTGATGGAC GAATGCCCTT 540
TCCGGTGAAC CATGGGCCCA GTTCAGAGGA CACCCTGCTG AAGGAOGCTG CCAAGGTGTG 600
CAGAGRAATC ACCGAGCGTG AGCAAGGAGA AGTCCGCTTC TCTGCGGTG CTCTCTGCAA 660
GGCAGCCTAA TGCTCTGTGG GAGGGACTTT GCTGATTTC CCTCTTCCCT TCAACATGAA 720
AATATATACC CCCCATGCG TCTAAAATGC TTCAGTACT GTGAAACACA GCTGTCTTC 780
80 TGTCTCGAG ACACGCTTC CCTCAGCCA CACCCAGGCA CTTAAGCACA AGCAGAGTGC 840
ACAGCTGTCC ACTGGGCCAT TGTGGTGTGA GCTTCAGATG GTGAAGCATT CTCCCCAGTG 900
TATGTCTTCT ATCGATATC TAACGCTTTA AATGGCTACT TTGTTTCTG TCTGTAGTT 960
AAGACCTTGG ATGTGGTTAT GTTGTCTTAA AGAATAAATT TTGCTGATAG TAGC

Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_004172

1 11 21 31 41 51
 5 MLNKLVSRLG VAGQWRFVDV LGLEESLGS VPAPACALLL LPPLTAQHEN FRKKQIEELK 60
 GQEVSPKVPYF MKQTIGNSCG TIGLIHAVAN NQDKLGFEDG SVLKQFLSET EKMSPEDRAK 120
 CFENEAIAQA AEDVAQEGGQ CRVDDKVNPH FILFNNVDGH LYELDGRMPF FVNHGASSED 180
 TLKDAARKVC REPTEREQGE VRPSAVALCK AA

10 Seq ID NO: 129 DNA sequence
 Nucleic Acid Accession #: NM_000213
 Coding sequence: 127-5385

1 11 21 31 41 51
 15 GCGCCGCGCG CTGCAGCCCC ATCTCCTAGC GGCAGCCGAG GCGCGGAGGG AGCGAGTCCG 60
 CCGGAGGGA GGTCCAGGAC GGGGCGACAG CAGCAGCCGA GGTGGGCGGG GAGAGGGGAG 120
 AAGAGGATGG CAGGGCCACG CCCGAGCCCA TGGGCCAGGC TGCTCCTGGC AGCCTTGATC 180
 AGCGTCAGCG TCTCTGGGAC CTTGGCAAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC 240
 20 ACGGAGTGTG TCGGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC 300
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	GACACGCCCA	CCCGCCTGCT	GTTCTCTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
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	GGGGATATCG	TGGCTACCT	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCGAG	AGCCCGCTGA	CGTGGCGGG	CCTCAGCGAG	5040
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	GAGGGCATCA	TCACTACAGA	GTCCACGAGT	GGAGGACCCCT	TCCCGCAGCT	GCGCAGCCGT	5160
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15	AGGCCACACG	AGCCCTTCTC	AGTGGATGGG	CCGACCCCTG	GGGCCACGCA	CCTGGAGGCA	5280
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	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCGCCATC	GTCCCACTAG	GGTCTCTCCC	GACTCTCTCT	CCGGAGCCTC	CTCAGCTACT	5460
20	CCATCTCTGC	AGCCCTGGGG	GCCAGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
	TCCTGGGAGG	CATGAAGGGG	GCAAGGTCCG	TCCTCTGTGG	GCCCAACCT	ATTGTATAAC	5580
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	ACTG						

25 Seq ID NO: 130 Protein sequence:
Protein Accession #: NP_000204

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	EVFEPLESFV	DLVILMDPSN	SMSDDLNLK	RMGQNLARVL	SQLTSDYITIG	FGKPVDKVSU	180
	PQTDMPREKL	KEPWPNSDPP	PSFKNVISLT	EDVDEPRNKL	QGERISGNLD	AFEGGPDAIL	240
	QTAVCTRDIG	WRPDSLHLV	PSTESAFHYE	ADGANVLAGE	MSRNDERCHL	DTTGTYYQVR	300
35	TQDYPSPVFTL	VRLLAKHNII	PIFAVTNYSY	SYYEKLEHTY	PVSSGLVLQE	DSSMTVELLE	360
	EAFNRIRSNL	DIRALDSPRG	LRTEVTSKMF	QKTRTGSPFH	RRGEVGIYQV	QLRALEHVDG	420
	THVQQLPEDQ	KGNLHLKPSF	SDGLKMDAGI	ICDVCTCELQ	KEVRSARCSF	NGDPVOCQCV	480
	CSBGWSGQTC	NCSTGSLSDI	QPCLRBEGDK	PCSGRGECCQ	GHCVCYGBGR	YEQFCEYDN	540
40	PQCPRTSGFL	CNDRGRCSMG	QCVCEPGWTG	PSCDCPLSNA	TCIDSNGGIC	NGRGHCEOGR	600
	CHCHQQSLYT	DTICEINYSY	IHPGLCEDLR	SCVQCQAWGT	GEKKGRICEE	CNFKVKMDE	660
	LKRAEEVVVR	CSFRDEDDDC	TYSYTMEDG	APGPNSTVLV	HKKXDCPPGS	PWWLIPLLLL	720
	LLPLALLLLL	LCWKYCACCK	ACLALLPCCN	RGHMVGFKEQ	HYMLRENLMA	SDHLDTPLMR	780
	SGNLGRDVRV	RWKVTNNMQR	EGFATHAASI	NPTLVPYGL	SLRLARLCTE	NLLKPDTRRC	840
45	AQLRQVEVEN	LNEVYRQISG	VHKLQTKFR	QQPNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
	LTEKQVBQRA	FHDLKVAPGY	YTLTADQDAR	GMVEFQBGVE	LVDVRVPLFI	RPEDDDEKQL	960
	LVEAIDVPAG	TATLGRRLVN	ITIIKQARD	VVSFEQPEFS	VSRGDQVARI	PVIRRVLDGG	1020
	KSQVSRTPQD	GTAGQNRDVI	PVSGELLQFP	GEAWKELQVK	LLELQEVDSL	LRGRQVRRFH	1080
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50	RKIHFNWLPF	SGKPMGYRVK	YWIQDSESE	AHLDSKVPS	VELTNLYPCV	DYEMKVCAYG	1200
	AQGGEPYSSL	VSCRTHQEPV	SEPGRLAFNV	VSSVTQLSW	AEPATNGEI	TAYEVCYGLV	1260
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60	LFQHPQLQSY	SSITTTHTSA	TEPFLVDGPT	LGAQHELAGG	SLTRHVTQEP	VSRTLTSTGT	1740
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Nucleic Acid Accession #: BC004372
Coding sequence: 132..2231

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70	CTCGGACAC	CATGGACAAG	TTTTGGTGGC	ACGCAGCCTG	GGGACTCTGC	CTCGTGCCGC	180
	TGAGCCTGGC	GCAGATOGAT	TTGAATATAA	CCTGCCGCTT	TGCAGGTGTA	TTCCAGCTGG	240
	AGAAAAATGG	TGCTACAGC	ATCTCTCGGA	CGGAGGCCGC	TGACCTCTGC	AAGGCTTTCA	300
	ATAGCACTT	GCCACAAATG	GCCAGATGG	AGAAAGCTCT	GAGCATCGGA	TTTGAGACCT	360
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75	GTGCAGCAAA	CAACACAGGG	GTGTACATCC	TCACATCCAA	CACCTCCAG	TATGACACAT	480
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	AGAAAGGAGA	ATACAGAACG	ATCCTGAAG	ACATCTACCC	CAGCAACCC	ACTGATGATG	660
	ACGTGAGCAG	CGGCTCTCTC	AGTGAAGAGA	GCAGCACTTC	AGGAGGTTAC	ATCTTTTACA	720
80	CCTTTTCTAC	TGTACACCCC	ATCCAGACG	AAGACAGTCC	CTGGATCACC	GACAGCACAG	780
	ACAGAAATCC	TGCTACCAAG	AGTCTTCAA	ATACCATCTC	AGCAGGCTGG	GAGCCAAATG	840
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	ACCCAGAAAG	ACACCCCTCC	CTCAITCACC	ATGAGCATCA	TGAGGAAGAA	GAGACCCAC	1140
	ATTCTACAG	CACATCCAG	GCAACTCCTA	GATGATCAAC	GGAAGAAACA	GCTACCCAGA	1200
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Seq ID NO: 132 Protein sequence:
Protein Accession #: AAH04372

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GSSSSRSSTS GGYIFYTTFST VHPIPDEDSF WITDSTDRIP ATSTSSMTIS AGWEPNEENE 240
DERDRLSFS GSGIDDDDEF ISSTISTTFR APDHTKQND WTQWNPESHN PEVLLQTTTR 300
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FGNRWHEGYR QTPREDSSHST TGTAASAHT SHPMQGRITP SPEDSSWTFD FNPI SHFMGR 420
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KDHPTTSTLT SSNRNDVTGG RRDPNHSEGS TTLLEGYTSR YPTKESRTF IPVTSARTGS 540
FGVTAVTVGD SNSNVNRSLS GDQDTFEPSP GSHTTHGSES DGHSHGSQEG GANTTSGPIR 600
TPQIPWELII LASLLALALI LAVCIAVNSR RRCQKKKLV INSGNGAVED RKP SGLANGEA 660
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Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_002882
Coding sequence: 150-755

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Seq ID NO: 134 Protein sequence:
Protein Accession #: NP_002873

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VWNTHADPAD ECPKPELLAI RPLNAENAQK PKTKPECRK EIEREREKAG SGKNDHAEKV 180
AEKLEALSVK EETKEDABEK Q

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Seq ID NO: 135 DNA sequence
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Coding sequence: 277-742

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GCCTTGGCT GACTGGCTGG CCACGGCCGC GGGCCGGGGT CGGGTAGAGG AGGTGCGGGC 360
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AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCACTG TGTGGAGTT TTCTGGAGTG 1020
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GAAGCTGTGC ACTTCATGAC AAGCAATTTG TGAAC TAGG AAGCTCAGG GGGTTACTGG 1140
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Protein Accession #: NP_000068.1

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LGRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

Seq ID NO: 137 DNA sequence
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Coding sequence: 104-421

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GCCCCACACC TGGCTCTGAC CATTCGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
CGAGTGGCG QAGCTGCTGC TGCTCCACCG CGCGGAGCCC AACTGCGCGC ACCCGGCCAC 180
TCTCACCCGA CCGGTGCAGC ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGTCT 240
GCACCGGGCG GGGGCGCGCG TGGAGGTGCG CGATGCCTGG GCGCGTCTGC CGGTGGACCT 300
GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACTCG CGCGCGGCTG CGGGGGGCAC 360
CAGAGGCACT AACCATGCCG GCATAGATGC CGCGGAAGGT CCTCAGACA TCCCGGATTG 420
AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAACCTTAG ATCATCAGTC ACOGAAGGTC 480
CTACAGGGCC ACAACTGCCC CGGCCACAAC CCACCCCGCT TCGTAGTTT TCATTAGAA 540
AATAGAGCTT TTAATAATGT CCTGCCTTT AACGTAGATA TAAGCCTTTC CCCACTACCG 600
TAAATGCCA TTTATATCAT TTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACTCAOCG CCTAAGCGCA 720
CAITCATGTG GGCATTTCTT GCGAGCCTCG CAGCCTCCCG AAGCTGTGCA CTTATGACA 780
AGCATTTGT GAACTAGGGA AGCTCAGGGG GGTACTGGC TTCTCTTGAG TCACACTGCT 840
AGCAATGCG AGAACCAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCCTC

Seq ID NO: 138 Protein sequence:
Protein Accession #: NP_478103.1

1 11 21 31 41 51
MMGSSARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG 60
RLPVDLAEBL GHRDVARYL RAAAGGTRGS NHARIDAAEGP SDIPD

Seq ID NO: 139 DNA sequence
Nucleic Acid Accession #: NM_058197.1
Coding sequence: 272-684

1 11 21 31 41 51
CCCAACCTGG GCGACTTCA GGTGTGCCAC ATTOGCTAAG TGCTCGGAGT TAATAGCACC 60
TCCTCGAGC ACTCGCTCAC GGCCTCCCTT TCCCTGGAAA GATACCGCGG TCCCTCCAGA 120
GGATTTAGG GACAGGGTGC GAGGGGGCTC TTCGCGCAGC ACCGAGGAA GAAAGAGGAG 180
GGGCTGGCTG GTCAACAGAG GGTGGGGCGG ACCCGGTGCG CTGCGCGGCT GCGGAGAGGG 240
GGAGAGCAG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
GCCGCGCGCG GGGAGCAGCA TGGAGCCTTC GGTGACTGG CTGGCCACCG CCGCGGCCCG 360
GGSTCGGGTA GAGGAGGTGC GGGGCTGCT GAGAGCGGGG GCGCTGCCCA ACGCACCGAA 420
TAGTTACGGT CCGAGGCGCA TCCAGGTGGG TAGAAGTCT GCAGCGGGAG CAGGGGATGG 480
CGGGGAGCTC TGGAGGACGA AGTTTGCAAG GGAATTGGAA TCAGGTAGCG CTTGATTCT 540
CGGAAAAAG GGGAGGCTTC CTGGGAGTT TTCAGAAGGG GTTTGTAATC ACAGACCTCC 600
TCCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAAG 720
TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGCG GCGGAGCCCA 780
ACTGCGCCGA CCGCGCACT CTCACCGGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC 840
TGGACACGCT GGTGGTGTCT CACCGGCGCG GGGCGCGGCT GGAAGTGGC GATGCTGGG 900
GCCGTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTGCA CGGTACTGTC 960
CGCGGCTGCG GGGGGGACCC AGAGGCGAGTA ACCATGCGCG CATAGATGCC GCGGAAGGTC 1020
CCTCAGACAT CCGCGATTGA AAGAACCGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
CATCAGTAC CGAAGGTCTC ACAGGGCCAC AACTGCCCGC GCCACAACCC ACCCGCTTT 1140
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCCCTTTAA GGTAGATATA 1200
TGCCCTTCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1260
TGTAATAAAG AAAAAACCGC CTTCTGCTTT TTCATGTGT TGGAGTTTC TGGAGTGAGC 1320
ACTCAGCGCC TAAGCGCACA TTCAATGTGG CAITTTCTGC GAGCCTCGCA GCCTCGGAA 1380
GCTGTGACT TCATGACAAG CATTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT 1440
CTCTTGAGTC AACTGCTAG CAAATGGCAG AACCAGAGCT CAAATAAAAA TAAATAAATT 1500

Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

5
1 11 21 31 41 51
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVRLAL EAGALPNAPN SYGRRPIQVG 60
10 RRSAAAGAGDG GRLWRTKFAF ELESQSASIL RCKGRLPGEF SEGVCNHRPP PGDALGAWET 120
KEEE

Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

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1 11 21 31 41 51
CCTCCCTACG GGGCCCTCCG GCAGCCCTTC CCGCGTGGCG AGGGCTCAGA GCGTTCGGA 60
20 GATCTTGGAG GTCGGGGTGG GAGTGGGGGT GGGGTGGGGG TGGGGGTGAA GTGGGGGGG 120
GGCGCGCTC AGGAAGGGCG GGTGGCGCC TGGGGGGCGG AGATGGGCAG GGGGGGTGC 180
GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GTTGCCAAAG 240
GGCGGGCGAG CGGCTGCCGA GCTCGGCCCT GGAGGGCGCG AGAACATGGT GCGCAGGTT 300
TTGGTGACCC TCOCGATTGG GCGCGCGTGC GGGCCGCGCG GAGTGAGGGT TTTCTGGTT 360
25 CACATCCCGC GGCTCACGGG GGAGTGGGCA GCGCCAGGGG CGCCCGCCGC TGTGGCCCTC 420
GTGCTGATGC TACTGAGGAG CCAGCGTCTA GGGCAGCAGC CGCTTCTAG AAGACCAGGT 480
CATGATGATG GGCAGCGCCC GAGTGGCGGA GCTGCTGCTG CTCCAAGCGG CGAGCCCAA 540
CTGCGCGGAC CCGCGCACTC TCACCCGACC CGTGCAAGAC GCTGCCCGGG AGGGCTTCT 600
GGACAAGCTG GTGGTGTCTG ACCGGGCGGG GGGCGGCGTG GACGTGCGCG ATGCTTGGGG 660
30 CGGTCTGGCC GTGGACCTGG CTGAGGAGCT GGGCCATCGC GATGTGCGAC GGTACCTGG 720
CGCGGCTGGG GGGGGCACCA GAGGCAGTAA CCATGCCCGC ATAGATGCGG CGGAAGGTCC 780
CTCAGACATC CCCGATTGAA AGAACCCAGAG AGGCTCTGAG AAACCTCGGG AAACCTTAGT 840
CATCAGTCAC CGAAGGTCTT ACAGGGCCAC AACTGCCGCC GCCACAACCC ACCCGCTTT 900
CGTAGTTTTC ATTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTAA CGTAGATATA 960
35 TGCTTCTCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1020
TGTAATAAAG AAAAACACCG CTTCTGCCCT TTCACTGTGT TGGAGTTTTC TGGAGTGAGC 1080
ACTCAGCCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA 1140
GCTGTGCACT TCATGACAAG CATTGTGTA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT 1200
40 CTCTGAGTC AACTGCTAG CAATGGCAG AACCAAGACT CAAATAAAAA TAAATAAATT 1260
TTCATTCATT CACTC

Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

45
1 11 21 31 41 51
MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AELGPGGGE NMVRRPLVTL RIRACGPPR 60
VRVFFVHIFR LTGEWAAPGA PAAVALVLM LRSQRLGQOP LPRRPGHDDG QRPSCGAAAA 120
50 PRRGAQLRRP RSHPTARR CPGLPGHAG GAAPGRGAAG RARCLGPSAR GPG

Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

55
1 11 21 31 41 51
GAAATTGCAC ACTTAAGAC ATCAGTGGAT GAAATCACAA GTGGGAAAGG AAAGCTGACT 60
60 GATAAAGAGA GACAGAGACT TTTGGAGAAA ATTGAGTCC TTGAGGCTGA GAAGGAGAAG 120
AATGTCTTATC AACTCACAGA GAAGGACAAA GAAATACAGC GACTGAGAGA CCAACTGAAG 180
GCCAGATATA GTACTACCGC ATTGCTTGAA CAGCTGGAAG AGACAACGAG AGAAGGAGAA 240
AGGAGGGAGC AGGTGTTGAA AGCCTTATCT GAAGAGAAAG ACGTATTGAA ACAACAGTTG 300
TCTGTGCAAA CCTCAGAAAT TGCTGAACTT GAAAGCAAAA CCAATACACT CCGTTTATCA 360
65 CAGACTGTGC TTCCAAACCTG CTTCAACTCA TCAATAAATA ATATTATGA AATGGAATA 420
CAGCTGAAG ATGCTCTGGA GAAAAATCAG CAGTGGCTCG TGTATGATCA GCAGCGGGAA 480
GTCTATGTAA AAGGACTTTT AGCAAAAGATC TTTGAGTTGG AAAAGAAAAC GGAACAGACT 540
GCTCAITTCAC TCCACAGCA GACAAAAAAG CCTGAATCAG AAGGTTATCT TCAAGAAAGAG 600
AAGCAGAAAT GTTACAAAGA TCTCTGGCA AGTGCAAAA AAGATCTTGA GGTGAAACGA 660
70 CAAACCATAA CTCAGCTGAG TTTTGAACCTG AGTGAAATTC GAAGAAAATA TGAAGAAACC 720
CAAAAAGAAG TTCACAATTT AATCAGCTG TTTGATTAC AAAGAAGGGC AGATGTGCAA 780
CATCTGGAAG ATGATAGGCA TAAACAGAG AAGATACAAA AACTCAGGGA AGAGAATGAT 840
ATTGCTAGGG GAAAACTTGA AGAAGAGAAG AAGAGATCCG AAGAGCTCTT ATCTCAGGTC 900
CAGTCTCTTT ACACATCTCT GCTAAAGCAG CAAGAAGAAC AAACAGGGGT AGCTCTGTTG 960
75 GAACAACAGA TGCAAGCATG TACTTTAGAC TTTGAAATG AAAAATCTGA CCGTCAACAT 1020
GTGAGCATC AATGTCAATG AATCTTAAG GAGCTCOGAA AAGCAAGAAA AAATAACACA 1080
GTGGAATCC TTGAAACAGC TTCAATGAGT TGCCATCACA GAGCCATTAG TCACTTTCCA 1140
AGGAGAGACT GAAACAGAG AAAAAGTTGC CGCTCACCA AAAAGTCCCA CTGCTGCACT 1200
CAATGGAAGC CTGGTGAAT GTCCCAAGTG CAATATACAG TATCCAGCCA CTGAGCATCG 1260
80 CGATCTGCTT GTCCATGTGG AATACTGTTT AAAGTAGCAA AATAAGTATT TGTTTTGATA 1320
TTAAAAGATT CAATACATGA TTTTCTGTTA GCTGTGGGGC ATTTTGAAAT ATATATTCA 1380
CATTTTGCAAT AAAACTGCCT ATCTACCTTT GACACTCCAG CATGCTAGTG AATCATGTAT 1440
CTTTTAGGCT GCTGTGCAIT TCTCTGGCA GTGATACCTC CCGACATGGS TTCATCATCA 1500
GGCTGCAATG ACAGAAATGTG GTGAGCAGCG TCTACTGAGA TACTAACATT TTGCACTGTC 1560
85 AAAAATCTTG GTGAGGAAAA GATAGCTCAG GTTATTGCTA ATGGSTTAAT GCACCAGCAA 1620
GCAAAATATT TTATGTTTCG GGGGTTTGA AAAATCAAAG ATAATTAAAC AAGGATCTTA 1680
ACTGTGTTGC CATTTTATAT CCAAGCACTT AGAAAACTTA CAATCCTAAT TTTGATGTCC 1740
ATTGTTAAGA GGTGGTGATA GATACTATT TTTTTCATA TTGTATAGCG GTTATTAGAA 1800

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AAGTTGGGGA TTTCTTGAT CTTTATTGCT GCTTACCATT GAAACTTAAC CCAGCTGTGT 1860
TCCCAACTCT TGTCTCTGCG ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA 1920
CACACAATGT TTTCTCTTAT GTTATCTGGC AGTAACCTGT ACTTGAATTA CATTAGCACA 1980
TTCGTCTTAG CTAAATTTGT TAAATAAACC TTAAATAAAC CCATGTAGCC CTCTCATTTG 2040
ATTGACAGTA TTTTAGTTAT TTTTGGCAAT CTAAAGCTG GGCATGTAA TGATCAGATC 2100
TTTGTTTGTC TGAACAGGTA TTTTATACA TGCTTTTGT AAACCAAAA CTTTAAATT 2160
TCTTCAGGTT TTCTAACATG CTTACCACTG GCGTACTGTA AATGAGAAAA GAATAAAATT 2220
ATTTAATGTT TT

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Seq ID NO: 144 Protein sequence:
Protein Accession #: NP_060601

15
20
25

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1 11 21 31 41 51
| | | | |
MBIQLKDALE KNQQLVYDQ QREVVYKGLL AKIFELEKKT ETAHSLPQQ TKKPESEGYL 60
QEEKQKCYND LLASAKKDLR VERQTITQLS FELSEPERKY EETQKEVHNL NQLLYSQRRR 120
DVQHLEDDRH KTEKIQLRE ENDIARGKLE EEKRSSEELL SQVQSLYTSI LKQQEEQTRV 180
ALLDQQMQAC TLDPENEKLD RQHVQHQHLV ILKELRKARK NMTVGILETA S

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Seq ID NO: 145 DNA sequence
Nucleic Acid Accession #: NM_001168
Coding sequence: 50..478

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40
45
50
55

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1 11 21 31 41 51
| | | | |
CCGCCAGATT TGAATCGCGG GACCGTGTGG CAGAGGTGGC GCGCGGGCCA TGGGTGCCCC 60
GACGTTGCCC CCGTCCCTTCT AGCCCTTCTT CAAGGACCAC CGCATCTCTA CATTCAAGAA 120
CTGGCCCTTC TTGGAGGGCT GCGCCTGCAC CCGGAGCGG ATGGCCGAGG CTGGCTTCAT 180
CCACTGCCCC ACTGAGAAAG AGCCAGACTT GCGCCAGTGT TTCTTCTGCT TCAAGGAGCT 240
GGAAGCTCGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGGTTG 300
CGCTTTCTTT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTTGGTGAAT TTTTGAAACT 360
GGACAGAGAA AGAGCCAAGA ACAAATTGTC AAAGGAAACC AACATAAGA AGAAAGAATT 420
TGAGGAAACT GCGAAGAAAG TGCGCGGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG 480
CCTCTGGCCG GAGCTGCCTG GTCCAGAGT GCGTGCACCA CTTCCAGGGT TTATTCCCTG 540
GTGCCACCAG CCTTCTCTGT GGCCTCTTAG CAATGTCTTA GGAAGGAGA TCAACATTTT 600
CAAAATAGAT GTTCAACTG TGCTCCTGTT TTGTCTTGAA AGTGGCACA GAGGTGCTTC 660
TGCTCTGTGA GCGGCTGCTG CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTTTT 720
GGGGGCTCAT TTTTGTCTGT TTGATTCCTG GGCCTACCAG GTGAGAAATG AGGGAGGAAG 780
AAGGCAAGTT CCGTTTGTCT AGAGCTGACA GCTTTGTTOG CGTGGGCAGA GCGCTTCACA 840
GTGAATGTGT CTGACCTCTA TGTGTGTGAG GCTGTACAG TCCTGAGTGT GGAAGTGGCA 900
GGTGCTCTTT GAATCTGAGC TGCAGGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG 960
ACAGTTTTTT TGTGTGTGTG TTTTGTGTGT TTTTGTGTGT GGTAGATGCA TGACTTGTGT 1020
GTGATGAGAG AATGGAGACA GAGTCCCTGG CTCTCTACT GTTTAAACAC ATGGCTTTCT 1080
TATTTTGTGT GAATGTGTTA TTCACAGAA AGCACAAACT ACAATTAAAA CTAAGCACAA 1140
AGCCATCTTA AGTCATTGGG GAAACGGGGT GAACTTCAGG TGGATGAGGA GACAGAAATG 1200
AGTGATAGGA AGGCTCTGGC AGATACTCCT TTTGCCACTG CTGTGTGATT AGACAGGCCC 1260
AGTGAGCCGC GGGGACATCG CTGGCCGCTC CTCCCTCAGA AAAAGGCAGT GGCCTAAATC 1320
CTTTTAAAT GACTTGGCTC GATGCTGTGG GGGAGTGGCT GGGCTGTGTC AGGCCGTGTG 1380
TCTGTACGCC CAACCTTCAC ATCTGTACAG TTCTCCACAC GGGGAGAGGA CGCAGTCCGC 1440
CCAGTCCCCC GCTTCTTTTG GAGGCAGCAG CTCCCGCAGG GCTGAAGTCT GGCCTAAGAT 1500
GATGGATTGG ATTCCGCCCT CTCCTGTGCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC 1560
GCTGGAACCC TCTGGAGGTC ATCTCGGCTG TTCTGAGAA ATAAAAAGCC TGTCATTTT

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Seq ID NO: 146 Protein sequence:
Protein Accession #: NP_001159

60
65

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1 11 21 31 41 51
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MGAPTLPPAM QPFLKDHRS TFRKNWPLEG CACTPERMAB AGFIHCPTEN EPDLAQCFPC 60
FKELEGWEPD DDPFIEHKKH SSGCAPLSVK KQFELTLGSE FLKLDREARX NKIAKETNNK 120
KKEFBETAKK VRRAIQLAA MD

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Seq ID NO: 147 DNA sequence
Nucleic Acid Accession #: NM_014176.1
Coding sequence: 127-720

70
75
80
85

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1 11 21 31 41 51
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AGTGATCCCC AGGCAGCTCT TAGTGTGGAG CAGTGAACCT TGTGTGGTTC CTCTACTTGT 120
GGGATCATCG AGAGAGCTTC ACGTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA 180
CCCCAGGCA TCACATGTTG GCAAGATAAA GACCAATAGG ATGACCTCGG AGCTCAAATA 240
TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT 300
GAGAGGTACC CATTGAACC TCCTCAGATC CGATTTCTCA CTCCAATTTA TCATCCAAC 360
ATTGATCTCG CTGGAAGGAT TTGTCTGGAT GTTCTCAAAAT TGCCACCAAA AGGTGCTTGG 420
AGACCATCCC TCACATCGC AACTGTGTTG ACCTCTATTC AGCTGCTCAT GTCAGAACCC 480
AACCCGTATG ACCCGCTCAT GCGTGACATA TCCTCAGAAAT TTAATATATA TAAGCCAGCC 540
TTCTCAGAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA GACAGAAACA AAAGGCTGAT 600
GAGGAAGAGA TGCTTGATAA TCTACCAGAG GCTGGTGAAT CCAGAGTACA CAATCAACA 660
CAGAAAGAGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTTCATCC TGATGTTTAG 720
GGGACTTGTG CTGGTTTATC TTAGTTAATG TGTCTTTTGC CAAGGTGATC TAAGTTGCCCT 780
ACCTGAATT TTTTAAAAA TATATTGAT GACATAATT TTGTGTAGTT TATTATCTTT 840
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Seq ID NO: 148 Protein sequence:
 Protein Accession #: NP_054895.1

5
 1 11 21 31 41 51
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 10 MQRASRLKRE LHMLATEPPP GITCWQDKDQ MDDLRAQILG GANTPYEKGV FKLEVIIPER 60
 YPFEPQIRF LTPYIHFNID SAGRICLDVL KLPPKGAWRP SLNIATVLTS IQLIMSEFNP 120
 DDPLWADISS EFKYNKPAFL KNARQWTEKH ARQKQKADDE EMLDNLPEAG DSRVENSTQK 180
 RKASQLVGIE KKFEPDV

Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_003812
 Coding sequence: 224-2722

15
 1 11 21 31 41 51
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 20 TCCTCTGGT CCGCCCCCGG GAGTGGCTGC GAGGCTAGGC GAGCCGGGAA AGGGGGCGCC 60
 GCCAGCCCCC GAGCCCCCGG CCCCGTGCOC CGAGCCCGGA GCCCCTGCC CGCGCGGCCA 120
 CCATGCGCGC CGAGCCCGGC TGACCGGCTC CGCCCGCGGC CGCCCGCGAG CTAGCCCGGC 180
 GCTCTGCGCG GCCACACGGA GCGGCGCCCG GGAGCTATGA GCCATGAAGC CGCCCGGCAG 240
 CAGCTGCGCG CAGCCGCCCC TGCGGGGCTG CAGCCTTGCC GGCGCTTCTT CGGCGCCCCA 300
 AGCGGGCCCC CGCGGCTCGG TGCCCTGCCAG CGCCCGGCCC CGCAGCGCGC CCGCGCGCCT 360
 25 GCTTCTGCTC CTTCTCTGTC TGCCCTCGCT CGCCCGCTCG TCCCGGCCCC GCGCCTGGGG 420
 GGCTGCTGCG CCCAGCGCTC CGCATTGGAA TGAAGTGA GAAGAAATTT TGGGAGTCTT 480
 GGCGATGAA GACAAATACAT TGCAACAGAA TAGCAGCAGT AATATCAGTT ACAGCAATGC 540
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 AAGCCCTTAT CAGCTTCTTG ACACAAAGGC AAGACACAGC CAAAAACATA ATAAGGCTGT 660
 30 CCATCTGGCC CAGGCAAGCT TCCAGATTGA AGCCTTCGGC TCCAAATTCA TTCTTGACCT 720
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 ACCACAGTAC TTAAGGGTGG GAGAGCACTG TTAATACCAT GGAAGCATCA GAGGCGTCAA 840
 AGACTCCAGG GTGGCTCTGT CAACCTGCAA TGGACTTCAT GGCACTGTTG AAGATGATAC 900
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 35 ACATATAATC CAGAAACCTT TGGCAGGACA GTATTCTAAG CAAATGAAGA ATCTCACTAT 1020
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 AGCAGTGAAT CCATCAGCTG GTATATTGTA AGAATGAAA TATTGGAAC TTATGATTGT 1140
 TAATGATCAC AAAACGTATA AGAAGCATCG CTCCTTCAT GCACATACCA ACACTTTGCG 1200
 AAAGTCCGTG GTCACCTTGT TGGATTCTAT TTCAAGGAG CAGCTCAACA CCAGGTTGT 1260
 40 CCTGGTGGCT GTAGAGACCT GGACTGAGAA GGATCAGATT GACATCACC CCAACCTGT 1320
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 45 ACAAGTATTA TCGCAGAGCC TGCTCTCAAA CCTTGAATC CAATGGGAAC CTTCTAGCAG 1560
 AAAGCCAAAA TGTGATGCA CAGAACTCTG GGTGGGCTGC ATCATGGAGG AAACAGGGGT 1620
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 AGGAGGTGGA GCTGCTCTT TCAACAGGCC AACAAAGCTA TTTGAGCCCA CGGAATGTGG 1740
 AAATGGATCA GTGGAAGCTG GGGAGGAGTG TGATTGTGT TTTCAATGAG AATGCTATGG 1800
 50 ATTATGCTGT AAGAAATGTT CCTCTCCAA CGGGGCTCAC TGCAGGAGC GCGCCTGCTG 1860
 TAACAATACC TATGCTCTTT TTCAGCCACG AGGGTATGAA TGCCGGGATG CTGTGAACGA 1920
 GTGTGATATT ACTGAATATT GTACTGGAGA CTCTGGTCAG TGCCCAACCA ATCTTCATAA 1980
 GCAAGACGGA TATGATGCA ATCAAAATCA GGGCGGCTGC TACAATGGCG AGTGCAGAGC 2040
 CAGAGACAC CAGTGTCACT ACATCTGGGG AACAAAGGCT GCAGGCTCTG ACAAGTCTCT 2100
 55 CTATGAAAAG CTGAATACAG AAGGCACTGA GAAGGAAAC TGCCGGAAGG ATGGAGACCG 2160
 GTGGATTACG TGCAGCAAA ATGATGTGTT CTGTGGATTC TTAATCTGTA CCAATCTTAC 2220
 TCGAGCTCCA CGTATTGGTC AACTTCAGGG TGAGATCATT CCACTTCCT TCTACCATCA 2280
 AGGCGGGGCT ATGATGCA GTGGTGCCCA TGTAGTTTGA GATGATGATA CGGATGTGGG 2340
 CTATGTAGAA GATGGAACCG CATGTGCCCC GTCTATGATG TGTTAGATC GGAAGTGCT 2400
 60 ACAAAATCAA GCCCTAAATA TGAGCAGCTG TCCACTCGAT TCCAAAGGTA AAGTCTGTTT 2460
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 AGATTGCACT ATCCGGGATC CAGTTAGGAA CCTTCAACCC COCAAGGATG AAGGACCCAA 2580
 GGTCTCTAGT GCCACCAATC TCATAATAGG CTCCATGCT GGTGCCATCC TGTAGCAGC 2640
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 65 TACTCAGCAA GGCOCCTACT GAATCAGCTG CGCTGGATGG ACACCGCCTT GCATCTGTGG 2760
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 CTGTCTCTTT TGGAAATAAT GTCAAAGAAC ACCTTTTACC ACCTGTCACT AAACGGGGGA 2940
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 70 ACGAAGGAAC AACACACACA CAAAAATTAA ATGCAATAAA GGAATCATTAAAA

Seq ID NO: 150 Protein sequence:
 Protein Accession #: NP_003803

75
 1 11 21 31 41 51
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 80 MKPPGSSSRQ PPLAGCSLAG ASOGPQGPAP GSVPASAPAR TPPCRLLLVL LLLPFLAASS 60
 RPRAWGAAAP SAPHNWETAB KNLGVLADED NTLQNNSSSN ISYSNAMQKE ITPSLRIYY 120
 INQDSSEPHY VLDTKARHQ KHNKAVHLAQ ASFQIEAPGS KPILDILN GLLSSDYVEI 180
 HYENGKPYYS KGGHCYYHG SIRGVKDSKV ALSTCNLHG MPEDDTFVYM IEPLLVHDE 240
 KSTGRPHIQ KTLAQYYSKQ MNLTMERGD QWPLSELQW LKRRKRAVNP SRGIFEMKY 300
 LELMIVNDHK TYKKHRSSEA HTNNFAKSV NLVDSIYKEQ LNTRVVLVAV ETWTEKDID 360
 ITTNPVQMLH EFSKYRQRIK QHADAVHLIS RVTFRYKRSS LSYFGVCSR TRGVGVNEYG 420
 85 LPMAVAQVLS QSLAQMLGT WEPSSRKPKC DCTESWGGCI MEETGVSHSR KFSKCSILEY 480
 RDLFQRGGGA CLFNRPTKLF EPTCEGNGYV EAGEBCDCGP HVCYGLCCX KCSLNGAHC 540
 SDGPCCNMTS CLFPPRGYEC RDAVNECDIT EYCTGDSQC PPNLEKQDGY ACNQNQRCY 600
 NGBCKTRDNQ CQYIWTGKAA GSKDFCYEKL NTEGTEKGNC GKDGRWICQ SKHDVPOGFL 660

WO 02/086443

LCTNLTRAPR IGQLQGEIIP TSFYHQGRVI DCSGARFVLD DDTGVGVVED GTPCGSPSMHC 720
LDRKCLQIQ A LAMSSCPDLS KGRVCSGHGV CSNEATCI CD FTWAGTDCSI RDPVRNLEPP 780
KDEGPKGPSA TNLIGSIAG AILVAIVLIG GTGWFKNVK KRRFDPTQGG PI

PCT/US02/12476

5 Seq ID NO: 151 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 250-1326

10 1 11 21 31 41 51
GGCAOGAGGG TTTCGTTTTC ATGCTTTACC AGAAAATCCA CTTCCTGCCC GACCTTAGTT 60
TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
CCCAOGCCTC AATGTCCTCC AAGTGTITTC TGACACGCAT CTTTGTCTAC AGTGCAATCAC 240
15 AACTGAAGAA TGGGGTTCAA CTTGAOGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCGAG GAAAGAACAC CACCTTTCAC 360
AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTGTG GGCAAGCATC 420
TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
TTCTATCTCA AAAACATAGT GGTTCGAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
20 ATAGTCCATG ATGACGAGT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
TCAGTTTGTG TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
GATCGCTATC TGAAGTGGT CAAGCCATTG GGGGACTCTC GGATGTACAG CATAACCTTC 720
ACGAAGGTTT TATCTGTITG TGTITGGGTG ATCATGGCTG TTTGTCTTT GCCAAACATC 780
ATCCTGACAA ATGCTCAGCG AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAGT 840
25 CCTTTGGGGG TCAAAATGGA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
GTGCTGTGTA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
GTGGCTGTG CTTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
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30 ATTACACTTT TCTGTCTGCG GTGTAATGTT TGCTTGGATC CAATAAATTA CTTTTCATG 1200
TGTAAGTCAT TTTCAGAAAG GCTGTTCAAA AAATCAAATA TCAGAACCG GAGTGAAAGC 1260
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35 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 152 Protein sequence:
Protein Accession #: NP_076404

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FYANMYTSIV FLGLISIDRY LKVVKPPGDS RMYSTPTKV LSVCVWVIMA VLSLPNIILT 180
45 NGQPTENDIH DCSKLKSPLG VEWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
ISQSSRRKXH NQSTRVVAVV FFTCFLPYHL CRIPPTPSHL DRLLDESAQK ILYYCKEITL 300
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50 Seq ID NO: 153 DNA sequence
Nucleic Acid Accession #: D80008.1
Coding sequence: 149-739

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65 GTGTCTAAAA GACTATGGAG AATTGGAAG TGATGATGGC ACTTCAGTCC TATTAATAAA 660
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70 AGGACTTTCT TTTTAAAG TGATACACTA TTCTTCTTAC TCTTTTGGG TTTTGGTTT 960
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AGTCTCTCCA CCTTAGCTTC TCAAAGTGT GAGATCACAG GGTGAGCCA CTGACCCCG 1080
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75 GTGTGTTTTT TAAATGAAAG TAAACATGGT TACATTTGAA TCTCTTAAAT AAGCAGTCAC 1200
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CAAGCTAGAG AGCTGAATT CTGAGATACA CATTTTCAAA TCACATGCAA GTGAAGATGA 1320
TGTCTGTAG AAATTTTAC TATATATAAT GTTAAATGAC ATACTAATTT ATCATCTGGC 1380
TATTTGGGAA GGAAGGACAC ACATGGATT TGCAATTTC CACCATGGTG GCTGGTGTGG 1440
CTGTGCTGTA TGGGGTGATC ACCAGTATCA CCATTTGGA AGGGGACAGT GAAATTTGGG 1500
80 CTAGAGAAAG AACTTGTATC AGTTTCCCT GAGATTGAGA TTGACTGAAA AGTCACATGA 1560
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TCCCAAGATC ACAATTTTTT TTCTTTTATA CTTCTAGAAG TGTATAAAT TTAAGCTTTA 1740
TACTTTGGTC TATGACCOGT TTTTTTTTTT GTTTTGTGTT GTTTTTCGT TGTGTTCTTT 1800
85 GTTTTGAAT GGAGCTTGT TCTGTCAACC AGGCTGGGGT GCAGTGGCGT GATCTTGGCT 1860
CACTGCAATC TCTATCCCT GGGTTCAAGT GATTCTCTTG TCTCAGCCTC CCAAGTAGCT 1920
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	TTTACCATG	TGGCCAGGC	TGGTTTCAAA	CTCCTGACCT	CAAGTGACCC	ACCTTGGCCT	2040
	CCCAAAGTTT	TGGGATTACA	AGTGTGGGCC	ACCGCGGCCA	GCCTATGATC	CATTTTGAAT	2100
	GAATTTTFTA	TATGGTGCAA	GGTGTCAATC	CACCTTCACT	TTTCTTGGG	AATATAGATA	2160
5	TCAGCTGTT	TCACACCAT	TTTTGAAAG	GACTGOCCTT	TGCTCTATCA	CCTTTGCAAT	2220
	TTTGTAAAA	AGTAGTTGTC	AATGTATATG	TGGGTTTATT	TCAGGACTCT	GTTTGTGTC	2280
	ATTGAACCTG	TTTTCTCTCC	TGAATGCCAA	TACCATATTT	GTATGTAGTG	TATGTAATTT	2340
	TCTAATAATT	CTTGAACAG	ATAGTATTAA	TGTGTCTAT	TTTTGCTGTT	GTTTGTATTT	2400
	TTTGTAGAGA	TGGGTTTCA	CCGTGTGGC	CAGGCTGTGT	TGAATCCTG	AGCTAAAGCA	2460
10	ATACACTTGC	CTGTCCTCC	CCATGTGCTG	GGATTACAGG	CGTGAGCCTT	GGTGTGGGCC	2520
	CAGTGTACCA	CATTCTTTT	TGAGATTGT	TTTGGCTATG	TTAAGTCCTT	TGCTTTTGAT	2580
	GTGAATTTG	GGAACAGGCA	GGGTGTGGTG	GCTTATGCCT	GTAATCCTAG	AACTTTGGGA	2640
	GGCTAGATG	GGTGGATCAC	TTGAGCTCAG	GAGTTCACAG	CCAGCCCGGG	CCTATGGCAA	2700
	AACTCCGCTC	CTACAAAAA	TAGAAAAAAT	TAGCCAGGTG	TGGTGGTGCA	TGCTGTAGT	2760
	CACAGTTACA	CGGCAGGCTC	AGGTGGGAGG	ATCACTTGAA	CCCCAGAGGT	CAAGACTGCA	2820
15	GTGAGCTGAG	ATCACACCC	TGTACTCCAG	CCTGGGTGAC	AAAGTGAGAC	TCTATCTCAA	2880
	AAAGAAATTA	GGATCAATTT	GTCAATTTCT	ACAAACAACA	CAACAAAAAC	CCCTGTTGGG	2940
	CACCTTGATT	GAGATTGCAAT	TGAATTTATA	TAAACTGTT	GGGAGAATTG	ACATCTTAAT	3000
	AATATTGAGT	CTTCTGGCCT	ATAACAAGG	TCTGTCTTCC	TAGGTATTAA	TGTTTTGTCT	3060
20	TCTATTCTTC	TCTAATATCT	TTTGTAGTTT	TCAGTGATCA	GGTCTACCAT	GTGAGCATTT	3120
	CATAGTTTGT	ATGCTAAATG	GTATTTTAAA	ATTTCAAATT	CTAACCACTT	GTGCTAGTA	3180
	AATAGAAATA	CAATTGATGT	TGAACCTGTA	TCCTTCAGCC	TTGCTAAACT	GTGAGTTCTC	3240
	ATGGTGTGTT	TGTAATATAC	ATCAACAGTC	ATGTGTTCTA	TGAATAAAGA	GTTTTACTCC	3300
	TTC						

25 Seq ID NO: 154 Protein sequence:
Protein Accession #: BAA11503.1

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30	MFCEKAMELI	RELHRAPEQG	LPANFEDGLR	QVLEEMKALY	BQNQSDVNEA	KSGGRSDLIP	60
	TIKFRHCSSL	RNRRTVAYLY	YDRLLRIRAL	RWEYGSVLPH	ALRFHMAAEE	MEWFNNYKRS	120
	LATYMRSLGG	DEGLDITQDM	KPPKSLYIEV	RCLKDYGEFE	VDDGTSLVLLK	KNSQHFPLRW	180
	KCBQLIRQGV	LEHLIS					

35 Seq ID NO: 155 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-709

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	CGAAAGGATT	GAGGCGCCGA	GAGCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTTGGC	120
	AAGCGCGCGG	GAGTGGGAAG	CGTCCGCCAT	GTTCTGCGAA	AAAGCCATGG	AACTGATCCG	180
	CGAGCTGCAT	CGCGCGCCCG	AAGGGCAACT	GCCTGCCTTC	AACGAGGATG	GACTCAGACA	240
45	AGTTCTGGAG	GAGATGAAAG	CTTTGTATGA	ACAAAACACC	TCTGATGTGA	ATGAAGCAAA	300
	GTCAAGTGGA	CGAAGTGATT	TGATACCAAC	TATCAAAATT	CGACACTGTT	CTCTGTTAAG	360
	AAATCGACCG	TGCACTGTAG	CATACCTGTA	TGACCGCTTG	CTTCGGATCA	GAGCACTCAG	420
	ATGGGAATAT	GGTAGGCTCT	TGCCAAATGC	ATTAGGATTT	CACATGGCTG	CTGAAGAAAT	480
	GGAGTGGTTT	AATAATTATA	AAAGATCTCT	TGCTACTTAT	ATGAGGTAC	TGGGAGGAGA	540
50	TGAAGGTTTG	GACATTACAC	AGGATATGAA	ACCACCAAAA	AGCCTATATA	TTGAAGCTGG	600
	ATGCAGTGGC	GGATCTCTGG	CTCAACCTGC	AACCTCCACC	TCCCAGGTTT	ACCTCAACTG	660
	CAACCTCCAC	CTCCAGGCTC	CGGTGTCTAA	AAGACTATGG	AGAAATTGAA	GTGATGATG	720
	GCACCTCACT	CCTATTAAAA	AAAAATAGCC	AGCACTTTTT	ACCTCGATGG	AAATGTGAGC	780
	AGCTGATCAG	ACAAAGGATC	CTGGAGCACA	TCCTGTCTAT	ACCATGCGCC	GAGGCACCTC	840
55	CAGGCTTCAC	TCAACTCATG	GACTCCTCTG	TACTCACTCT	CTCCACCACT	CCCTTCACCT	900
	CCCTCTTTGA	TTTTAGAAAG	TATAGACATT	GTTTAAAGATA	ACTAAGATA	CTTGGCTAAG	960
	AAGTATAATT	TGCTAATCAT	TAAGGACTTT	CTTTTITTA	TGTTGTACAC	TATCTCTCCT	1020
	ACTCTTTTTT	GGTTTGGTTT	TTGTTTGTGA	GAGACTGTCT	CACATGTTTG	CCCAAGCTGG	1080
	TCTCAAACCT	CTGGCCTCAA	GCACTCCTCC	CACCTTAGCT	TCTCAAAGTG	TTGAGATCAC	1140
60	AGGCGTGAGC	CACGTGACCC	GGCCCCACT	CCTTTTTCTA	ATAAGCTGTA	TCTGTAACTA	1200
	CAGCATCTCT	ACAGTTGTTA	CAGTGTGTTT	TTTAAATGAA	AGTAAACATG	GTTACATTGT	1260
	AATCTCTTAA	ATAAGCAGTC	ACTTGGCTGG	ACAGGAAGAA	GGTAGATCCT	GTGTGCTCTG	1320
	TTTTCTGGTC	ATGTGTATTG	TACAAGCTAG	AGAGCTGAAT	TTCTGAGATA	CACATTTTCA	1380
	AATCACATGC	AAGTGAAGAT	GATGGTCTGT	AGAAATTTTC	AGTATATATA	ATGTTTAATG	1440
65	ACATACTAAT	TTATCATCTG	GCTATTTGGG	AAGGAAGGAC	ACACATGGAT	TTTGACATT	1500
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	GAAGGGGACA	GTGAATTTGG	GGCTAGAGAA	GGAACTTTGT	ACAGTTTTCCT	CTGAGATTCA	1620
	GATTGACTGA	AAAGTCACAT	GAAGAGTTGA	TGTCTTTTA	ATGGTATGTT	TTAAACAGCT	1680
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70	GCATCCGAGA	AATCTTTTCC	CATCCCAAGA	TCACAAATTT	TTTTCTTTT	TACTTCTAGA	1800
	AGTGTATATA	TTTTAAGCTT	TATACITTGG	TCTATGACCC	GTTTTTTTTT	TTGTTTGTGT	1860
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	GTGCACTGGC	GTGATCTTGG	CTCACTGCAA	TCTCTATCCC	CTGGGTTCAA	GTGATTCTCT	1980
	TGCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACAGGC	CGCCACGCCT	GGCTAATTTT	2040
75	TGTATTTTTA	GTAGAGACAG	AGTTTACCA	TGTTGGCCAG	GCTGGTTTCA	AACTCCTGAC	2100
	CTCAAGTGAC	CCACTTTGGC	CTCCCAAAGT	TTTGGGATTA	CAAGTGTGGG	CCACCGCGGC	2160
	CAGCCTATGA	TCAATTTTGA	ATGAATTTT	TATATGGTGC	AAGGTGTCAA	TCCACCTTCA	2220
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80	TTTCAGGACT	CTGTTTGTGT	CCATTGACCT	GTTTTTCTCT	CCTGAATGCC	AATACCATAT	2400
	TTGATGTAGT	TGATGTGAAT	TTTCTAATAA	TCTCTGAAC	AGATAGTATT	AATGTGTGAT	2460
	ATTTTTGCTG	TGTGTGTAT	TTTTTGTAGA	GATGGGGTTT	CACGTGTTG	GCCAGGCTGT	2520
	GTTGAACCTC	TGAGCTAAAG	CAATACACTT	CCCTGCTCCT	CCCATGTGTC	TGGGATTACA	2580
	GGCGTGAGCC	TGAGTGCTGG	CCCAGTGAC	CACATTTCTT	TTTGAGATTT	GTTTGGGCTA	2640
85	TGTTAAGTCC	TTTGCTTTTG	ATGTGAAATT	TGGGAACAGG	CAGGCTGTGG	TGGCTTATGC	2700
	CTGTAATCCT	AGAACTTTGG	GAGGCTTAGA	TGGGTGGATC	ACTTGAGCTC	AGGAGTTCCA	2760
	GACCAGCCCG	GGCCTATGCG	AAAACCTCCGT	CTCTACAAAA	AATAGAAAAA	ATTAGCCAGG	2820

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TGTTGGTGGT CATGCTGTGA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG 2880
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ACAAAGTGAG ACTCTATCTC AAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAC 3000
AACCAACAAA ACCCGTGTG GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAACTG 3060
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CCTAGGTATT AATGTTTGT CTCTATTTC TCTTAATAAT CTTTGTAGT TTTGAGTGA 3180
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Seq ID NO: 156 Protein sequence:
Protein Accession #: Eos sequence

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TIKFRHCSLL RNRRTCTVYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS 120
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KRLMRI

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Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-621

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CGGTGTCTAA AAGACTATGG AGAATTTGAA GTTGATGATG GCACCTTCAGT CCTATTAAAA 540
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Seq ID NO: 158 Protein sequence:
Protein Accession #: Eos sequence

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TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRPHMAAE VRCLRDYGEF 120
EVDGTSVLL KNSQHFLEPR WKCEQLIRQG VLEHILS

5 Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-229

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CGAGCTGCAT CGCGCGCCCG AAGGSCAACT GCCTGCCTTC AACAAATTAG TGGGTGTGGT 240
GGCACACACC TGTAGTCCCA GCAACTTAGG AGGCTGAAGT GAGAGGATTG CATGGCTCCA 300
GGAAAGTTGAA ACTGCACTGA ACTGTGTGCA CGCTATTACA CTCCAGCCTG GGTGACAGAC 360
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AAGCTTTGTA TGAACAAAAC CAGTCTGATG TGTCTCTGT TAAGAAATCG ACGTGCACAT 480
GTAGCATACC TGTATGACCG CTTCCTTCGG ATCAGAGCAC TCAGATGG

Seq ID NO: 160 Protein sequence:
Protein Accession #: Eos sequence

25 1 11 21 31 41 51
ATGTTCTGCG AAAAAGCCAT GGAAGTATC CGCGAGCTGC ATGCGCGCGC CGAAGGGCAA 60
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30 Seq ID NO: 161 DNA sequence
Nucleic Acid Accession #: U10694
Coding sequence: 1333-2280

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AGGAACCTAA GGGAGGATCG AGGTACCTC CAGGCCAGAG AAATCTCTAG ATCAAGAGAG 180
TTTGCCCTGC CCTACTGTTC ACCCCAGAGA GCCCGGGCAG GGCTGTCTGC TGAGGTCCCT 240
CCTTTATCCT GGGATCACTG GTGTGCGGGA GGGCTGGCCT TGGTCTGAGG GGGCTGCACT 300
CAGTCAAGCA GAGGGAGGCT CCCAGGCCCT GCCAGGAGTC CAGGTGCAGA CTGAGGGGAC 360
CCCACTCACC AAACACAGAG GACCTAGCCC CACCTGCCCC CTGTGTCTAG CTGAGGGGAG 420
CGCTGGGCTG GATGACTCC CCTCACTTCC TCTTCAGGTG TCTCCTGGAG ATAGGGCTC 480
AGGTCAACAG AGGGAGGGTT CCAGACCCCTG CAGGCATCAA GATGAGGACC AGGCAGTATC 540
CTACCCCAAG GACACATGGA CCCCATTTAA TTTAGACATC TCTTACTGTA CTTCGAGGA 600
AACCCTGGGC AGGTGTGGGC AGATGTTGGT TGGGGCATGT CCTCTGTTC CATATCAGGG 660
ATGTGAGCTC CTGATCTGAG AGACTCTCAG GCAAGTAGAG GAGTAGAGTC CAGTCCCTGC 720
CAGGAGAAAG GTCAGGGCCC TGAGTGAGCG CAGAGGGGAC CATCCACCCC AAAAGTGTGT 780
AGAACTCAAG AGTGTCCAGC CCGCCCTCTT GACAGCACTG AGGGACCGGG GCTCTGCCTG 840
CAGTCTGACG CCTAAGGGCC CCTCGATTCC TCTTCCAGGA GCTCCAGGAA GCAGGCAGGC 900
CTTGTCTGTA GACAGTGTCC TCAGGTGCGA GAGCAGAGGA GACCCAGGCA GTGTGAGCAG 960
TGAAGGTGAA GTGTTCACCC TGAATGTGCA CCAAGGGCCC CACCTGCCCC AGCACACATG 1020
GGACCCCATG GCACCTGGCC CCATTCCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC 1080
AGGTAGCTG CAGCTGAGT AGCCCTCTCA CTCTCTCCTC CAGGTCTCTG GACAGGCTA 1140
ACCAGAGAGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAACTCA 1200
GCCTTTGTTA GACAGTCCAA GGTTCGGTTC TCAGCTGAAG TCTCTCACAC ACTCCCTCTC 1260
TCCCCAGGCC TGTGGGTCTC CATGCCCCAG CTCCTGCCCA CGCTCCTGAC TGCTGCCCTG 1320
ACCAGAGTCA TCATGTCTCT CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT 1380
GAAGCCCAAG GAGAGGACTT GGGCCTGATG GGTGCACAGG AACCCACAGG CAGGAGGAG 1440
GAGACTACCT CCTCCTCTGA CAGCAAGGAG GAGGAGGTGT CTGCTGCTGG GTCATCAAGT 1500
CCTCCACAGA GTCTCTCAGG AGGCGCTTCC TCCTCCATTT CGTCTACTA CACTTTATGG 1560
AGCCAAATGG ATGAGGGCTC CAGCAGTCAA GAAGAGGAAG AGCCAAGCTC CTCGGTCCGAC 1620
CCAGCTCAGC TGGAGTTCAT GTTCCAAAGAA GCACTGAAAT TGAAGGTGGC TGAGTTGGTT 1680
CATTTCTGCG TCCACAAATA TCGAGTCAAG GAGCCGCTCA CAAAGGCAGA AATGCTGGAG 1740
AGCCTCATCA AAAATTACAA GCGCTACTTT CCTGTGATCT TCGGCAAGC CTCGAGTTC 1800
ATGCAGGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGAAC CGCCCGGCCA CTCCTACATC 1860
CTGTCTACTG CTCTTGGCCT CTCGTGCGAT AGCATGTGCG GTGATGGTCA TAGCATGCC 1920
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GCCCATGTG ACATGAGGCC CATCTCTGCG TCTGTGTTG AAGAGAGCAA TCAGTGTCT 2400
CAGTGGCAGT GGGTGAAGT GAGCACACTG TATGTCTCT CTGGTTCCCT TGTCTATTGG 2460
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AGTTTAATGA ACTTACCAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATTGCTGTTT 2580
ATGTTATTTA GAGTAAAGAT TCTTCTTTT GAGTCAATG GGGAAATCCC TGTATTATTG 2640
TGAATTGGGA CAGATAACA TAGCAGAGGA ATTAATAAAT TTTTGAAGC TGAAGCTTAG 2700
CAGCAAAATA GAGCTCATA AGAAATAGT AAATGAAAAT GTAGTTAAT CTGCTTTAT 2760
ACCTCTTTCT CTCTCCTGTA AAATTAAGC ATATACATGT ATACCTGGAT TTGCTTGGCT 2820
TCTTTGAGCA TGTAAAGAAA ATAAATTTG AAAGAATAAT TTTTCTGTT CACTGGCTCA 2880
TTTTTTCTTC AGACACGCAC TGAACATCTG TTATTGGGAA CACCTGGGT T

Seq ID NO: 162 Protein sequence:
Protein Accession #: AAA68877.1

1 11 21 31 41 51
MSLEQSRSPHC KPDEDELAQGE EDLGLMGAQE PTGEEKEETS SSDSKEEEVS AAGSSSPFQS 60
5 PQGGASSSIS VYTTLSQFD EGSSSQEEEE PSSVDPAQL EFMFQALKL KVAVLVEFL 120
HKYRVKEPVT KAEMLESVIK NYKRYFFVIF GKASEPMQVI PGTDVKEVDP AGHSYILVTA 180
LGLSCDSMLG DGHSMFKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGREHMFYGE 240
PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAEY SYEKVINYLVL MLNAREPICY 300
10 PSLYEVLIGE EQEGV

Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: AF292100
Coding sequence: 30-809

1 11 21 31 41 51
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20 CTCAAAATGA CTGGAAGTTA GATGTTGCAA CAGATAATTT TTTCCAAAAT CCTGAACCTT 180
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ATGACCTGGC ACTCGATCCA GCCAGCATTA GTGTGTTGAT TATTCGTGGG AAGTTCAGAG 360
CAGCAACACA GTGCGAGTTC TCCAAACAGG AGTTCATGGA TGGCATGACA GAATTAGGAT 420
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ACACTTGGAA TCTTCTTTTA GACTTCAGTA CGATGATTGC AGATGACATG TCTAATTATG 720
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30 TTGCTGGGAG AAAAAGTACA ACAGTGTAGC ACTAAAGGAA CCTTTTAGAA TGTACATAGT 840
CTGTACAATA AATACAAACAG AAAATTGCAC AGTCAATTTT TGCTGGCTGG ACTGAACTGA 900
AGATCAATCC TCACAAATCA GACTGAGGGT TGAGACAAAA CTTTAAGGAT ACATCTTGGA 960
CCATATCGTA TTTCATTCTT CTAATGGTGG TTTGGGCTTG TCTCTAGTC TGGGCGCTC 1020
TAAACATTTA TAATCCCAAC ATTGTGGATT TCATCTTATA TCTGTGGACC ATCCTAGTTT 1080
35 ATTCCTCCAT AAGTCTTAGA AGCTTTATGG TGATTATTTT GAGGTTTTCA TTCTCGCATA 1140
AAGCACAATG CTGTCTTCAT CAGAAAACAG TTGGCATAAG AATTAACAT ATGAACATCA 1200
CAAAACAATG TATATAAATC TCTTAAATAT ACGCTTTGGG CTAGTTGCAA AGACTATGCT 1260
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40 ATGAAAAAAC AATGTCAGAA TAACCGACAT GAAAAATTTT TAGGATAACT TGGTGCCTAC 1440
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45 TGCTTTTGAA ATGCTTATCT GCTGTGCACA TAAGTTAAAC TATTTAATTT GTTTTGAATG 1680
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TTTTACTTTT TTTTGTTCAT TGCACTATGG AACACAAATG AAATCTCTCT AATTATATAAG 1800
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AATTACTTTA ACTGCTAATC ACTGTGGTGG CCAAAATATT ACTTCAGAG CAAAGATTTT 1980
50 CAAACAAAGC AATGTCAGATG AAAATACAG TCTGGCTTCT AGTCTATTTA CTGTTTTGTT 2040
TCACTCAGAT TAGCTCAGTT TTCTCATCAA AGCAGAATGC TATCTTGGCT GTGTGTGTGT 2100
GTGTGTGTGT GTGTGTGTGT GTATGTGTGT ATATATATAT ATATATATAT ATATATATTT 2160
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TAAGGCAGGC TAGAAATGTA ATACTTCAAA TGTTTGATGA TTATGGTCTT TTGATAGGAA 2340
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AGGAATGTAC TTAGAATAGC AGTACATTTT ATGCAAATAT GGAATATTAT TTAAGAAACA 2460
ATGACATATC AAAACTGCTT TTTACATGAT TTTGAAATAG ACTAGAAAGC TTTCCCTATA 2520
60 GACATATTAA TATTCCAATC ATAACTTTAA TTCAAGAAATG CAGTTTTACC AAAAGAAAAA 2580
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ATCTGTCTGC TTTCAGTATT TCCTGATTTT TTTGTAATAA TAAAGAGGAA CTTCATTTAT 2700
GAAAAATTTT TAAAGATAT ATATCTATAT ATATCTATAT ATATGTACTG TTTTGTTC 2760
70 TGCTTTGAAG ATTTTGAGTT ATGTTTATG GTTTCAGATT GATTAAATCA CATATGCTGT 2820
GTTTTCTTTA AAAGTCATAT GGGTTCGTGG CCTAATGCCT TGGATTTTAC ATATTTTTCT 2880
TTTTAAATGC AAAACCTTTT CAACAAAAATA GTGTTTGTCA TCAGGTTGGT ACTAAACATT 2940
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TAAAGTTTAA GGTGTGTCAC TATGATGSCA TCTTAGAATT AAACAAACT TTTACTAGGG 3060
CTGAAAAGAG AAGACTGATT TAATGTGGTG TGATTATTCT GAAGATAAAT GTCTGGCTAC 3120
75 AGGGAATATT TTGACTAAA AAATGATTAC ACATATGGCT GTGTGTGTTT GAGTCTGTGT 3180
CTGTGAGAGA GCCAGAGAGA GTGAGAGAGA TTGACAGAGA AAGGGAGAGA CACACACAG 3240
CCCTTTGAAT TGCTTTAACT CCTAAGTGTT TCAGTCTCTA TTCCGGTAAA CTCCCATGTC 3300
TGATTCCTTG TTTTAAACTG AACCATAGGT ACAGTTTCTT TTTTGCCAAA TGTCAAAACA 3360
GGTACAAATT TTAAATGTGA ATGCTTTTAA AATAGAAAAA TGTATAAAAT TAGAAGTGCC 3420
CACATATAAA AAATAGTTGA GATGAAGATT ATCTTTAGTG AATATCATCT GCATATCTCT 3480
80 GTAAGTTCAA TTGTGTTTCT TACAGTCCTT GTCATATTAC CAACAGAGGC AATAAAAGCT 3540
GCAGTGAAT TG

Seq ID NO: 164 Protein sequence:
Protein Accession #: AAG00606

1 11 21 31 41 51
MNKLKSSQXD KVRQPMIFTQ SSEKTAVSCL SQNDWKLQVA TDNFFQNPQL YIRESVKGSL 60
85 DRKLEQLYN RYKDPQDENK IGIDGIQFPC DDLALDPASI SVLILAWKFR AATQCEFSKQ 120
EFMDGHTLGL CDSIEQLKQK IPKMEQELKE PGRFKDFYQF TFNFAKNPGQ KGLDLEWALA 180
YWNVLVNGRP KFLDLWNKFL LEHHRKSIPIK DTWNLLDPS TMIAADMSNY DEBGAWPVLI 240
DDFVEFARPO LAGTRSTTV

Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

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	GCCTACGGGG	TGCGGTGGGG	GGCGCGCGGG	CACCGCGCAG	GGCGCGCCAG	TCCCGCTTC	120
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	CAGCGCGGGG	GCTGCGGGAG	CGACCAAGTG	GCTCCTGCGA	TGGCGGCGGA	AGAGGAGGCT	240
	GGCGCGGGAG	GTAAAGTGTT	GAGAGAGGAG	AACCAAGTGA	TGCTCCTGT	GGTTTCCAGC	300
	CGCGTGAGTC	CAGGGAACAAG	ACCAACAGCT	ATGGGGTCTT	TCAGCTCACA	CATGACAGAG	360
	TTTCCACGAA	AAGCAAAAGG	AAGTGATTCA	GACCCATCCC	AAGTGAAGA	TGGTGAACAC	420
15	CAAGTTAAAA	TGAAGGCCTT	CAGAGAAGCT	CATAGCCAAA	CTGAAAAGCG	GAGGAGAGAT	480
	AAAATGAATA	ACCTGATTGA	AGAAGTGTCT	GCAATGATCC	CTCAGTGCAA	CCCCATGGCG	540
	CGTAAACTGG	ACAAACTTAC	AGTTTAAAGA	ATGGCTGTTT	AACACTTGAG	ATCTTTAAAA	600
	GGCTTGACAA	ATTTCTTATGT	GGGAAGTAAT	TATAGACCAT	CATTCTTCTA	GGATAATGAG	660
	CTCAGACATT	TAATCCCTAA	GACTGCAGAA	GGCTTCTTAT	TGTGGTGTGG	ATGTGAAGA	720
20	GGAAAAATTC	TCTTCGTTTC	TAAGTCAGTC	TCCAAAATAC	TTAATTATGA	TCAGGCTAGT	780
	TTGACTGGAC	AAAGCTTATT	TGACTTCTTA	CATCCAAAAG	ATGTTGCCAA	AGTAAAGGAA	840
	CAACTTTCTT	CTTTTGATAT	TTTCCCAAGA	GAAAAGCTAA	TAGATGCCAA	AAGTGGTTTG	900
	CAAGTTCACA	GTAATCTCCA	CGCTGGAAGG	ACACGTGTGT	ATTCTGGCTC	AAGACGATCT	960
	TTTTCTGTCT	GGATAAAGAG	TGTAAATATC	TCTGTCAAAG	AAGAGCATGG	ATGCTTACCC	1020
25	AACCTCAAGA	AGAAAGAGCA	CAGAAAATTC	TATACTATCC	ATTGCACTGG	TTACTTGAGA	1080
	AGCTGGCCTC	CAAAATATTGT	TGGAATGGAA	GAAGAAAGGA	ACAGTAAGAA	AGACAACAGT	1140
	AAITTTACCT	GCCTTGTGGC	CATTGGAAGA	TTACAGCCAT	ATATTGTGCC	ACAGAACAGT	1200
	GGAGAGATTA	ATGTGAAACC	AACCTGAATTT	ATAACCCGGT	TGCAAGTGA	TGGAAAAATT	1260
	GTCTATGTGT	ATCAAGGGCG	AACACGGATT	TTAGGATATC	TGCTCAGGA	ACTTTTGGGA	1320
30	ACTTCTTGTT	ATGAATATTT	TCATCAAGAT	GACCACAATA	ATTGACTGTA	CAAGCACAAA	1380
	GCAGTCTACT	AGAGTAAGGA	GAAAATACTT	ACAGATTCTT	ACAAATTCAG	AGCAAAAGAT	1440
	GGCTCTTTTG	TAACCTTTAA	AAGCCAAATGG	TTTAGTTTCA	CAAACTCTTG	GACAAAAGAA	1500
	CTGGAATATA	TGTATCTGT	CAACACTTTA	GTTTTGGGAC	ATAGTGAGCC	TGGAGAAGCA	1560
	TCATTTTATC	CTGTGAGCTC	TCAATCATCA	GAAGAATCCT	CTAGACAGTC	CTGTATGAGT	1620
35	GTACCTGGAA	TGCTACTCGG	AACAGTACTT	GGTGCTGGTA	GTATTGGAAC	AGATATTGCA	1680
	AATGAAATTC	TGGATTTACA	GAGGTTACAG	TCTTCTTCAT	ACCTTGATGA	TTGAGTCCA	1740
	ACAGGTTTAA	TGAAAGATAC	TCATACTGTA	AACCTGAGGA	GTATGTCAAA	TAAGGAGTTG	1800
	TTTCCACCAA	GTCTCTCTGA	AATGGGGGAG	CTAGAGGCTA	CCAGGCAAAA	CCAGAGTACT	1860
	GTGCTGTGCC	ACAGCCATGA	GCCACTCCTC	AGTGATGGTG	CACAGTTGGA	TTTGGATGCC	1920
40	CTATGTGACA	ATGATGACAC	AGCCATGGCT	GCATTATGTA	ATTACTTAGA	AGCAGAGGGG	1980
	GGCTCGGGAG	ACCTCGGGGA	CTTCAGTGAC	ATCCAGTGA	CCCTCTAGCC	TTGATTTTTT	2040
	AACCTCAAAA	ATGAGAAACA	TTTTAAAGCA	TTATTTACGA	AAAAACTGTC	TCAACTATTC	2100
	TTAAGTACTG	TATTGATATT	GTTTGTATCT	TTTATTAATG	TTCTACCACT	TTTTATAGAT	2160
	TTGCATCTTC	CTGTCACAGG	GATGTGGGGA	AATACGTTTT	CCTCCCAAGA	GAACCAAGTT	2220
45	TATTATAGAC	TCTTTTATTC	AGTGAAATGG	CTTATAATCC	ACTAGTTGCC	ATATTTTTCG	2280
	TAAATATATT	CTAACCAAGA	ATACTACTTA	CATATTGTTT	TGGCTTTGTT	TTATTTTGA	2340
	TGCACTTTTG	TTTGTGTGAG	GTAATGTAAT	ATATTGATGT	TTTCTTTTGT	GTCTAAGATT	2400
	GATTTATAT	AGTAGGTTTG	TATAATTTGG	AACATTTTCC	ATGCTTGGG	AATTTCTCTA	2460
50	ATTGAGGATA	GGGCTTACAC	ACTTTAAGAA	AACAGTGAGT	ACTTGAACAT	TTAAAGGGAC	2520
	AGTGCAATTT	ATAGTCATAA	TCACATTGAA	TACTGTATTT	GATCTTTGGA	GACTTAGGCA	2580
	AGCACAGAGC	TGGGATATTT	ATGCTCAGTT	GAGCACTTTA	AGATGAATTT	TAAGTGAGAT	2640
	GATTTCTTGC	TTTAAACTCA	GAAAGTCAAA	AGAGTTTCAG	CTTTCTTAC	AGAAAAGGAA	2700
	GGATCTTGGG	CCCTAGATCT	TGGGGATTAA	CCTCTGCATA	TAAGATTAC	TCTTAATAGG	2760
55	CCAGAGGTGG	TGCTACGGCC	TGTAATCCCA	GTACTTTGGG	AGGCTGAGAC	GGGCGAGTCA	2820
	CTTGAGGTGA	GGAGTCTAAG	ACCAGCCTGG	CCAATATGGT	GAACCCCGCT	TTCTACTAAA	2880
	AATACAAAAA	AAATTAACCA	GGCACTCACT	CTGAGGTAA	CTAACCAACT	CCCACGATA	2940
	TGACAGTCCA	TTCAATGAGG	CAAGGGCCTC	ATGACCTAAT	GGCACACACC	TGTAATCCCA	3000
	ACTGCTTGGG	AGGCTGAGGC	GAGAGGATTG	CTTGAACCTG	GGAGGCAGAG	GTTCAGGTGA	3060
60	GCCGAGATCG	CACCCTGCA	CTCCAGTCTG	GGCAACAGAG	TGAGACTTCA	TCTCAAAAAA	3120
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	GATTAAATGT	CTTGTGTAAA	GTACACATT	AAATTCAATC	ACACATTAAA	TTATAGAGT	3300
	TTTAAATGTT	TAATGTATAT	AAACAGTTT	CTTTATACAC	ATTGGGAAA	ACATTTGCTT	3360
	CACAGATTAA	ATGATTAAC	AACTGACCCA	GGAACTAGTT	GTAGCTTTCT	AAGTAATTAG	3420
65	GCAATTACAG	TTATTGCTTG	TAACCAAGG	TAATAAACA	AAATGACAAG	TACATGTTTA	3480
	AAATTTAGAG	GCAATGAGAA	ATAATTTAAA	AACCAATTTT	CTAGTTATAA	TTTAAAAATT	3540
	GGAGAGCAT	TTTAAACAGTA	ATTAATCCAG	AGGTGGCTCA	AATTGAGTAT	AAGAATTAA	3600
	ATTATTTAAA	ATACTGCATG	TCTACCTTCT	CGGGATCAT	ACTTTATAAC	ACTTTCTGCT	3660
70	TCAGTAGCTC	TTATAGCTT	GCCAGATATG	CTCCCATATT	TTCTCTCTCG	TGCTCTCGAA	3720
	ATGAAAGTCA	GATAGGCTGG	GAACTCATGG	GGCAGCCCTC	AGACTTCAAT	GTGGGCTTCA	3780
	AATCCAGTTT	CCCTGTCTAT	ATGGTGCTAC	ATCTTTCAG	AAAAATTTCC	TCAGAGCCCC	3840
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	CATTGCAAGT	TAGACTTGTC	TTCCAAAGAG	TCTGCTTAAG	CCAGGGGTGG	CAGGATAGGC	4320
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	ACTCTGTGCA	TGGTTTGATC	CTTTATTAGT	TCGCTCTAAT	ATTTTCTGT	AGATCCTTTT	4560
	GTCTGAGACT	CAAAATCTAA	TCCATGCATT	GTATGATACC	GTAGCTCTCC	TAAGGTTTGT	4620
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	CATATTTTAA	TGGTATACAC	TATGTTCTCT	TTTCTACTG	CGAGTCAATT	TTTGAATTTT	4740
	TGCTGAGAAA	GAATATATCT	ACAAATTGCA	CGAAAGTATC	ATAAAAACAG	TACTCTAGAG	4800

5	CAGCGCTGTC	CAATAGAAAT	ATAATCTGAG	CCACATGTAT	AATTTTATTT	TCTTCTAGCC	4860
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	CAAAATATCA	TTTGAACATG	TAATTAATAT	AAAATTATTA	ATGTGATATT	TTACATTCTT	4980
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	GTACTAGCCA	CATTGCAAGT	GCTCAGTAGC	CACATGTGGC	TAGTGGCTAC	TGCACTGGAC	5100
	AGCACAGTTC	TAGGTTCCAC	CCTAACACCC	AACTCCTGTG	GATTAGAATC	CCAGAAATCAG	5160
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	CCAGGCACCT	TCCCACTCC	ACTACATTAC	TGTAGTGGTA	ATTCTTAGGG	TTAAAAAAG	5340
10	TGTAGAGTAG	GCCGGGCGCA	GTGGCTCATG	CCTGTAATCC	CAGCACITTG	GGAGGCCGAA	5400
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	CTCTACTGAA	AATACAAAGC	AAAATTAGCC	AGGTGTGGTG	GCGGGCGCCT	GTGGTCCCG	5520
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	AGATCGGCGC	ACTGCACCCC	AGCCTGGGCG	ACAGAGCGAG	ACTCCATCTC	AAAAAAGG	5640
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	GAAGTAGACC	AAAGTTTATA	CCATAAGGAT	ATTTTCTCTT	AAATACCATG	TTTGAAGAAC	5760
	AATTATTATG	TGATCCTTGA	ATCTGTAAAG	TCAAATAACA	AGTCTCTATC	CATGTTACCA	5820
	AATTTAACCT	TTTGAATAA	ATAAACTTTA	AAATATCAGA	TGTGTTATTA	CAGGATGATA	5880
	CTTGAATCAA	AGTGAATGA	GTTTATATGG	CATCACTAAA	TTTAGAAATC	TATTGTGAAA	5940
20	CAAGACAAA	CAGAAAGTGA	CAGAAATAG	ACTTTTAGTA	AATAAATGGA	ATTTAAAGAA	6000
	AAGTGTATAT	TTACAGGTGC	ACGACAGAAA	AGGATGTCTT	TGTTGTGATA	GTCTTTGAGG	6060
	GATCTCTGTA	GAATCTGGGG	CACAGGTACA	AGAAATAGCC	AATATTAGT	TCCAGACCA	6120
	TGTTTAGTAG	TGTCAGATT	CAGATCATGC	TGCCAAGAGG	TATCTCCCCC	TGAGGTGGGT	6180
	CATCACTGAG	CCCTGGAATT	GGAGACTCAT	ACTTGCCAG	CACAAATGTA	CGGCGAGACA	6240
25	GGCGCAGCAT	TATGATTAG	TAGAAGCCAT	AAAGAAAGC	TGCTAAGTGG	CCACTAGGTG	6300
	CCACTTTTCT	GTTTGTGATA	TGCTTTTATT	AGCAGATCTT	TTTTTCCAA	GCTCCATGGG	6360
	GCCTATGAGA	GGCATTATG	ATTTTGTGTC	CTACAATAAG	TCAGCCTGTC	TGGTGTGAGT	6420
	TGTTTATGTA	GAATGTCTT	CCAAGGGAGG	TCTAGGAAGA	TCTGACACA	TAGAACTTT	6480
	GGCTTAGAGA	GCTTTCCAGG	TGTAGTGCCA	ATAAACTG	ACCTGGAAG	AAAACCTGCC	6540
30	CAGCAOAGAA	CATGCTTTCT	GAATCTACTT	GAGAGGTGAT	GGTGTATGTC	ACTTCTCATA	6600
	TATTTCTGAG	TTTAGATTG	TCTTTTATAC	AATTTTATAG	TCTTTTCCAG	TTCACTTGTG	6660
	CTGCTCTGTA	TATGTGTTAT	TTTAAATTTT	TGTGTTAAAT	AATGAAAGAA	GTGAAATTAT	6720
	ATTTTATAAT	TACTCATTTG	TAGTTTTTTT	TTTTAATTTA	ATAAACTTCC	TCCAAAAGT	6780
35	GCTCCCTTAA	AA					

Seq ID NO: 166 Protein sequence:
Protein Accession #: AAG34652

40	1	11	21	31	41	51	
	MAAEEREAAG	QKVLREENQC	IAPVVSSRV	PGTRPTAMGS	PSSHMTFPR	KRKGSDSDPS	60
	QVEDGEHQVK	MKAFREAHQS	TEKRRRDKMN	NLIEELSAMI	PQCNPMARKL	DKLTVLRMAV	120
	QHLRLSLKGLT	NSYVGSNYRP	SFLQDNELRH	LILKTBAGFL	FVVGCEGRKI	LFVSKSVSKI	180
45	LNVDQASLTG	QSLPDLHPK	DVAKVKQLS	SFDISPREKL	IDAKTGLQVH	SNLHAGRTRV	240
	YSGRRSFPC	RIKSKISVK	EHGCLPNSK	KKEHRKFYTI	HCTGYLRSWP	PNIVGMBEER	300
	NSKKDNENFT	CLVAILRLQ	YIVPQNSGEI	NVKPTEFITR	FAVNGKFVYV	DQRATAILGY	360
	LPQELLGTSC	YEYFHQDDHN	NLTDKHKAVL	QSKKILTDS	YKPRAKDGSP	VTLKSQWFSF	420
	TNPWTKELEY	IVSVNTLVLG	HSEPGESFL	PCSSQSSEES	SRQSCMSVPG	MSTGTVLGAG	480
50	SIGTDIANEI	LDLQRLQSSS	YLDSSPTGL	MKDTHTVNCR	SMSNKLFPF	SPSEMGELEA	540
	TRQNSQTVAV	HSHEPILLSG	AQLDFDALCD	NDDTAMAAFM	NYLEAEGGLG	DPGDFSDIQW	600
	TL						

Seq ID NO: 167 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

60	1	11	21	31	41	51	
	GGTTACTCAT	CCTGGGCTCA	GGTAAGAGGG	CCCGAGCTCG	GAGGCGGCAC	ACCCAGGGGG	60
	GACGCCAAGG	GAGCAGGACG	GAGCCATGGA	CCCCGCCAGG	AAAGCAGGTG	CCAGGCCCAT	120
	GATCTGGACT	GACGGCTGGC	TGCTGCTGCT	GCTGCTTCGC	GGAGGAGCGC	AGGCCCTGGA	180
	GTGCTACAGC	TGCGTGCAGA	AAGCAGATGA	CGGATGCTCC	CGGAACAAGA	TGAAGACAGT	240
	GAAGTGGCGG	CCGCGCGTGG	ACGCTGTCAC	CGAGGCCGTG	GGGGCGGTGG	AGAACCATCA	300
65	CGGACAAATC	TGCTGTCGAG	TGCGGGGTGG	CGGTTGGGGA	CTCCCCGGCA	AGAAATGACG	360
	GGGCGGTGAT	CTTCAAGGGC	TTCTGGGCTT	CATCCAGCTG	CAGCAATGCG	CTCAGGATCG	420
	CTGCAACGCC	AAGCTCAACC	TCACCTGCGG	GGCGCTCGAC	CGGCAGGTA	ATGAGAGTGC	480
	ATACCCGCCC	AACGGCGTGG	AGTGCTACAG	CTGTGTGGGC	CTGAGCCGGG	AGGCCTGCCA	540
	GGGTACATCG	CCGCGGCTCG	TGAGCTGCTA	CAACGCCAGC	GATCATGTCT	ACAAGGCTCG	600
70	CTTGAAGCGC	AACGTCACCT	TGACGGCAGC	TAATGTGACT	GTGTCTTTCG	CTGTCCGGGG	660
	CTGTGTCCAG	GATGAATCTT	GCACCTCGGA	TGGAGTAACA	GGCCCAAGGT	TCAAGCTCAG	720
	TGGCTCCTGT	TGCCAGGGGT	CCCGCTGTAA	CTCTGACCTC	CGCAACAAGA	CCTACTTCTC	780
	CCCTGGAATC	CCACCCCTTG	TCCGGCTGCC	CCCTCCAGAG	CCACGACTG	TGGCCTCAAC	840
	CACATCTGTC	ACCACCTCTA	CCTCGGCCCC	AGTGAGACCC	ACATCCACCA	CCAAACCCAT	900
75	GCCAGGCCCA	ACCAGTCAGA	CTCCGAGACA	GGGAGTAGAA	CACGAGGCTT	CCCGGATGTA	960
	GGAGCCGAGG	TTGACTGGAG	GCGCGCTGGG	CCACCCAGGAC	CGCAGCAATT	CAGGGCAGTA	1020
	TCTTGCAAAA	GGGGGGCCCC	AGCAGCCCCA	TAATAAAGGC	TGTGTGGCTC	CCACAGCTGG	1080
	ATTGGGAGCC	CTTCTGTGTT	CCGTGGCTGC	TGGTGTCTTA	CTGTGAGCTT	CTCCACCTGG	1140
	AAATTTCCCT	CTCACTACTT	TCTCTGGCCC	TGGGTACCCC	TCTTCTCATC	ACTTCTCTGT	1200
80	CCCAACACTG	GACTGGGCTG	GCCAGCCCCC	TGTTTTTCCA	ACATTCGCCA	GTATCCCCAG	1260
	CTTCTGCTGC	GCTGTTTGGC	GGCTTTGGGA	AATAAAATAC	CGTGTATAT	ATTCTGGCAG	1320
	GGGTGTTCTA	GCTTTTGTAG	GACAGCTCCT	GTATCCTTCT	CATCCTTGTG	TCTCGGCTTG	1380
	TCTCTTGTG	ATGTTAGGAC	AGAGTGAGAG	AAGTCAGCTG	TCAAGGGGAA	GGTGAGAGAG	1440
	AGGATGCTAA	GCTTCTACTT	CACTTTCTCC	TAGCCAGCCT	GGACTTTGGA	GCGTGGGGTG	1500
85	GGTGGGACAA	TGGCTCCCCA	CTCTAAGCAC	TGCTCCCTCT	ACTCCCGCCA	TCTTTGGGGA	1560
	ATCGGTTCCC	CATATGTCTT	CCTTACTAGA	CTGTGAGCTC	CTCGAGGGCA	GGGACCGTGC	1620
	CTTATGTCTG	TGTGTGATCA	GTTTCTGGCA	CATAAATGCC	TCAATAAAGA	TTTAATTACT	1680

TTGTATAGTG AAAAAAA

Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

5
10
15

1	11	21	31	41	51	
MDPARKAGAQ	AMINTAGWLL	LLLLRGGAQA	LECYSCVQKA	DDGCSFNKMK	TVKCAPGV DV	60
CTEAVGAVET	IHQFSLAVX	GCGSGLPGKN	DRGLDLHGLL	APIQLQCAQ	DRCNALNLT	120
SRALDPAGNE	SAYPPNGVEC	YSCVGLSREA	CQGTSPFVVS	CYNADHVYK	GCDFGNVILT	180
AANVTVSLPV	RGCVQDEPCT	RDGVTGPGPT	LSGSCCQGSR	CNSDLRNKTY	FSPRIPLVR	240
LPPPEPTTVA	STTSVTTSTG	APVREPTSTK	PNPAPTSQTP	RQGVHEASR	DEEPRLTGGA	300
AGHQDRNSNG	QYPARGGPQQ	PENKGCVAPT	AGLAALLLAV	AAGVLL		

Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

20
25
30
35
40
45
50
55

1	11	21	31	41	51	
GAATTGGGCA	CGAGCGCGCG	GCGAATCTCA	ACGCTGGGCC	GTCTGGGGGC	GCTTCGGGGC	60
CACCAAGTTT	TCTGCTTTTC	ACCCTGGGCG	CCCCAGCCCC	TGGCTCCCCA	GCTGGGCTGC	120
CCCCGGGCTC	CACGCCCTGC	GGGCTTAGCG	GGTTCAGTGG	GCTCAATCTG	CGCAGCGCCA	180
CCTCCATGTT	GACCAAGCCT	CTACAGGGGC	CTCCCGCGCC	CCCCGGGACC	CCCACGCCGC	240
CGCCAGGAGG	CAAGGATGCG	GAAGGTTTGG	AGGCGGAGTA	TGGACTCGGC	CCCCTCCTGG	300
GTAAGGGGGG	CTTTGGCACC	GTCTTCGCAG	GACACCGCCT	CACAGATCGA	CTCCAGGTGG	360
CCATCAAGAT	GATTCGCCCG	AATCGTGTGC	TGGGCTGGTC	CCCTTGTGCA	GACTCAGTCA	420
CATGCCCACT	CGAAGTCGCA	CTGCTATGGA	AAGTGGGTGC	AGGTGGTGGG	CACCTGGGCG	480
TGATCCGCTT	GCTTGACTGG	TTTGAGACAC	AGGAAGGCTT	CATGCTGGTC	CTCGAGCGGC	540
CTTTGCCCGC	CCAGGATCTC	TTTGACTATA	TCACAGAGAA	GGGCCCCACT	GGTGAAGGCC	600
CAAGCGCGTG	CTTCTTGGCG	CAAGTAGTGG	CAGCCATCCA	GCACTGCCAT	TCCCGTGGAG	660
TTGTCCATCG	TGACATCAAG	GATGAGAACA	TCCTGATAGA	CCTACGCCGT	GGCTGTGCCA	720
AACTCATTGA	TTTTGGTTCT	GGTGCCCTGC	TTTATGATGA	ACCCTACACT	GACTTTGATG	780
GGACAAGGGT	GTACAGCCCC	CCAGAGTGGG	TCTCTCGACA	CCAGTACCAT	GCACTCCCGG	840
CCACTGTCTG	GTCACTGGGC	ATCCTCCTCT	ATGACATGGT	GTGTGGGGAC	ATTCCCTTTG	900
AGAGGGACCA	GGAGATTCTG	GAAGCTGAGC	TCCACTTCCC	AGCCCATGTC	TCCCCAGACT	960
GCTGTGCCCT	AATCCGCGCG	TGCTGGGCCC	CCAAACCTTC	TTCCGAGCCC	TCACTGGAAG	1020
AGATCCCTGT	GGACCCCTGG	ATGCRAACAC	CAGCCGAGGA	TGTTACCCCT	CAACCCCTCC	1080
AAAGGAGGCC	CTGCCCTTTT	GGCCTGGTCC	TTGTACTCCCT	AAGCCTGGCC	TGGCCTGGCC	1140
TGGCCGCCAA	TGCTGTGCAC	AGCCATCCCA	TGGCCATGTC	ACAGGGATAG	ATGGACATTT	1200
GTGCACTTGG	TTTACAGGTT	CATTACCACT	CATTAAAGTC	CAGTATTACT	AAGGTAAGGG	1260
ATTGAGGATC	AGGGGTTAGA	AGACATAAAC	CAAGTTTGCC	CAGTTCCTCT	CCCAATCCTA	1320
CAAAGGAGCC	TTCTCTCCAG	AACCTGTGGT	CCCTGATTTT	GGAGGGGAA	CTTCTTGCTT	1380
CTCATTTTGC	TAAGGAAGTT	TATTTTGGTG	AAGTTGTTC	CATTTTGAGC	CCCGGGAGCT	1440
TTATTTTGAT	GATGTGTCAC	CCACATTTGG	CACCTCCTAC	TACCAACACA	CAAACTTAGT	1500
TCATATGCTT	TTACTTGGGC	AAGGGTGCTT	TCCTTCCCAT	ACCCAGTAG	CTTTTATTTT	1560
AGTAAAGGGA	CCCTTTCCCT	TAGCCTAGGG	TCCCATATTG	GGTCAAGCTG	CTTACCTGCC	1620
TCAGCCGAGG	ATTTTATTAT	TTGGGGGAGG	TAATGCCCTG	TTGTACCCCT	AAGGCTTCTT	1680
TTTTTTTTTT	TTTTTTTTTG	GGTGAGGGGA	CCCTACTTTG	TTATCCCAAG	TGCTCTTATT	1740
CTGGTGAGAA	CGGCTTAATT	TCCATAATTT	GGGAAGGAAT	GGAAGATGGA	CACCAACCGA	1800
CACCAACAGA	CAATAGGATG	GGATGGATGG	TTTTTTGGGG	GATGGGCTAG	GGGAAATAAG	1860
GCTTGCTGTT	TGTTTTCCTG	GGGCGCTCCC	TCCAATTTTG	CAGATTTTTC	CAACCTCCTC	1920
CTGAGCCGGG	ATTGTCCAAT	TACTAAAATG	TAAATAATCA	CGTATTGTGG	GGAGGGGAGT	1980
TCCAAGTGTG	CCCTCCTTTT	TTTTCTCGCC	TGGATTATTT	AAAAAGCCAT	GTGTGGAAAC	2040
CCACTATTTA	ATAAAGTAA	TAGAATCAGA	AAAAAATAAA	AAAAAATAAA		

Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

60
65
70

1	11	21	31	41	51	
MLTKPLQGGP	APPPTPTPPP	GGKDREAFEA	EYRLGPLLGG	GGPGTVFAGH	RLTDRLQVAI	60
KVIPRNEVLG	WSPLSDSVTC	PLEVALLWKV	GAGGGHPGVI	RLLDWFETQE	GFMLVLERPL	120
PAQDLFDYIT	EKGPLGEGPS	RCFFGQVVAA	IQHCHSRGVV	HRDIKDENIL	IDLRRGCAKL	180
IDFGSGALLH	DEPTTDFDGT	RVYSPPEWIS	RHQYHALPAT	VWSLGILLYD	MVCGDIPFER	240
DQEILEAEHL	FPFHVSPDCC	ALIRRCCLAPK	PSSRPSLEBI	LLDPWMTQTP	EDVTPQPIQR	300
RPCPFGLVLA	TLSLAWPGLA	PNGQKSHFMA	MSQG			

Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

75
80
85

1	11	21	31	41	51	
GCGGCGCGGA	GCGGCGCTGC	TGAGCCCCGG	CGGCGGGCCC	GGCATGGGCG	TCTCCGCGGG	60
GCCCTTCGGC	GGCGGGGGCT	AGGGCCGGAT	GGAGCCGGGG	GACGGTAGCC	CCGAGGCGCG	120
GAGCAGCGAC	TCCGAGTCGG	CTTCGCGCTC	GTCCAGCGGC	TCCGAGCGCG	ACGCGGGTCC	180
CGAGCGCGAC	AAGGCGCGCG	GGCGACTCAA	CAAGCGGGCG	TTCCGCGGGC	TGCGGCTCTT	240
CGGCGCAGG	AAAGCCATCA	CCAAGTCGGG	CCTCAGCAC	CTGGCCCCCC	CTCCGCCACC	300
CCCTGGGGCC	CCGTGCAGCG	AGTCAGAGCG	GCAGATCCGG	AGTACAGTGG	ACTGAGAGGA	360
GTTCAGGACA	TATGGGGAGC	ACATCTGGTT	CGAGACCAAC	GTGTCCGGGG	ACTTCTGCTA	420
CGTTGGGGAG	CAGTACTGTG	TAGCCAGGAT	GCTGAAGTCA	GTGTCTCGAA	GAAAGTGGCG	480
AGCCTGCAAG	ATTGTGTGTC	ACAAGCCCTG	CATCGAGCAG	CTGGAGAAGA	TAAATTTCCG	540
CTGTAAGCGG	TCTTTCGGTG	AATCAGGCTC	CAGGAATGTC	CGGAGCCCAA	CCTTTGTACG	600
GCACCACTGG	GTACACAGAC	GACGCCAGGA	CGGCAAGTGT	CGGCACTGTG	GGAAGGGATT	660
CCAGCAGAAG	TTACCTTCCC	ACAGCAAGGA	GATTGTGGCC	ATCAGCTGCT	CGTGGTGCAA	720

	GCAGGCATAC	CACAGCAAGG	TGTCCTGCTT	CATGCTGCAG	CAGATCGAGG	AGCGGTGCTC	780
	GCTGGGGGTC	CACGCGAGCC	TGGTCATCCC	GCCCCCTGG	ATCCTCCGCG	CCCGGAGGCC	840
	CCAGAAATCT	CTGAAGACAA	GCAAGAGGAA	GAAGAGGGCA	TCCTTCAAGA	GGAAAGTCCAG	900
5	CAAGAAAGGG	CCTGAGGAGG	GCCGCTGGAG	ACCCCTCATC	ATCAGGCCCCA	CCCCCTCCCC	960
	GCTCATGAAG	CCCCTGCTGG	TGTTTGTGAA	CCCCAAGAGT	GGGGGCAACC	AGGGTGCAAA	1020
	GATCATCCAG	TCCTTCTCTCT	GGTATCTCAA	TCCCAGACAA	GTCTTGGACC	TGAGCCAGGG	1080
	AGGGCCCAAG	GAGGCGCTGG	AGATGTACCG	CAAAAGTGAC	AACCTGCGGA	TCTTGGCGTG	1140
	CGGGGGCGAG	GGCAGCGTGG	GCTGGATCCT	CTCCACCCGT	GACCAAGTAC	GCGCTGAAGCC	1200
10	GCCACCCCTT	GTTCGCATCC	TGCCCCGSGG	TACTGGCAAC	GACTTGGCCC	GAAACCTCAA	1260
	CTGGGGTGGG	GGCTACACAG	ATGAGCCTGT	GTCCAAGATC	CTCTCCACAG	TGAGGAGGGG	1320
	GAACTGGTA	CAGCTGGACC	GCTGGGACCT	CCACGCTGAG	CCCAACCCCG	AGGCAGGGCC	1380
	TGAGGACCGA	GATGAAGCGG	CCACCGACCG	GTGGCCCTTG	GATGTCTTCA	ACAACTACTT	1440
	CAGCCTGGGG	TTTGAAGCCC	ACGTCAACCT	GGAGTTCAC	GAGTCTCGAG	AGGCCAACCC	1500
	AGAGAAATTC	AACAGCCGCT	TTGGGAATAA	GATGTTCTAC	GCGGGACAG	CTTTCTCTGA	1560
15	CTTCTGATG	GGCAGCTCCA	AGGACCTGGC	CAAGCACATC	CGAGTGGTGT	GTGATGGAAT	1620
	GGACTTGACT	CCCAAGATCC	AGGACCTGAA	ACCCCACTGT	GTGTTTTTCC	TGAACATCCC	1680
	CAGGTACTGT	GCGGCGACCA	TGCCCTGGGG	CCACCTGGGG	GAGCACCAAG	ACTTTGAGCC	1740
	CCAGCGGCAT	GACGACGGCT	ACCTGAGGCT	CATTGGCTTC	ACCATGACGT	CGTTGGCCGC	1800
	GCTGCAGGTG	GGCGACACCG	GCGAGCGGCT	GACGAGTGT	CGGAGGTGG	TGCTCACCAC	1860
20	ATCCAAGGCT	ATCCCGGTGG	AGGTGGATGG	CGAGCCCTGC	AAGCTTGACG	CCTCAAGCAT	1920
	CCGATCGCC	CTGCGCAACC	AGGCCACCAT	GGTGACGAAG	GCCAAGCGGC	GGAGCGCGGC	1980
	CCCCCTGCAC	AGCGACGAGC	AGCCGCTGCC	AGAGCAGTTG	CGCATCCAG	TGAGTGGCGT	2040
	CAGCATGCAC	GACTATGAGG	CCCTGCACTA	CGACAAGGAG	CAGCTCAAGG	AGGCCTCTGT	2100
	GCGCTGGGC	ACTGTGGTGG	TCCCAGGAGA	CAGTGACCTA	GAGCTCTGCC	GTGCCACAT	2160
25	TGAGAGACTC	CAGCAGGAGC	COGATGGTGC	TGGAGCCAAG	TCCCAGACAT	GCCAGAAACT	2220
	GTCCCCCAAG	TGGTGCTTCC	TGAGCGCCAC	CAGTCCACG	CGCTTCTACA	GGATCGACCG	2280
	AGCCAGGAG	CAGCTCAACT	ATGTGACTGA	GATCGACAG	GATGAGATT	ATATCTTGGA	2340
	CCCTGAGCTG	CTGGGGGCAT	CGGCCCGGCC	TGAACCTCCA	ACCCCACTT	CCCTCTCTCC	2400
30	CACCTCACCC	TGCTCACCCA	CGCCCGGTGC	ACTGCAAGGG	GATGCTGCAC	CCCCTCAAGG	2460
	TGAAGAGCTG	ATTGAGGCTG	CCAAGAGGAA	CGACTTCTGT	AAGCTCCAGG	AGCTGCACCG	2520
	AGCTGGGGGG	GACCTCATGC	ACCGAGACGA	CGAGAGTCCG	ACGCTCTCTG	ACCAAGCAGT	2580
	CAGCATCTGC	AGCAAGAGATG	TGGTCCGCTA	CCTGCTGGAC	CACGCCCCCG	CAGAGATCCT	2640
	TGATGCGGTG	GAGGAAAACG	GGGAGACCTG	TTTGACCAAA	GCAGCGCCCC	TGGGCCAGCG	2700
35	CACCATCTGC	CAGTACATCG	TGGAGGCGCG	GGCCTCGCTC	ATGAAGACAG	ACCAGCAGGG	2760
	CGACACTCCC	CGGCGAGCGG	CTGAGAAGGC	TCAGGACACC	GAGCTGGCCG	CCTACTTGGA	2820
	GAACCGGCAG	CAGTACCAGA	TGATCCAGCG	GGAGGACAG	GAGACGGCTG	TGTAGCGGGC	2880

Seq ID NO: 172 Protein sequence:

Protein Accession #: NP_003637

40	1	11	21	31	41	51	
	MEPRDGSPEA	RSSDSESASA	SSSGSERDAG	PEPDKAPRRL	NKRRFPGLRL	FGRKAITKS	60
	GLQHLAPPPP	TPGAPCSESE	RQIRSTVDWS	ESATYGEHIN	PETNVSGDFC	YVBQYCVAR	120
45	MLKSVSRRC	AACKIVVHTP	CIEQLEKINF	RCKPSFRESG	SRNVREPTFV	RHHVHRRRQ	180
	DGKCRHCGRG	PQOKFTFHSK	EIVAISSWC	KQAYHSKVSC	FMLQOIEBPC	SLGVHAAVVI	240
	PPTWILRAAR	PQNTLKASKK	KIRASFKRKS	SKKGPEBGRW	RPFIIRPTPS	PLMKPLLVFV	300
	NPKSGGNQGA	KIIQSPFLWYL	NFRQVFDLSQ	GGPKALEMY	RKVHNLRLA	CGGDTGVGWI	360
	LSTLDQLRLK	PPPPVAILPL	GTGNDLARTL	NWGGSYTDEP	VSKILSHVEE	GNVVQLDRWD	420
50	LHAEPNFEAG	PEDRDEGATD	RLPLDVFNNY	PSLGFDAHVT	LEPHESREAN	PEKPNRSFRN	480
	KMFYAGTAFS	DFLMGSSKDL	AKHIRVVC DG	MDLTFKIQDL	KPCQVVLINI	PRYCACTMPW	540
	GHPGEHHDPE	PQRHDDGYLE	VIGPTMTSLA	ALQVGHGER	LTQCREVVLIT	TSKAIPVQVD	600
	GEPCKLAASR	IRIALRNQAT	MVQAKRRSA	APLHSDQPPV	PEQLRIQVSR	VSMHDYEALH	660
	YDKBQLKEAS	VPLGTVVVPG	DSDELICRAH	IERLQQEPDG	AGAKSPTCQK	LSPKWCFLDA	720
55	TTASRPRYRD	RAQEHNLNYT	EIAQDEIYIL	DFELLGASAR	PDLPTPTSPL	PTSPCSPTPR	780
	SLQGDAAFPQ	GEELIEAAKR	NDFCKLQELH	RAGGDLMRD	DQSRLLHLHA	VSTGSKDVVR	840
	YLLDHAPPBI	LDAVEZENGT	CLHQAALGQ	RTICHIYIVEA	GASLMKTDQO	GDTPRQRAEK	900
	AQDTELAAYL	ENRQHYQMIQ	REDQETAV				

Seq ID NO: 173 DNA sequence

Nucleic Acid Accession #: AF232772

Coding sequence: 1-1662

65	1	11	21	31	41	51	
	ATGCGGCTGC	AGCTGACGAC	AGCCCTGCGT	GTGGTGGGCA	CCAGCCTGTT	TGCCCTGGCA	60
	GTGCTGGGTG	GCACTCTGGC	AGCCTATGTG	ACGGGCTACC	AGTTTATCCA	CACGAAAAG	120
	CAGTACTCTG	CTTTCGGCCT	GTACGGCGCC	ATCCTGGGCC	TGCACCTGCT	CATTGAGAGC	180
70	CTTTTGCCT	TCCTGGAGCA	CGGCGCATG	CGACGTGCGG	GCCAGGCCCT	GAAGCTGCCC	240
	TCCCGCGGCG	GGGGCTCGGT	GGCACTGTGC	ATTGCCGCAT	ACCAGGAGGA	CCCTGACTAC	300
	TTGCGCAAGT	GCCTGCGCTC	GGCCACGCGC	ATCTCCTTCC	CTGACCTCAA	GGTGGTCAATG	360
	GTGGTGGATG	GCAACCGCCA	GGAGGACGCC	TACATGCTGG	ACATCTTCCA	CGAGGTGCTG	420
	GGCGGACCGG	AGCAGGCGGG	CTTCTTTGTG	TGGCGCAGCA	ACTTCCATGA	GGCAGGCGAG	480
	GGTGAGACGG	AGGCGACGCT	GCAGGAGGGC	ATGAGCCGTG	TGCGGGATGT	GGTGGCGGCC	540
75	AGCACCTTCT	CGTGCACTAT	GCAGAAAGTG	GGAGGCAAGC	GCGAGGTGAT	GTACAAGGCC	600
	TTCAAGGCCCT	TCCGGGATTC	GGTGGACTAC	ATCCAGGTGT	GCGACTCTGA	CAGTGTGCTG	660
	GATCCAGCCT	GCACCATCGA	GATGCTTCGA	GTCTGGAGG	AGGATCCCCA	AGTAGGGGGA	720
	GTCCGGGGAG	ATGTCCAGAT	CCTCAACAAG	TACGACTCAT	GGATTTCCTT	CCTGAGCAGC	780
	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCCTGCC	AGTCTACTTT	TGGCTGTGTG	840
80	CAGTGTATTA	GTGGGCCCTT	GGGCATGTAC	CGCAACAGCC	TCCTCCAGCA	GTTCCTGGAG	900
	GACTGTGTACC	ATCAGAAGTT	CCTAGGCAGC	AAGTGCAAGT	TCGGGGATGA	CCGCAACCTC	960
	ACCAACCGAG	TCCTGAGCCT	TGGCTACCGA	ACTAAGTATA	CGGCGCGCTC	CAAGTGCCTC	1020
	ACAGAGACCC	CCACTAAGTA	CCTCCGGTGG	CTCAACAGC	AAACCGCGCT	GAGCAAGTCT	1080
	TACTTCCGGG	AGTGGCTCTA	CAACTCTCTG	TGGTTCCATA	AGCAACCACT	CTGATGACCC	1140
85	TACGAGTCAG	TGGTCAAGGG	TTTCTTCCCC	TTCTTCTCTA	TGCGCAAGGT	TATACAGCTT	1200
	TTCTACCGGG	GCGGCATCTG	GAACATCTCT	CTCTTCTCTG	TGAAGGTGCA	GCTGGTGGGC	1260
	ATTATCAAGG	CCACCTACGC	CTGCTTCTCT	CGGGGCAATG	CAGAGATGAT	CTTCATGTCC	1320

	CTCTACTCCC	TCCCTCTATAT	GTCCAGCCTT	CTGCCGCGCCA	AGATCTTTGC	CATTGCTACC	1380
	ATCAACAACAT	CTGGCTGGGG	CACCTCTGGC	CGAAAAACCA	TTGTGGTGAA	CTTCATTGGC	1440
	CTCATTCTCGT	TGTCATCTCTG	GGTGGCAGTT	CTCCTGGAGG	GGCTGGCCTA	CACAGCTTAT	1500
	TGCCAGGACC	TGTTCAAGTA	GACAGAGCTA	GCCTTCCTTG	TCTCTGGGGC	TATACTGTAT	1560
5	GGCTGCTACT	GGGTGGCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG	1620
	AAGAAGCCGG	AGCAGTACAG	CTTGGCTTTT	GCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	CGGGTAAATG	GCAATGGGTA	AGGGAGGGAA	GGGGAATGGA	AGAGAAAAGA	CAGGGTGGGA	1740
	GGGAGGAGGG	AGTGTGTGT	TTTAGTCTCT	TAATGGTCCA	AAGGACAAAT	CTAAAAATGCA	1800
	AAGAACCGTG	ATGTAGTATG	GCCTGACAGC	TCTGTTTAGA	GGAGGCAACA	CTGATCCCCC	1860
10	AGATGCAGGG	CTGCAGGGGA	TTCTGTGTTT	TCAGACTGCC	TGCTGTGCTG	CATCTGCACA	1920
	TAGGCAGTAG	CCTCCTCCTG	GGCTCCAGAG	GGCACTCAGA	AGTTGTGCTA	AACCAAGTTA	1980
	AGTCCCATTC	AGTGGCAACT	TGTGATAGGT	ACCTGAGTGA	CGGCAACCTG	CGGAAGGAGG	2040
	TTCTCCACGC	CCATCTGAAC	ACAACCAGAG	GTGGCAGGAG	AATTTCTACT	GAGCGAGGTG	2100
	GGCCGGTTAG	TGTATGTCAC	CCCCACCCCA	CCCATAACTA	GTCACTCAATG	CAATAAGATT	2160
15	GGCGTGAGGA	TACAAGGCC	AGAAGCCTGA	TCTTTGGGCA	TCAGAAAAAC	GGGTCCAGGA	2220
	ATGGTGCTTT	ATGTGAGATA	CCCCACTCCA	CATCAACATT	CCAGGGATGA	GCCAAACAGG	2280
	CAGGAGGTGA	GCACTGAACT	GCTTTTAAAA	GTGCACATTA	AAAAGGAAAG	TTTGCCAGGA	2340
	GGAAACAAAG	GATTGTGGTG	GTGCTAAAGG	AGGCCATAAG	CTACACAGAG	GCCTTGGGTG	2400
	TTCCACCTGG	AAACTGCTCA	GACGTCTAGA	TGGGTTCTTA	GCTTGTCTGT	GATCTCTGCT	2460
20	GGGAGATATA	AAAGATTAA	CCCCAACATG	TTGAGAAAAG	AAGTGAAGTC	TTGGGTATTT	2520
	TAACTGTAT	ACTCTTGAAT	TCCTCTCAAA	TTGAGCTCTG	ATCTGAGGCT	AAGACACACT	2580
	CCCCACTTCA	CTTCTTCAA	AGCCACATT	TTTGAGGTAT	CACCTGCAGT	ACCTCTTCTA	2640
	CCCTCATCAT	CATAGGTAAG	GTTTTCAGG	TGGCAATTGG	GGCGAGGCC	CGGCTTCTTA	2700
	TAGAAGCTTC	AGCAGGAGGC	AAGCGTGTTC	TCAGCACATA	TGGGAACAT	GAGGAGCCTC	2760
25	TGATCAAAAT	GGCTACAAAT	TTGGAGCTGC	TTGGACGGAT	TCCTTGGCAG	CGGGTTAGC	2820
	ATGTGTGACT	TTACAGCTAC	TGTTCTTGAC	AATCATCTCC	AATGGAAAGC	TTTTCACTGT	2880
	TCCCAAGAGT	AACCTCTCAA	TCCAAATGG	TTATCTTTGA	GACCATCCAT	TCTCCTCAGT	2940
	GGCTTCTCCA	GGGAATCTT	ACAGCCAAGT	TGTGACAGTC	ACTGCATTG	CCTGCTTCTT	3000
	TCCAGAAACC	AAACTAGGAG	ATGAACTGG	TTCTACATC	CTAAGGTTCT	TGCTTTCTCT	3060
30	CTCATGCCCT	CTGAGGCTGT	TTTTGGCTGT	TTTCCCTCTG	CTGCTTTTGG	GGAATGAGGG	3120
	GAAGCCATT	TCCAAGTGAC	TTGCAATCCA	GGCTGTTCTC	AGCGTTTTGA	GTTTAAACC	3180
	TGGATCCTTG	CTAAGCCTT	TGACTTAAGG	GTTGCTTGCT	TGCCCTCCAA	ATGCTCTTTC	3240
	TCAAAGGGGC	CAACTAACCC	GTGCAGAAC	AGCACTAAGG	TGGACAGCAG	ACAAGAGGGC	3300
	AAGCCTCTAA	TGTACCAAGT	GCTTCTTACA	AAGACGCAAG	GTGTGCTCCG	AACCACAGAT	3360
35	GGGCAAAACC	TGGTGCCTTC	CTTCACTCTC	CACGAACTCA	AGGGTTTTCC	AAGTGTAGCT	3420
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	CCAACCCATT	GAAGGCTGGA	AGGCAGCAGG	CATTGTCTAA	GGCAGCTGAT	CCAGGCAATC	3540
	GTTCTGCTGG	CCAGAAGATT	AAACTATTTT	GAGCATTAGA	ATGGAGGAAA	TCCGTCAGC	3600
	CAAGTGCAGA	GTTCAAGCTT	CGCTAAGGGC	TTGTTTTTCT	TCAGCATTTA	CTTGAAGATT	3660
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	GTCACCTTTC	CTCAATCAA	AAACAGGCAG	GTACAGGTAG	TGGGCTCACA	ACGTTTGACC	3780
	TOGACTGGTT	TTTCTAAGTT	ATTTTGTACA	TTTTTCAGCA	GCAAAACCAA	ACTGGGCTCT	3840
	CAGCTTTATC	CCCGTTTCTT	GCAAGGGAAG	AGCCTTTATA	CAATTGGACG	CATTTTGGTT	3900
	TTTCTCTATT	GAGAATTCAA	ATCCTCTTTT	GTATTGTTTC	TACATAAATT	TGTAACATA	3960
45	TTTATTTTAA	CTGCTTTTTC	TTTTTTTTTT	TAATTTTCAG	GTCAAGTTTT	TTATACTGCA	4020
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Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

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55	VVDGNRQEDA	YMLDIFHEVL	GGTEQAGFFV	WRSNFHEAGE	GETEASLQEG	MDRVRDVVRA	180
	STFSCIMQKW	GGKREVMYTA	FKALGDSVDY	IQVCDSDTVL	DPACTIEMLR	VLEEDPQVGG	240
	VGGDVQILNK	YDSWISFLSS	VRWMAFNVE	RACQSYFGCV	QCISGPLGMY	RNSLIQQFLE	300
	DWYHQKPLGS	KCSFGDDRHL	TNRVLSLGYR	TKYTARSKCL	TEPTPKYLRL	LNQQTNRWSKS	360
	YFREWLYNLS	WFHKHRLWMT	YESVVTGFFP	PFLIATVIQL	FYRGRINWIL	LFLLTVQLVG	420
60	LIKATYACPL	RGNALMIFMS	LYSLLYMSSL	LPKIPAIAT	INKSGWGTSG	RTKIVNVFIG	480
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	KKPEQYSLAF	AEV					

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Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

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	TTCCAGCAGC	TGGAGGCGCT	GCAGCGCCTG	ATCCAGGAGC	AGGAGCAGGA	GCTGGTGGGC	180
	GCGCTGGCCG	CAGACCTGCA	CAAGAATGAA	TGGAACGCCT	ACTATGAGGA	GGTGGTGATC	240
75	GTCCTAGAGG	AGATCGAGTA	CATGATCCAG	AAGCTCCCTG	AGTGGGCGCG	GGATGAGCCC	300
	GTGGAGAAGA	CGCCCCAGAC	TCAGCAGGAC	GAGCTCTACA	TCCACTCCGA	GCCACTGGGC	360
	GTGTCTCTCG	CTATTGGCAC	CTGGAACCTAC	CCCTTCAACC	TCACCATCCA	GCCCATGGTG	420
	GCGGCCATCG	GTCAGGGAAG	CGCAGTGGTC	CTCAAGCCCT	CGGAGCTGAG	TGAGAACATG	480
	CGAGGCTGTC	TGGCTACCAT	CATCCCCCAG	TACCTGGACA	AGGATCTGTA	CCAGTAATC	540
80	AATCGGGGTG	TCCCTGAGAC	CACGGAGCTG	CTCAAGGAGA	GGTTCGACCA	TATCCTGTAC	600
	ACGGGCAGCA	CGGGGTGGGG	GAAGATCATC	ATGACGGCTG	CTGCCAAGCA	CCTGACCCCT	660
	GTCACGCTGG	AGCTGGGAGG	GAAGAGTCCC	TGCTACGTGG	ACAAGAACTG	TGACCTGGAC	720
	GTGGCCTGCG	GACGCTACGC	CTGGGGGAAA	TTTCATGAACA	GTGGCCAGAC	CTGGGTGGCC	780
	CCAGACTACA	TCTCTCTGTA	CCCTCGATC	CAGAACCAAA	TTGTGGAGAA	GCTCAAGAA	840
85	TCACTGAAG	AGTTCTACGG	GGAAGATGCT	AAGAAATCCC	GGGACTATGG	AAGAATCATT	900
	AGTGCCCGGC	ACTTCCAGAG	GGTGATGGGC	CTGATTGAGG	GCCAGAAGGT	GGCTTATGGG	960
	GGCACCGGGG	ATGCCGCCAC	TGCTACATA	GCCCCACCA	TCTCACGGA	CGTGGACCCC	1020

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CCCATGGGAG TGGCGCACAC CCTCACTGGC TCTCTGGGCC CTGGAGAATC GCTCTCTGAG 1500
CCCCAGCCCA GCCCACATCC TCTGCTGACC TGCTGACCTG TGCACACCCC ACTCCCAT 1560
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CAATTTTCTA ACTCGG

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Seq ID NO: 176 Protein sequence:
Protein Accession #: NP_000682

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TIQPMVGAIA AGNAVVLKPS ELSENMAILL ATII PQYLDK DLYPVLINGV PETTELLKER 180
FDHILYTGST GVGIKINTAA AKHLTPVLE LGGKSPCYVD KNCGLDVACR RIWAGKFMNS 240
GQTCVAFDYI LCDPSIQNQI VEKLEKSLKE FYGEDAKKSR DYGRILSARH PORVMGLIEG 300
QKVAYGGTGD AATRYIAPTI LTDVDQSPV MQEELFGFVL PIVCVRSLEE AIQFINQREK 360
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Seq ID NO: 177 DNA sequence
Nucleic Acid Accession #: NM_001067.1
Coding sequence: 108-4703

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 Protein Accession #: NP_001058.1

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Seq ID NO: 179 DNA sequence
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	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAAACAA	TTCCGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GSAAAGGAAG	AGATTTCATGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
	TGGGAAGAGC	CTGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGTG	CAGATGGCTA	TCAAGACTTG	1260
15	GGTGTATTTC	TCATAAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATCA	GGAAGAAAGG	ACCCAGATTT	TCTACCAACA	CACACTACAA	TGSCATAGGG	1560
20	ACGAAATAGA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAGG	ATAATTTCTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCTCTTCT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
	AACCTGTGCG	GGAGTCGAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAAAT	TGAGGAGGAG	1860
25	AGTTTATTTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTCTCG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAAGG	TCATAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
30	AGCTTCTCC	AGACTAATTA	CACGTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTCTCG	CAGGCCCATG	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATCTTA	CGTTTGCTTA	CTTCCCACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTGGT	CTCCAAGGTC	AACGTGGTAT	ACTGCGAGAC	AACCCAAACG	2400
35	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
	ACCCCTTTGT	TGCTTGAACA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TCGGCCTTGC	ATGCTAGCGC	TGTATTTCCC	AGTGTGATG	TGTCAATTGA	ATCCATCCTG	2580
	TCCTCCTATG	ATGCTGCAAC	TTTGCTTCCA	TTTCTCTG	CTTCTTCAG	TAGTGAATTG	2640
	TTTCGCCATC	TGCTATACAGT	TTCTCAATC	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
40	GATAAGGTGC	CCTTGATGCT	TTCTTGCCA	GTGGCTGGGG	GTGATTGCT	ATTAGAGCCC	2760
	AGCCTTGCTG	AGTATCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GAOCCTGGAA	2820
	TTTGTAGTAG	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTAGTG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTCCTTACA	GTTCGCAAT	ACCTGTGCAT	3000
45	GATTTCTGTG	GTGTAACTTA	TCAGGGTTCC	TTATTTAGCG	GCCTTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	TGCTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACTAT	TTCTTCACT	GTTCCTGTAG	CTGAATTAC	ATATACAAAC	3240
	TCGTGTGTTG	TGCTGATATA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATAGAG	3300
50	ACTGAAGTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGCGAT	GTTTCCAGGG	TCCCTTGCTC	ATACCAACCAC	TAAAGTTTTC	3480
	GATCATGAGA	TGATCAAGT	TCCAGAAAAAT	AACTTTTAG	TTCAACCTAC	ACATACGTGC	3540
	TCTCAAGCAT	CTGGTGACAC	TTGGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
55	TCCTCTGACC	CTGCTTCTAG	TGAATATGTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTG	CTTTTATGAT	TGAAGTATG	CTACAACTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TAAACCTGT	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTGAAACCC	3780
	CCCAAGTTG	ATAAAATTAG	TTCTACAATG	TGCTATCTCA	TTGATCAAA	TTCTGCTTCA	3840
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	GTTTTGTATA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAAC	CAGGCCATC	CCCCAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AAATGATGAA	CCATTAAATA	CACTAATAAA	TAAAGCTTATA	4140
	CATTCOGATG	AAATTTTAA	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
65	ATTCCAACAG	TGCTTCTGTA	TACATTTGTA	TCTACTGATC	ATTCCTGTTC	TATAGGAAAT	4260
	GGGCAAGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCTGTAA	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAGGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
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70	CAGGAAAAGG	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAAATAAT	4560
	CCAACTCAT	ACTCATATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
	TCAGACAGTC	AACTGCTAT	GGACAGAAGT	CCTGCTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGCTAG	TGCTCTGCTT	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
75	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTGTGA	4860
	GACACTAATG	AAAAGATGTC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCAC	AGTCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAGT	GTTCCAAGTT	4980
	TCAGAGGACG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTGTTA	TTGGTCTAGC	TGAGGGGTTG	5040
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATGTTGT	CAGCCCTGAC	TTTTTCTGTT	5100
80	CTAGTGGTTT	TGTTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAAGAT	ATGTCGGAGC	AAATCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTAA	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACCAAG	5400
	CACAGAAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
85	CTTGTGTA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	5580
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	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
5	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CTGACCTTTG	TGAGAAAGGC	AGCCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGC	5940
	CACGTGAGTG	CTGAGGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	6000
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAAACACAT	CCGTTCACAA	6060
	AGAAATTATT	TGGTACAAAC	TGAGGAGCAA	TATGTTCTCA	TTCATGATAC	ACTGGTTGAG	6120
10	GCCATACCTA	GTAAGAGAAAC	TGAGGTGCTG	GACAGTCATA	TTCAATGCCA	TGTTAATGCA	6180
	CTOCTCATT	CTGAGCCAGC	AGGCCAAACA	AAGCTAGAGA	AACAATCCCA	GCTCCTGAGC	6240
	CAGTCAAAAT	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAGAG	6300
	AATCGAATCT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	6360
	GGAGAAAGCA	CAGACTACAT	CAATGCCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTTATCATTA	CCCAGCACCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
15	GACCATTAAT	CCCACTCTGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATCTGT	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAATAT	TCTATCTAAT	GAGGAAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAAGT	TCCTAAATGG	6720
20	CCAAATCCAG	ATAGCCCCAT	TAGTAAAACT	TTTGAACCTA	TAAGTGTATT	AAAAGAAGAA	6780
	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
	ACTTTCCTGT	CTCTGACAAC	CCTTATGCAC	CAACTAGAAA	AAGAAAATTC	CGTGGATGTT	6900
	TACCAGATAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
25	TCCACCTCTC	TGGACAGTAA	TGGTGACAGA	TTGCCTGATG	GAAATATAGC	TGAGAGCTTA	7080
	GAGTCTTTAG	TTTAAACAG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTTCTCT	7140
	TTCTTAAAT	TAGGCAGGAA	AATCAGTCTA	GTTCTGTTAT	CTGTTGATTT	CCCATCACCT	7200
	GACAGTAACT	TTCTATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTTA	CAATGTGTGC	7260
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	GCTGTATTTC	TAGCAATTTAT	CAGGTTTGCT	AGAAATATAA	CTTTTAATAC	AGTAGCCGTG	7500
	AAATAAAACA	CTCTTCCATA	TGATAATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAATAACT	GCCCTAGTGT	CTCCATGGAC	CAAATTTATA	7620
35	TTTATAATG	TAGATTTTTTA	TATTTTACTA	CTGAGTCAAG	TTTTCTAGTT	CTGTGTAATT	7680
	TTGTAGTTTA	ATGACGTAGT	TCATTAGCTG	GTCTTACTCT	ACCACTTTTC	TGACATTGTA	7740
	TGTGTTTACC	TAACTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAATAA	7800
	GAAATACCTT	CATTTTGAAA	GAAGTTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTTCA	7860
40	AATGGTTTTT	ATCCAAGGAA	TTGCAAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAAAATA	7920
	AAAAAAAAAA	AAAAAAAAAA	AAAA				

Seq ID NO: 180 Protein sequence:
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQVNVNLKLL	KFQGWKDTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	FKAGKITFEW	GKCMMSDGS	EHSLEGGKFP	LEMQIYCFDA	DRFSSFEBAV	KKGKLRALS	180
	ILFEVGTSEN	LDFKAIIDGV	ESVSRPGKQA	ALDPFILLNL	LPNSTDKYII	YNGSLTSPCC	240
50	TDTVDMIVFK	DTVSISSQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEEAV	CSSEPEVQVA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDTGYQ	LAILNLNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLVDMPT	DNPELDLFFE	420
	LIGTEEIIKE	EEEGKDLIEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHVNRI	GTKYNEAKTN	480
	RSPTRGSEPS	GKGDVPNTSL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPPHY	VEGTSASLND	540
55	GSKTVLRSFH	MNLSGTAESL	MTVSIIEYEE	ESLLTSPLKD	TGAEDSSGSS	PATSAIPPIS	600
	ENISQGVIPS	SENPETITVD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWVFPSSTDI	660
	TAQPDVGSGR	ESFLQNTNTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAFYP	720
	TEVTPHAFTP	SSRQODLVST	VNVVVSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
	LMTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSE	LPRHLHTVSQ	840
60	ILPQVTSATE	SDKVPLHSLH	PVAGGDLLE	PSLAQYSDVL	STTHAASETL	EPGSESGVLY	900
	KTLMFQVQEP	PSSDAMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVTYQG	960
	SLPSPGSEHIP	IPKSLITPT	ASLLQPTHEAL	SGDGEWSGAS	SDSEFLLEPDT	DGLTALNISS	1020
	PVSVAETTYT	TSVPGDDNKA	LSKSRIIYGN	ETELQIPSPN	EMVYPSESTV	MPNMYDNVKN	1080
65	LNASLQETSV	SISSTKGMFP	GSLSHTTTKV	FDHEISQVPE	NNFSVQPTHY	VSQASGDTSL	1140
	KPVLSANSEP	ASSDPASSEH	LSPSTQLLFY	ETSASFSTEV	LLQSPSQASD	VDTLKTVLP	1200
	AVPSDPILVE	TPFKVDKISS	MLELIVNSNA	SSENMLESST	VPVFDVSPTS	HMHSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVPSLYSND	ELFQATANLEI	NQAHPPKGRH	VFATPVLSID	1320
	EPLNLTINKL	IHSDEILTST	KSSVTGKVFA	GIPTVASDTE	VSTDHSVPIG	NHGVAITAVS	1380
70	PERDGSVTST	KLLFPFKATS	ELSHSAKSDA	GLVGGGEDGD	TDDGDDDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQERVMNDSD	THENSMDQVN	NPISYSLSEN	SEEDNRVTSV	SSDSQTMGDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTSAL	LPLSPESKAM	AVLTSDSEESG	SGQGTSDSLN	1560
	ENETSTDPSP	ADTNEKDADG	ILAAGDSEIT	PGFPQSPSTSS	VTSENSEVPH	VSEAEASNSS	1620
	HESRIGLABG	LESEKKAVIP	LVIVSALTPI	CLVVVLGILI	YWRKCFQTAH	FYLEDSTSPR	1680
75	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCVTDLGI	1740
	TADSSNHPDN	KHKRYRYINTV	AYDESRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPRAYIAA	1800
	QGPLEKSTAE	PWRMIWEHNV	EIVVMITNLV	ERGRKKCDQY	WPADGSEEEY	NFLVTQKSVQ	1860
	VLAYTYVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFTVKKAA	1920
	AKREHAGPVV	VHCSAGVGRT	GTIIVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
80	QYVPIHDTLV	EAILSKSTEV	LDSHIAHYVN	ALLIPGPAGK	TKLERQFQLL	SQSNIIQSDY	2040
	SAALKQCNRE	NKRTSSIIIPV	ERSRVGISSL	SGEGTDYINA	SYIMGYQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDQGNMAED	EFVYWPKNDE	PINCESPKVT	LMABEKKCLS	2160
	NEEKLIIQDP	ILEATQDDYV	LEVRFQCQPK	WPNPDSPISK	TFELISVIKE	EANNRDGPMI	2220
85	VEDEHGGVTA	GTFPCALTTLM	HOLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVIL	2280
	SLVSTGREN	PSTSLDSNGA	ALPDGNIAES	LESILV			

Seq ID NO: 181 DNA sequence
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	CGGCGAGGGG	CGGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCGG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
10	CTTGTGGAAG	AGATTGGCTG	GTCCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAACCTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	ITCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTACGCGGAG	GAGTTTCAGA	AATGGTGTIT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
15	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTITTTAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTAGGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTITTTGGGA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
20	AATGGCTCAT	CTCGATCTCG	TOCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTAGACA	TCTCTGAAAG	CCAGTTGGCT	GTITTTTGTG	AAGTTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCCAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAT	AGGTGTITTC	CTCATACACT	GGAAAGGAAG	AGATTTCATG	AGCAGTTTGT	1080
	AGTTCAAGAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTATCA	1140
	TGGGAAGAC	CTCGATCTCG	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
25	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAGACTTGT	1260
	GGTGCTATTC	TCAATAATT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACATAAT	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGCATAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
30	GAAGAGGAAA	TAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTATCA	1500
	AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACCAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTAGTG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAATAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
35	GAAGGTACTT	CAGCTCTCTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCCATATG	1800
	AACCTGTGCG	GSACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATGTA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCATG	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAGAACCCG	AGACAAATAC	ATATGATGTC	CTTATACCGA	AATCTGCTAG	AAATGCTTCC	2040
40	GAAGATTCAA	CTCATGCGG	TTCAGAAGAA	TCACATAAAG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGTTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTCTC	AGACTAATTA	CAGTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTCTTG	CAGGCCAGTG	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATCTTA	CCTTTGCCCTA	CTTCCCAACT	GAGGTAAACAC	CTCATGCTTT	TACCCCATCC	2340
45	TCCAGAACAC	AGGATTGTGG	CTCCACGGTC	AACGTGGTAT	ACTGCGAGAC	AACCCAACCG	2400
	GTATACATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAAATCG	AGAAGAAGGG	AGTTATACCC	CTTGTGATGG	TGTGAGCCCT	GACTTTTATC	2520
	TGTTAGTGTG	TCTTGTGGG	TATTTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
	TTTTACTTAG	AGGACAGTAC	ATCCCTAGAG	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
50	CCAATTCTAG	ATGATGTCCG	AGCAATTCCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCGACAGCAAC	2820
	AAGCACAAGT	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
55	TACAACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGAGGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAAATG	TGATCAGTAC	TGGCCTCCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACCTTCTGG	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCTT	ATTATACTGT	GAGGAATTTT	3180
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60	GTACACAGAT	ATCACTACAC	GCACTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
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	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
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	CAAGAAATTT	ATTTGGTACA	AACGTGAGGAG	CAATATGTCT	TCATTCTATG	TACACTGGTT	3540
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70	GAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCCT	GAGGATGATA	3900
	TGGGACCAT	ATGCCCAACT	GGTGGTTATG	ATTCTCTGAT	GCCAAAACAT	GGCAGAAGAT	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAAAT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACAACA	ATGCTATCT	AATGAGGAAA	AACCTATAAT	TCAGGACTTT	4080
	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGCTCTAAA	4140
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	GGAACTTCT	GTGCTCTGAC	AACCCCTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
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	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCTTAA	AATTAGGCGA	GAAATCAGT	CTAGTTCTGT	TATCTGTTGA	TTTCCCATCA	4620
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	TGCCCTTTTG	CAAGACTTGT	AAITTACTTA	TTATGTTTGA	ACTAAAATGA	TGAAATTTTA	4740
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85	CAATTTATAG	CGTTTAGGAA	TTCCAAACTA	CAGAAAATGT	TTGTTTTTAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAATAAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980

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10 Seq ID NO: 182 Protein sequence:
 Protein Accession #: Eos sequence

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 VEVIVMITNL VEGRRKRCQW YWPADGSEZY GNFVLTQKSV QVLAYYTVRN FTLRNTKIKK 1020
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 35 VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
 VERSRVGISS LSGEGTDYIN ASYIMGYQS NEFIITQHPL LHTIKDPWRM IWDHNAQLVV 1260
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 VLEVRHFQCP KWNPDSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
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Seq ID NO: 183 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4494

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 GAGATGCAAA TCTACTGCTT TGATGAGAG CGATTITCAA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAAAGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAAATTG 720
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 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTGTG AAGTCTTAC AATGCAACAA 960
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 TTCTCTAGAC AGGTGTTTTT CTCTACACTC GGAAAGGAAG AGATTCTATG AGCAGTTTGT 1080
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 80 GCAACTTCTG CTATCCCATC CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCTCTC 1980
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5	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
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	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAAACAGC	ACAAGAAATCG	ATACATAAAT	2820
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10	GCTGCCCAAG	GCCCACTGAA	ATCCAAGCTC	GAAGATTCTT	GGAGAATGAT	ATGGGAACAT	3000
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	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGG	CGTGTGGTCA	CACAGTATCA	CTACAOCGAG	3240
15	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	TGACCTTTGT	GAGAAAGGCA	3300
	GCCTATGGCA	AGCGCCATGC	AGTGGGGCCT	GTGTGCTGCC	ACTGCAGTGC	TGGAGTTGGA	3360
	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	AGATTCAACA	CGAAGGAACT	3420
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	GAGGAGCAAT	ATGCTTTCAT	TCATGATACA	CTGGTTGAGG	CCATACCTAG	TAAAGAAACT	3540
20	GAGGTGCTGG	ACAGTCATAT	TCATGCCCTAT	GTTAATGCAC	TCCTCATTC	TGGACCAGCA	3600
	GGCAAAACRA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	AGTCAAAATAT	ACAGCAGAGT	3660
	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAGAA	ATCGAACTTC	TTCTATCATC	3720
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25	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	ACCATAATGC	CCAACCTGGT	3900
	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	TTGTTTACTG	GCCAAATAAA	3960
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Seq ID NO: 184 Protein sequence:
Protein Accession #: EOS sequence

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60	ILFEVGTREN	LDFKAILDGV	ESVSRPFGQA	ALDPPILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSP	300
	TGKEEIEHAV	CSSEPEVQQA	DFENYTSLLV	TWERPRVVDY	TMIEKFAVLV	QQLDGEDQTK	360
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	LIGTEELIKE	EEEGKDIEEG	AI VNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
65	RSPTRGSEPS	GKGDVPTSL	NSTSQPVTKL	ATEKDILSLT	QTVTELPFHT	VEGTSASLND	540
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	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAIVP	780
70	LVIVSALTFI	CLVVVLGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
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Seq ID NO: 185 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

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	CGAAATACAA	TGAAGCCAG	ACTAACCGAT	CCCCAACAA	AGGAAGTGAA	TTCTCTGGAA	1620
30	AGGGTGATGT	TCCCAATACA	TCCTTAAAT	CCACTTCCCA	ACCAAGTCACT	AAATTAGCCA	1680
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	GTCTATTGAC	CAGTTTCAAG	CTTGATACCT	GAGCTGAAGA	TTCTTCAGGC	TCCAGTCCCG	1920
35	CAACTTCTGC	TATCCCATTC	ATCTCTGAGA	ACATATCCCA	AGGGTATATA	TTTTCTCTCG	1980
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	AAGATTCAAC	TTCTATCAGT	TCAGAGAAT	CACTAAAGGA	TCCTTCTATG	GAGGGAAATG	2100
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40	CCTTTCTGCG	AGGCCCAAGT	ATGTCACAGG	GTCCCTCAGT	TACAGATCTG	GAATGCGCAC	2280
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	CCAGACAACA	GGATTTGGTC	TCCACGGTCA	ACGTGGTATA	CTCGCAGACA	ACCCAACCGG	2400
	TATACAATGA	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	GAGGGTTTGG	2460
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Seq ID NO: 186 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 187 DNA sequence
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5	TGGAGATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTGTGGGAG	3060
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Seq ID NO: 188 Protein sequence:
Protein Accession #: B0S sequence

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55	ILFVGVTEEN	LDFKAIIDGV	ESVSRFGKQA	ALDPPILLNL	LPNSTDKYYI	YNGSLTSPPC	240
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Seq ID NO: 189 DNA sequence
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Seq ID NO: 190 Protein sequence:
Protein Accession #: NP_002811

30 1 11 21 31 41 51
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 35 HHLIAEIHIA EIRATSEVSP NSKPSFNTKN HPVRFSGDDE GRYLTQETNK VETYKEQPLK 120
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Protein Accession #: NP_005679.1

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 CGCCCTGCTT GTTTGTAGTA ATTTTATAGG ACCAAATCTC CCTCATCTTC TAGTGCCATT 2460
 CTCCTCTCTG TTACAGTAAA TGTCACACTG TGCCCAAGAT GGATGACCAG GAACCTTAAA 2520
 GAGTGGCTGA AAAGATTGCA GAGTTATCAT AATAAATTGC TAACTTGCCT

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Seq ID NO: 196 Protein sequence:
 Protein Accession #: NP_006461

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1 11 21 31 41 51
 MASELDLMAFG PLPRATAQPP APLSPDSGSP SPDSGSASPV EEDVGSSEK LGRETEBQDS 60
 DSABQGDPAE EGKEVLCDPC LDDTRRVKAV KSCLTCMVNY CEEHLQPHQV NIKLOSHLLT 120
 EPVVDENWRY CPAHHSPLSA FCCPDQCCIC QDCQEHSGH TIVSLDAARR DKEAELQCTQ 180
 LDLEERLKLIN ENAISRLQAN QKSVLVSVE VKAVAEWQFG ELLAAVRKAQ ANVMLFLEEK 240
 EQAALSQANG IKARLEYRSA EMEKSKQELE RMAAISMTVQ FLEEYCKPKN TEDITFPSVY 300
 VGLKDLKSGI RKVITESTVH LIQLLENYKK KLQEFSEKBE YDIRTQVSAV VQRKYWTSKP 360
 EPSTRBQFLQ YAYDITTFDP TAHKYLRLQE ENRKVTNTTP WEEPPYDLPV RFLHWRQVLS 420
 QQSILYHRY FEVEIFGAGT YVGLTCKGID RKGBERNSCI SQWFSWLSQ WNGKEFTAWY 480
 SDMETPLKAG PFRRLGVYID PFGILSPFY VEYDTMTLVH KFACKFSEPV YAAFWSLKEE 540
 NAIRIVDLGE EPEKPAPSLG VTAP

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Seq ID NO: 197 DNA sequence
 Nucleic Acid Accession #: NM_004316
 Coding sequence: 433-1149

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1 11 21 31 41 51
 CCCGAGACCC GGCAGAGAG AGCGCAGCCT TAGTAGGAGA GGAACGCGAG ACAGCGGAGA 60
 GCGCGTTTCA CACTGACTTT TGCTGCTGCT TCTGCTTTT TTTTCTTTAG AAACAAGAAAG 120
 GCGCCAGCGG CAGCCTCACA CGCGAGCGCC ACGCGAGGCT CCGAAGCCA ACCCGGGAAG 180
 GGAGAGGGGG AGGGAGGAGG AGGGCGGTTG CAGGGAGGAG AAAAAGCAAT TTCACCTTTT 240
 TTGCTCCAC TCTAAGAAGT CTCGCGGGA TTTGTATAT ATTTTAAAC TTCGTCAGG 300
 GCTCCCGCTT CATATTTCTT TTTCTTTCCC TCTCTGTTCC TGACCCCAAG TTCTCTCTGT 360
 GTCCCGCTCG CGGCGCCCGC ACCTCGGCTC CGGATCGCT CTGATTCGCG GACTCCTTGG 420
 CGCGCGCTCG GCATGGAAG CTCTGCAAG ATGAGAGCG GCGCGCGCG CCAGCAGCCC 480
 CAGCCGACG CCGCAGCGCC CTCTCTGCG CCGCAGCCT GTTCTTTGC CACGGCCGCA 540
 GCCCGCGCG CCGCAGCGCC CGCAGCGCA CGCAGAGCG CGCAGCAGCA GCAGCAGCAG 600
 CAGCAGCAGC AGCAGCAGCA GCAGCGCGCG CAGCTGAGAC CGGCGGCGGA CGGCGAGCCC 660
 TCAGGGGGCG GTACAAAGT AGCGCCCAAG CAAGTCAAGC GACAGCGCTC GTCTTCGCCC 720
 GAACCTGATC GCTGCAAAAG CCGGCTCAAC TTCAGCGGCT TTGCTACAG CCGCGCGCAG 780
 CAGCAGCGCG CGCGGTTGGC GCGCGCAAC GAGCGGAGC GCAACCGCGT CAAGTTGGTC 840
 AACCTGGGCT TTGCCACCTT TCGGGAGCAC GTCCCCAAC GCGCGGCCAA CRAAGAAGAT 900
 AGTAAGGTGG AGACACTGCG CTCGGCGGTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG 960
 GACGAGCATG ACGCGGTGAG CGCGCGCTTC CAGGCAGGCG TCCTGTGCGC CACCATCTCC 1020
 CCCAAGTACT CCAACGACTT GAACTCCATG GCGCGCTCGC CGGTCTCATC CTACTGCTCG 1080
 GACGAGGCTT CTTAGGACCC GCTCAGCCCC GAGGAGCAGG AGCTTCTCGA CTTCAACCAAC 1140
 TGGTTCTGAG GGGCTCGGCC TGGTCAGGCC CTGGTGCGAA TGGACTTTGG AAGCAGGGTG 1200
 ATCGCAACAT CTGCACTTTT AGTGCTTTCT TGTCAAGTGC GTTGGGAGGG GGAGAAAGAG 1260
 AAAAGAAAAA AAAAGAAAGA GAAGAAGAAA AGAGAAGAA AAAAAACGA AAACAGTCAA 1320
 CCAACCCCAT CGCCACTCAA GCGAGGCATG CCTGAGAGAC ATGGCTTTCA GAAACGGGA 1380
 AGCGCTCAGA ACAGTATCTT TGCACCTCAA TCATTCACCG AGATATGAAG AGCAACTGGG 1440
 ACCTGAGTCA ATGCGCAAAA TGCAGCTTGT GTGCAAAAGC AGTGGGCTCC TGGCAGAAGG 1500
 GAGCAGCACA CGGCTTATAG TAACTCCCAT CACCTCTAAC ACGCACAGCT GAAAGTTCTT 1560
 GCTCGGCTCC CTTCACCTCC CCGCCCTTTC TTAGAGTGCA GTTCTTAGCC CTCTAGAAAC 1620
 GAGTTGGTGT CTTTC

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Seq ID NO: 198 Protein sequence:
 Protein Accession #: NP_004307

1 11 21 31 41 51
 MESSAKMESG GAGQPPQPP QPFLPPAAC PFATAAAAAA AAAAAAQA QQQQQQQQQQ 60
 QQQQAPQLRP AADQPPSGG HKSAPKQVKE QSSSPFLMR CKRRLNFSGP GYSLPQQQPA 120
 AVARRNERER NRKVLNVLGF ATLREHVPNG AANKKMSKVE TLRSAVEYIR ALQQLLDEHD 180
 AVSAAPQAGV LSPITSPNYS NDLHSMAGSP VSSYSSEBGS YDPLSPREQE LLDPTNWF

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Seq ID NO: 199 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1-1005

1 11 21 31 41 51
 ATGACAGAGA ACTCGACAA AGTCCCAAT GCCCTGGTGG GACCTGATGA CGTGAATTC 60
 TGCAGCCCCC CGGGGTACGC TACGCTGACG GTGAAGCCCT CCAGCCCCGC GGGGCTGCTC 120
 AAGGTGGGAG CGGTGCTCTT CATTTGCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
 GCCTTCTACT TCTGGAGAGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGAGC CTGGGAACAA CTTGGAGACC 300
 TTTAAATGG GAGTTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC 360
 ACAGGAATTC GTTTTGTCTG AGGAGAGAAG TGCTACATTA AAGGCAAGT GAAGGCTCGT 420
 ATTCTTGAGG TGGGCGCGGT GACCAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAAGA AAATTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 GACACAGCTT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTCTCGG 600
 CTTAAACCAA CCTATCCAAA AGMAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAACCTA CCACAAAAG ACCACACAGT GGACACGGA GCAACCCAGG CGCTGGAAGA 720
 CTGAATAATG AAACAGAGCC CAGTGTTCAG GAGGACTCAC AAGCCTCAA TCCTGATAAT 780

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CCTTATCATC AGCAGGAAGG GGAAAGCATG ACATTGAGCC CTAGACTGGA TCACGAAGGA 840
ATCTGTTGTA TAGAATGTAG GGGAGGTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
GGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960
ATGCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTTATATAT 1020
CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTG AGGCAGGTG 1080
ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGTTTATTC TTGACACTCT 1140
TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAATGCA CTGAAAGGGT 1200
AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTTGTTAT TTTTATTGCG ATTGATTGCG 1260
CATAAGTCTT CCCTTGCTTG CATCTTCCA AGCTATTTCG AAATAAACAC GAAATTTTAC 1320
AGTTTGCC

Seq ID NO: 200 Protein sequence:
Protein Accession #: NP_008946

1 11 21 31 41 51
MTENSCKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
APYFWKSDS HIYNVHYTMS INKILQDGSN EIDAGNNLET FKMGSAGAEA IAVNDPQNGI 120
TGIRFAGGEK CYIKAQVKAR IPEVGAVTRQ SISKLEGI MPVKYRENSL IWAVDQPVK 180
DNSFLSSVKL ELQGLPIFW LKPTYPKEIQ RERREVVRI VPTTTKRPHS GPRSNPGAGR 240
LNNETRPVQ EDSQAFNPDN PYHQQBGESM TFDPRLDHES ICCIECRRSY THCQKICEPL 300
GGYYPWPYNY QGCRSACRVI MPCSNWVARI LGMV

Seq ID NO: 201 DNA sequence
Nucleic Acid Accession #: NM_000728.2
Coding sequence: 112..495

1 11 21 31 41 51
GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCACAGC AGGTGTGGTG TTCATCCCGG 60
GTCGACGGGC CGCTGCGCT GCCCTGAAAC TCTAGTCGCC AGAGAGGCGG CATGGGTTTC 120
CGGAAGTTCT CCCCCTTCT GGCTCTCAGT ATCTTGTGTC TGTACCAAGC GGGCAGCCTC 180
CAGGCGGCGC CATTGAGGTG TGCCCTGGAG AGCAGCCAG ACCCGGCCAC ACTCAGTAAA 240
GAGGACGGGC GCCTCTGCT GGCTGCACTG GTGCAGGACT ATGTGCAGAT GAAGGCCAGT 300
GAGCTGAAGC AGGAGCAGGA GACACAGGGC TCCAGCTCCG CTGCCAGAA GAGAGCCTGC 360
AACACTGCCA CCTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG 420
GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGCAG GCGCCGCGAG 480
GACCTTCAAG CCTGAGCAGA TGAATGACTC CAGGAAGAAG GTGTGTCTTA AATCCAATGA 540
CATATCTCTA TAAGAGATTC ACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC 600
AAGGAGGCAC AAGCCAAGGA AGTCTGTGTC TACCAGAAGC CAGAAATACA GAACAGTCTC 660
TGGAAGAAGA GCAGCCCTGC TGACACCTAG AGTTTGGACT TCCAGCTTCC AGAAGTGTGA 720
GAGAATAAAT TCTGTTGTTT TAAGCCACAA AGTTTGTGGT AATTGTGTAT GACAGCCCTA 780
GGAAACTAAT ACAATACATT TTCAATTAAT TTGGGTAAAT GCCTTGGAGT GGGATTGCTG 840
GGTTATTGGG AAAGTGTGTA TTTAACTCTG TAAGAAACTG CCAAACTATT TTCTGAAGTG 900
ACTGTACCAC TTCGCCCTCT TGCCAGCCAC ATATGAGAGC TCTAGTATT CCACAAATAG 960
GTATGTAGCA GTATCTCATT GCTGTTTAA TTTGTATTTT CCAATGACT AATGAGCTTG 1020
AGCATCTATT TTACCATATG TTTATCACCT TTATTGAAGG GTCTGTAAAT ATCTTCTGCT 1080
AAATTTTGTG TGGCTTGCTT GCTTTATTAG TGTGTAGTTT TTAGAGCTCT TTATATGTTG 1140
TGGATGCAAG ATTTCTTTCA GATATATAGT TTGGAACCTT CCTTCCCTCG AATCTGCGGA 1200
TTGCTTTTTC ATTTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA 1260
TCCAATTCAT CTTTTTTTTT CTTTTATGTA TTGTGCTTTT AGTTTCATGT TAAGAACTCT 1320
TTGCTAACT AAGGTCCCAA GGTCAACATA ACCTTATTCT ATACTTTCTT GTAAAAAGTT 1380
TATAGTTTTA TATTTATAT GTAGATTAGT GATCTATTTT GAGTTAATTT TTGTATAAGG 1440
TGAGAGGTGT AGGTGTAAAT TCATACCTGT GAATATAGAT ACCCAATTGT TTCAGTGCCA 1500
TTGTATAAAA AGACTGTAT TTCAACATTT AATTGCCCTT GCACCTTGT CAAAAGCAA 1560
CTGATCATAT TTGTGTGGGT ATATTTCGCG GTTCTCAATT CTGTCTCATT GATTGATTG 1620
ACCATCTCTT TGCCCAATGTC ATACTGCTT GATTAGTGTA GTGTAAAGT GAATCTCAA 1680
ACCAGATAAT GTGGGTCTAC CAACATGTTT CATTCTGTTT CAAAAGATT TTAGCTACAT 1740
CTAAATATTT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT 1800
TTCTGATGAG ATTTTAAATG GGATTGTGTT AAATCAGTGG GTTAATTTTG GGAGAATTAG 1860
CATATTAATA ATATTAAGTC GTTCAATTCA TGAACACAA ACATGTTTTC ACTTATTTAG 1920
GTTTTCTCTG TTTTTTTTTT TTTAACAGTG TTCTCAGTTT TCAACAGAAA TATTTACAC 1980
ATATCTGTTT AGATTTTAA CTATTTTATT TTTTGTGCT AATGTAAATG GTACTTAAAC 2040
ATTTTGTGTT TTAATTGTTT ATTCTAGTA GATAGAAATA CAATATTTAA AATATTAGGA 2100
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 202 Protein sequence:
Protein Accession #: NP_000719.1

1 11 21 31 41 51
MGFRKFPPL ALSILVLYQA GSIQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM 60
KASELKQEQE TQSSSSAAQK RACNTATCVT HRLAGLLSRS GGMVKSNEVP TNVGSKAFGR 120
RRRDLQA

Seq ID NO: 203 DNA sequence
Nucleic Acid Accession #: NM_001741
Coding sequence: 71..496

1 11 21 31 41 51
CTCTGGCTGG ACGCCGCGC GCGCGCTGCC ACCGCCCTCG ATCCAAGCCA CCTCCCGCCA 60
GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCTCG GCTCTCAGCA TCTTGTCTCT 120
GTTGCAGGCA GGCAGCCTCC ATGCAGCACC ATTCAAGTCT GCGCTTGGGA GCAGCCGAGC 180
AGACCCGCGC ACGCTCAGTG AGGACGAAGC GCGCTTCTCG CTGGCTGCAC TGGTGCAGGA 240
CTATGTGCAG ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT 300

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10
GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCATGCTGG GCACATACAC 360
GCAGGACTTC AACAACTTTC ACACGTTCCC CCAAACTGCA ATTGGGGTTG GAGCACCTGG 420
AAAGAAAGGC GATATGTCCA GCGACTTGGA GAGAGACCAT CGCCCTCATG TTAGCATGCC 480
CCAGATAGCC AACTAAATCT CTCCTTTTCC TTCTTAATTT CCCTTCTTGC ATCCTTCCTA 540
TAACTTGATG CATGTGGTTC GGTTCCTCTC TGGTGGCTCT TTGGGCTGGT ATTGGTGGCT 600
TTCTTGTGGG CAGAGGATGT CTCAACTTC AGATGGGAGG AAAGAGAGCA GGACTCAGAG 660
GTTGGAAGAG AATCACTGG GAAATACCA GAAATGAGG GCGCTTTGA GTCCCCCAGA 720
GATGTATCA GAGTCTCTCT GTCTGTCTTC TGAATGTGCT GATCATTGA GGAATAAAAT 780
TATTTTTCCT C

Seq ID NO: 204 Protein sequence:
Protein Accession #: NP_001732

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1 11 21 31 41 51
MGFPKFPFPL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVQ 60
MKASELEQEQ EREBSSLDSP RSKRCGNLST CNLGTYYTQDF NKPHTFPQTA IGVGAPGKKR 120
DMSSDLERDH RPHVSMFQNA N

Seq ID NO: 205 DNA sequence
Nucleic Acid Accession #: NM_005361
Coding sequence: 1-945

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1 11 21 31 41 51
ATGCTCTTTG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGGCCTTGA GGCCCGAGGA 60
GAGGCCCTTG GCTTGGTGGG TCGCAGGCT CCGTCTACTG AGGAGCAGCA GACCGCTTCT 120
TCCTCTCTTA CTCTAGTGGG AGTTACCTTG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT 180
CCTCCCCACA GTCTCAGGG AGCCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG 240
AGACAATCCG ATGAGGGCTC CAGCAACCAA GAAGAGGAGG GGCCAAGAAT GTTTCCCGAC 300
CTGAGGTCCG AGTTCACAAG AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG 360
CTCCTCAAGT ATCGAGCCAG GGAGCCGGTC ACAAAGGCAG AAATGCTGGA GAGTGTCTCT 420
AGAAATGTCG AGGACTTCTT TCCCGTGATC TTCAGCAAAG CCTCGAGTA CTTCGAGCTG 480
GTCTTTGGCA TCGAGGTGGT GGAAGTGGTC CCATCAGGCC ACTTGTACAT CCTTGTCAAC 540
TGCTTGGGCC TCTCTACGGA TGGCCTGCTG GCGACAAATC AGGTCTATGCC CAAGACAGGC 600
CTCTGATAA TCGTCTCTGG CATAATGCGA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA 660
ATCTGGGAGG AGCTGAGTAT GTTGAGGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCCGA 720
CATCCAGAGA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCGGCAG 780
GTGCCCGGCA GTGATCTCTG ATGCTACGAG TTCCTGTGGG GTCCAAGGGC CCTCATTGAA 840
ACCAGCTATG TGAAGTCTCT GCACCATACA CTAAGATCG GTGGAGAAC TCACATTTC 900
TACCCACCCC TGCATGAAAG GCTTTTGAAG GAGGAGAGAG AGTGA

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Seq ID NO: 206 Protein sequence:
Protein Accession #: NP_005352

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1 11 21 31 41 51
MPLEQRSQHC KPEEGLERAG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS 60
PPHSPQAGSS PSTTINYTLW RQSDGSSNQ EEEGPRMFPD LESEFQAALR RMVVELVHFL 120
LLKYRAREPV TKAEMLSEVL RNCQDFPVI FSKASEYLQL VPGIEVVEVV PISHLYILVT 180
CLGLSYDGLL GDNQVMPKTO LLIIVLAIIA IEGDCAPEEK IWEELSMLEV FBGREDVSPA 240
HPRKLLMQDL VQENYLEYRQ VPGSDPACYE FLWGPRLALIE TSYVKVLHHT LKIGSEPHIS 300
YPLHERALR EGEE

Seq ID NO: 207 DNA sequence
Nucleic Acid Accession #: NM_021115
Coding sequence: 743-2893

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1 11 21 31 41 51
AAAGGAAGGG AGGAGGGGAG AAAGGAGAAG TTGGTTTAGA GGCCAGCCGG ACAGACTTTG 60
GGCACCGCCC TTAGGAGGGC CACCCTCAGA GTCTGACAGC AGGTGAAGGT CCTAAATCTC 120
CCCAAACTAA CTGTGTCTTT TTCTCTCTTT CCAAGATGCT CTTCGCGAGG GAGATGCTAG 180
CCCTTTGGGT CCTTACCTCC TGCCCTCAGG AGCCCGGAG AGAGGCAGTC CTGGCAAAGA 240
GCACCCCTGA GAGAGAGTGG TAACAGCGCC CCCCACTTCC TCACAGTCGG CGGAAGTGCT 300
GGGCGAGCTG GTGCTGGATG GGAACCGCAC CTCTGCACAT CAACACATCC CAGCCCTGTC 360
ACCGCTGCTT CCAGAGGAGG CCGGCCCAA GCACGCTTG CCCCCAAGA AGAAACTGCC 420
TTGCTCAAG CAGGTGAAC CTGCCAGGAA GCAGCTGAGG CCAAGGCCA CCTCCGCGAG 480
CACTGTCCAA AGGCAGGGT CCCAGCCAGC GTCCAGGGC CTAGATCTCC TCTCTCTCTC 540
CAGGAGAAAG CCTGGCCAC CGGGGGACCC GGACCCCATC GTGGCTCCG AGGAGGCATC 600
AGAAGTGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCGGTC CTACAAACAC CGCACCCCTC 660
GCAAACTCTC CCTTCACTT GGCAGCCCTA TGTGGCCAC ACACCTCCCC AGAGGCCAGA 720
ACCGGGGAG CCTGGGCTG ACATGGCCCA GGAGGCCCCC CAGGAGGACA CCAGCCCAT 780
GGCCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAGG AGAGCCAGGA 840
GACCACTACC TCCACCATTA TCACCACCAC GGTCTATACC ACCGAGCAGG CACCACTCT 900
CTGCAGTGTG AGCTTCTCCA ATCTGAGGG GTACATTGAC TCCAGGAGT ACCCACTGCT 960
GCCCTCAAC AACTTCTGG AGTGACATA CAACGTGACA GTCTACACTG GCTATGGGGT 1020
GGAGCTCCAG GTGAGAGGTG TGAACCTGTC CGATGGGAAA CTGCTCTCCA TCGCGGGGT 1080
GGACGGCCCT ACCCTGACCG TCCTGGCCAA CCAGACACTC CTGTTGGAGG GGCAGGTAAT 1140
CCGAAGCCCC ACCAACACCA TCTCCGTCTA CTTCCGAGCC TTCCAGGAGC ACAGCCCTTG 1200
GACCTTCCAG CTTCACTACC AGGCCTTCAT GCTGAGCTGC AACTTTCCTC GCGGCGCTGA 1260
CTCTGGGGAT GTCAAGGTGA TGGACCTGCA CTCAGGTGGG GTGGCCCACT TTCAGTCCA 1320
CCTGGGCTAT GAGCTCCAGG GCGCTAAGAT GCTGACATGC ATCAATGCTC CCAAGCCGCA 1380
CTGGAGCAGC CAGAGGCCCA TCTGCTCAGC TCCTTGTGGA GGGGCACTGC ACAAATGCCA 1440
CATCGGCCGC GTCTCTCTCC CAAGTTACCC TGAACACACA AATGGGAGCC AATCTGCTAT 1500
CTGAGGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GCGTGTGCT 1560

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GCATGACAAG GACAGGATGA OGGTTACAG CGGGCAGACC AACAGTCAG CTCTTCTCTA 1620
CGACTCCCTT CAACACGAGA GTGTCCCTTT TGAGGCGCTG CTGAGCGAAG GCAACACCAT 1680
CGGCATCGAG TTCACGTCGG ACCAGGCCCG GGGCGCCTCC ACCTTCAACA TCCGATTGTA 1740
AGCGTTTGAG AAAGGCCACT GCTATGAGCC CTACATCCAG AATGGGAAT TCACTACATC 1800
CGACCCGACC TATAACATTG GGACTATAGT GGAGTTCACC TGGACCCCGG GCCACTCCCT 1860
GGAGCGGGCC CGGCGCATCA TCGAATGCAT CAATGTGGGG GACCCATACT GGAATGACAC 1920
AGAGCCCTG TGCAGAGCCA TGTGTGGTGG GGAGCTCTCT GCTGTGGCTG GGGTGGTATT 1980
GTCCCCAAAC TGGCCCGAGC CCTACGTGGA AGGTGAAGAT TGTATCTGGA AGATCCACGT 2040
GGGAGAAGAG AAACGGATCT TCTTAGATAT CCAGTTCCTG AATCTGAGCA ACAGTGACAT 2100
CTTGACCATC TACGATGGCG ACGAGGTTCAT GCCCCACATC TTGGGGCAGT ACCTTGGGAA 2160
CAGTGGCCCG CAGAACTGT ACTCCTCCAC GCCAGACTTA ACCATCCAGT TCCATTGGGA 2220
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AAGGAATGAC TCCTGCTCGG ATTTACCCGA GATCCAGAAAT GGCTGGAAAA CCACCTTCTCA 2340
CACGGAGTGT GTGCGGGGAG CCAGAATCAC CTACCAAGTGT GACCCCGGCT ATGACATCGT 2400
GGGGAGTGAC ACCCTCACTT GCCAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTITG 2460
TGAGAAAAAT ATGTACTGCA CGACCCCGG AGAGGTGGAT CACTCGACCC GCTTAAITTC 2520
GGATCCTGTG CTGCTGTGTG GGACCACCAT CCAATACACC TGCAACCCCG GTTTTGTGCT 2580
TGAAGGAGAT TCTCTCTCGA CCTGCTACAG CCGTGAAACA GGGACTCCCA TCTGGACGTC 2640
TCGCTGCCCC CAGAGCGGCT CAGAGCGGCG AGCAGAGACG TCGCTGGAAG GGGGGACAT 2700
GGCCTGGCT ATCTTCACTC CGGTCTCAT CATCTCCTTA CTGCTGGGAG GAGCCTACAT 2760
TTACATCACA AGATGTGCTG ACTATTCCAA CCTCGGCTG CCTCTGATGT ACTCCACACC 2820
CTACAGCCAG ATCAGCGTGG AAACCGAGTT TGACAAACCC ATTTACGAGA CAGGGGGAAC 2880
CCAAAAGTT TAGGGTTTCA TTTAAAAAGA GGTAACCTTT AAAAAGGGGC TTGTGAATCT 2940
AACCCCAATT TCCCGAGAGC ATTTATCCAA AGGCCCTGGG GGCCTTGATT TAAACCCCA 3000
AAAGGCGGCT GTTTTTTGGT TAAACTTTTT AACAAAGGT TACGGGTTTT TTCCCGGAT 3060
TTTATAAATT TTAAGATG

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30 Seq ID NO: 208 Protein sequence:
Protein Accession #: NP_066938

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1 11 21 31 41 51
MAQEPQEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN 60
PEGYIDSSDY PLLPIANFLE CTYNVTVTG YGVELQVRSV NLSGELLISI RGVDPGPTLV 120
LANQTLVVEG QVIRSPNTII SVYFRTFQDD GLGTFQLHYQ AFMLSNCNFP RPDSGDVTVM 180
DLHSGGVVAHF HCHLGYELQG AKMLTCINAS KPHWSSQEPi CSAPOGGAVH NATIGRVLSP 240
SYPTNTHSGQ FCINTIEAPE GQKLHLHFER LLLHDKDRMT VHSQGTNKA LLYDSLQTES 300
VPFEGLLSEB NTIRIEFTSD QARAASTFNI RFEAFERKHC YEPYIQNGNF TTSPTYNIG 360
TIVEFTCDPG HSLEQGPAIL ECINVRDPYV NDTEPLCRAM CGGELSAVAG VVLSFNWPEP 420
YVEGEDCIWK IHVGEERKIF LDIQFLNLSN SDILTIYDGD EVMPHILGQY LGNSGPQKLY 480
SSTPDLTIQF HSDPAGLIPG KQGFIMNYI EVSRNDSGSD LPEIQNGWKT TSHTELVRGA 540
RITYQCDPGY DIVGSDTLTC QNDLSWSSDP PFCEKIMYCT DPGEVDHSTR LISDPVLLVG 600
TTIQTNCNPG VLEGGSLLT CYSRETGTPI WTSRLPHCVS EAAETSLG GMNALAIFIP 660
VLIISLLLG AYIYITRCRY YSNLRLPLMY SHPYSQITVE TEFDNPIYET GGTQKV

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50 Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89-631

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1 11 21 31 41 51
AGCAGGGGGC GCTGTGTGTA CGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GCGCAGGCTT CCGAGCCCAT GCAGGCCGAA GCGCGGGGCA CAGGGGGTTC 120
GACGGGGGAT GCTGATGGCC CAGGAGGCCG TGGCATTCTT GATGGCCGAG GGGGCAATGC 180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCAGGGCG CAGGGGCAGC 240
AAGGGCCTCG GGGCGGGGAG GAGGCGCCCG GCGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
GCTGAATGGA TGCTGTCAGA GCGGGGCCAG GGGGCCGGAG AGCGGCTGCG TTGAGTCTA 360
CCTCGCCATC CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCTTGCCCCA 420
GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGTG TGTCCGGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTTCCC TGTGTATGTG GATCAOCGAG TGCTTTCTCG CCGTGTITTT 600
GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCAGCCTT GCGGCCCTT CCTAGGTGAT 660
GCCCTCTCCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
GTTTGTGCTT GGAGGAGGAC GGCTTACATG TTGTTTCTG TAGAAAAATA AACTGAGCTA

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70 Seq ID NO: 210 Protein sequence:
Protein Accession #: NP_001318.1

75

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1 11 21 31 41 51
MQAEGRGTTG STGDADGPGG PGIPDPGGGN AGGPGEAGAT GGRGFRGAGA ARASGPGGGA 60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLPVPG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCFLPVF LAQPPSPGQR

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80 Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52-459

85

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1 11 21 31 41 51
CCTGCTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
GAAGGCCAGG GCACAGGGGG TTGACGGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGTGTCCAC GGGCGGCAGA 180
GGTCCCGGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCGGA GAGGAGGCGC CCGCGGGGGT 240
CCGCATGGCG GTGCCCTTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGGCG 300

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GACAGCGGCC TGCCTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
 ATCAGCTCCT GTCTCCAGCA GCTTTCCTCTG TTGATGTGGA TCACGCACTG CTTTCTGCCC 420
 GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCCTCC 480
 TAGGTCTATG CTCCCTCCCT AGGGAATGGT CCCAGCAGA GTGGCCAGTT CATTGTGGGG 540
 GCCTGATTGT TTGTGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAATAAAG 600
 CTGAGCTA

Seq ID NO: 212 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGSPGEAGAT GGRGPRGAGA ARASGPRGGA 60
 PRGPHGGAAS AQDGRCPGGA RRPDSRLLOF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 PLFVFLAQAP SQRRR

Seq ID NO: 213 DNA sequence
 Nucleic Acid Accession #: NM_000555
 Coding sequence: 416..1498

1 11 21 31 41 51
 CTTATTTTTT ATGAATGTGG GATAGCTGCA CCAGCTTGGT GGGGAAAGGG TTGATGAAT 60
 AGCACAAAGA CACTGGCTGT TCCCTGGAGG CTGTCCCTTT AAAGGAGAAT CTTAGTTTAT 120
 TCTGGGGGGA GGGGATGCAC ACATTAGAGT AGGAAAGAGG GCTTGGGAATA AAATGAAAAC 180
 ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCTTAAGC TGGAGATGCT 240
 AACCTCTGGT AGCTCTCTCT GTTCTCTTCA AGGGGAATTT TGTCTAGGCTA TGGATTCATT 300
 TACAACGTGT AGTCATGTGG GCATGTGTGA GGAAACAGAT GCCAGTTTGA ATGTATTAG 360
 CCGGAAGTTC CAATTTGATA GGAGCCACTG TCACTCTCTG AGGTTCCACC AAAATATGGA 420
 ACTTGATTTT GGACACTTTG ACGAAAGAGA TAAGACATCC AGGAACATGC GAGGCTCCCG 480
 GATGAATGGG TTGCTTAGCC CCACTCAGAG CGCCCACTGT AGCTTCTACC GAAACAGAAC 540
 CTTGCAGGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
 CCGCTACTTC AAGGGGATGT TGTACGCTGT GTCCCTCTGAC CGTTTTCGCA GCTTTGACGC 660
 TCTGCTGGCT GACCTGACGC GATCTCTGTC TGACAACATC AACCTGCGCTC AGGGAGTGGG 720
 TTACATTTAC ACCATTGATG GATCCAGGAA GATCCGGAAGC ATGGATGAAC TGGAGGAAGG 780
 GGAAAGCTAT GTCTGTCTCT CAGACAACTT CTTTAAAAAG GTGGAGTACA CCAAGAAATGT 840
 CAATCCCAAC TGGTCTGTCA ACGTAAAAAC ATCTGCCAAT ATGAAAGCCC CCCAGTCCTT 900
 GGCTAGCAGC AACAGTGACG AGGCCAGGGA GAACAAGGAC TTGTGCGGCC CCAAGCTGGT 960
 TACCATCATC CCGAGTGGGG TGAAGCCTCG GAAGSGCTGT CGTGTGCTTC TGAACAAGAA 1020
 GACAGCCCAAC TCTTTTGGAG AAGTCTCTAC TGATATCACA GAAGCCATCA AACTGGAGAC 1080
 CGGGGTGTGC AAAAATCTCT ACACCTCTGA TGGAAAAAGC GTAACTGTGC TCCATGATTT 1140
 CTTTGGTGAT GATGATGTGC TTATTGCTGT TGGTCTGTGA AAATTTGCTC ATGCTCAGGA 1200
 TGATTTTCTC CTGATGAAAT ATGAATGCGG AGTCATGAAG GGAAACCCAT CAGCCACAGC 1260
 TGGCCCAAGG GCATCCCAAC CACCTCAGAA GACTTCAGCC AAGAGCCCTG GTCCCTATGG 1320
 CGAAGCAAG TCTCCAGCTG ACTCAGCAAA CGGAACCTCC AGCAGCCAGC TCTCTACCCC 1380
 CAAGTCTAAG CAGTCTCCCA TCTCTAGGCC CACCACTGCT GGCAGCCCTC GGAAGCAGAA 1440
 GGACCTGTAT CTGCTCTGTG CCTTGGATGA CTCGGACTCG CTTGGTGATT CCATGTAAAG 1500
 GAGGGGAGAG TGCTCAGAGT CCAAGATACA AATCCAAGCC TATCATTGTA GTAGGGTACT 1560
 TCTGCTCAAG TGTCACACAG GGCTATTGGT GCTTCAAGT TTTTATTTTG TTGTGTGTGT 1620
 TATTTTGAAA AACACATTGT AATATGTTGG GTTATTTTTC CTGTGATTTT TCCTCTGGGC 1680
 CACTGATCCA CAGTTACCAA TTATGAGAGA TAGATTGATA ACCATCCTTT GGGGCGAGCAT 1740
 TCCAGGATG CAAATGTGTC TAGTCCATGA CCTTCAATG GAAAGCTTAG GGGCCTGGGG 1800
 TAAATTTGCC CCGTTTAAAT TTGCCCAAAC AGTTTTCTCT TTGTAGAGGG GTGTTTAAAT 1860
 ATACAGCAAT TAAAAAGTTT GTGTGGGGAA AAAAAAACT CATTGGCAGA TCCAAGAAATG 1920
 ACAAAACAAA GTGCCCTTT TCTCTGGATC TCAAGAAATG TGGAGGACCC TGGAAAGACA 1980
 GCAAGGCAGC TCCCGACGCT CACTCTTAC TCTGTATGTA GGCCCGGGTT TGTGTGCCAG 2040
 CACCAATGAT CGCTGTCAAT GGGGAGAAAT AAACCAACAA CTTATAATTG TGACACAGA 2100
 TGCTTAGGAT CCTGCTGCTG GGTAGCTAAG GAGAATAGAC AGAATTGGAA AATAGTCAG 2160
 ACATTTCCGA AGAGTTTATA AAGCACAGTG AATCTCTGGT CAATCTCTCC ACTGAGGCAA 2220
 TTTGGAAATCA ATAAGCAATT GATAATAGTT TGGAGTAAGG GACTTCATAT ACCTGATTTCC 2280
 TCTAGAAGGC TGTCTAACAT ACCACATGAT TACATGAAT GTATGGTATC CATCTATCTC 2340
 TGTCTATTG AATGCTTGT TAACAGCCAA CACTGAAAAC ACTGTGAGAA TTTGTTTCA 2400
 GGTCTGACAC CTTTCACTCT CTTTTATAG CAAGAAATCA ATATCCTTTT TATAAAAAAT 2460
 CATGCTCTGA TTTTCAAGAG AAACCTCTTCA GGCTCCTTTT TTATAAACTG GTGATTTTTC 2520
 TTTTGTCTAA AAAACACATG AAGAAATTT ACCAGAAAAA AAAAAAAAG COGAAGAATA 2580
 ATGTTATTTA GAAATATGTC TGTCACTGCC AAACAGTAAC CTCCAGGAGA AAACAAGATG 2640
 AATAGCAGAG GCCAATTCAA TAGAATCAGT TTTTGTATAG CTTTTAACA GTTATGCTTG 2700
 CATTAAATAT TTCAATGTGG ACCAGACATT CTAATTATAT TTTAAATGAA ATGTTACAGC 2760
 ATATTTTAAG CAACTCTTTT TATCTATAAT CCTAATATTT CATACTGAAG ACACAGAAAT 2820
 CTTTCACTTG TCTTTAATAT TAGAAAGGAT TTCTCTTTAC TAAGGACTGA TCATTTGAAA 2880
 TAGTTTTCAG TCTTTTGAGA TACAGGTTTA TAACACTGCT TTTTTTTCC TGTAAACATA 2940
 GCCATAAATG GCAAAAAACA CTAATTTTAA TTGAAGTCT TGCTTGCCAN TCCTGTGTTG 3000
 GCTTTNACCA AATATAAAAA TTCCCTTATT CCTTGGTAAT GGTGCAAAAT TTTGAAAAGG 3060
 CACAGCATCC AAACCAAGCT GCTGTTTGGC TACTGAATGG CTTGCAGTTG TTCTTCACT 3120
 CTAATGGAA TGAGCTTGCT GTGTGTGTGT GTGGTGGTGG TGGGAGGGGG TGGTGCATGT 3180
 GTGTGTGTGT GTGTGCTCT GCAGCTGCTT CAAATTAAG AAATACTACA AGACACCCCT 3240
 GTAATGGATT GGTGGCACT GGTGAGTGTG ACTGTGTAGG GGGGAACCCA 3300
 GTGGTGGTGG GGTATCTCAA ATGCCCTAG ACAAGCTTCA GATGTCTGTA GCTACCAAAA 3360
 ACATTTTCGG TTCAAGAAAA GTGAGATGAT GGTAGTACTG GTTCTCTGTG AAATGAAAAA 3420
 ACCCCAAATG ATGAGATCT CTTTGTGCCC CTTCTCTCTT TTTTGTAAAC CCAATCAAAA 3480
 CCATTAATAA GCCCATTTTA CTAANCCCTT ATTTCTTTCT AGAAGCTCAG GGTTCNCTTA 3540
 GTGCCCTCCA NAACATTTTG TAGTTAATTG GGAAAAAGTG ATACTTGGAT TAGGGGGTGT 3600
 GGGCATAAAG AATGGTGGGA GGCTGTATT TAAAAATCAG GCCAGAACCC CCAATGACTC 3660
 CACCCATAGT NTCACITTAG GTCTCATTTA GTCCATCACC TTTATTTTAA GTTGAGGAAG 3720
 TGGAGGCTGG TAAAGAGCAG GACCAAGGGA AGAATOCAGA TTTCTTATG CTTGGGCTCT 3780
 ACACAGCTCT TMTAGTATT TCCTTGATTG CGGTATATGT ACTACTAGAA AATACCAAAT 3840
 GGATATATTT TCTTTAGGAT AACCTTTGAA CCAACAAATN TCAATAACAA TAGTACATCT 3900

	TCCATCTTAC	TTTAAATCGA	GTATAAGGAA	ATGTTTCTTT	ATGGCCATTT	TGGAGGGAGC	3960
	AGGGGATGAG	GCTTGGCATA	GTCCAAATTT	TAAGNCTCCA	ATAATTAATT	GCATTTTAAA	4020
	TTGTTTAAAA	TTGGCCCACT	TTCAAGGCAA	TTTTTTTTGT	GTGTCGTGAA	CTGAGCTCCT	4080
5	CCACCCCTGT	CATCACTTTC	CAATTTTACC	CAATCCAAAT	TTAGCACTCA	AGTTCCATTG	4140
	TGTTAATTTT	TGCACGGTCT	ACACACATCA	AGTCAGCAAG	CATTTGCCAC	CACCTCCCTAT	4200
	ACTTCTCCCT	CTTTTTTACA	CACACACACA	CACACACACA	CACAAATCCAT	CTCTTGCTTG	4260
	TTCTACGCTC	CCTGATTTT	CTTCCCTACA	GAATATAGAA	TAGGACAAAA	GAAGGGGAAA	4320
	ATGTATATAT	TGGGGCTGGG	CTGAACAACT	AACCTTCATA	GTAGTATTAA	CTAGGGGTAA	4380
10	ATTGAGAGAA	AAGCTCCTTT	TCTCTTCACT	GTTTGGGAAA	GGATAGCCAT	TAGCATGACT	4440
	GCTTTGTGTC	CTTATGGACT	TTAGTATTAG	CCTAGATTGA	ATTATAGCGT	TTTTCTAGCT	4500
	GAAGGAACCT	TAAGATCACA	TCATCTACTC	CTCTACTCCA	AATTTCTCAT	TCTTCAGGCC	4560
	AGGAAACCGA	GACACAGAGG	TAAAGTAAAT	TCCCCAAGGT	CACACAGCTG	GCTGGGGCAG	4620
	GATTGGGTTT	ACAACCCACA	TCTCCTGGCT	CTTATCCAG	GGCCTTTTCC	CACTAAGTAG	4680
15	TATTGCGCTT	CATTAGGCTC	CTGAGAGTTA	TTTCTCAGGG	TCATGTTGCA	TCTTGGAGCC	4740
	ACATGCTGCT	GCCCTGATCT	CAGTGGGAAA	TNCAACCCAGC	AACCTAATAC	AGCCCCTTTT	4800
	CCCTGCAATC	ACCTGGTTCC	CATCCACATG	GGTTGCAGAT	GTCCCTGAAG	AGAGTGGAGC	4860
	ATTGAGGGCC	AATAGGAGCA	ATGGGGTCCC	TGGCCTTGTC	CATCTGATTC	AGGAGATCAC	4920
	TGCTCCATCG	TGAGGAGCCC	TCTGAATAGC	CCCCCACTGA	ATGCTTGCGT	TGCCAAATG	4980
20	GAATGGAGGA	AGATTGATTT	TCTCCATCAG	TTCACTTTGT	GTCACTCAT	AATGGTTGGT	5040
	CTTTCCAGGC	TGAGGGAAT	GTTTCTTGTT	TCCANAGTAN	AAAAAAGAAA	GAGTGGAAACA	5100
	ATANCTTTGT	TCATCTCAAC	TTTCTGAGAT	GGCTTTTCAA	CATTTAAAAA	AAACTAGTGT	5160
	GGTACCATTG	ACTGGCAGTG	TTTNTTTTAG	AATATGGGAG	TAAGATGAGG	TAGAGAAAAA	5220
	AACCTGGTCT	CACGTGGGTT	GCCCTCATCC	ACAATGTCCC	CAAAGCCATC	CTGCTNTGAT	5280
25	GAGGACAAAT	TCCAGGTATA	AGCAAGGGGC	TTTGTGACAA	AAATGTACCC	TGGCTGATGT	5340
	TAAACATTTG	CTCCTGTGTT	TGCACCAAAA	TAGCAAGCTG	TGTGCTCTAT	ACACTCTTCC	5400
	CATCGTCTTG	TGTACACTGC	TCCTGTGGCC	TTCCACAGCA	GAACCCAGGG	CAAAAGGGTC	5460
	CAAAACATG	GTTTTCTGTT	CTGCAAGGCT	NTTCTGGGA	ACTAAGGGGG	TATTTATTAG	5520
	TTCACTTNTA	AGAGACCTCC	TTCTGGGCTT	ACCCCACTCC	TCAGGTACTT	CTCTCTCCTT	5580
30	CCTCCTTCTC	CTCCACAGTC	ACAAGTAACC	AAGGAACCTG	AAAGTGGATG	TGTAGCTATT	5640
	TGAAGAAGGC	AAGGAACCTG	GAGATTCTTC	TTTGAATCCT	TTAGTCCCAAG	TCTTAGACCA	5700
	GTGATTGGTG	CTTACCTTGA	ACAAAAATTT	GTCTGTGTTT	CTAATCCCTT	CAATACINTG	5760
	GGTACAAATG	TCCCAATCAC	CCTGCACATT	TGATTCTAAA	TGGCTTTTAT	TTTTTAAAAA	5820
	TCCATATCCC	TAGGACAAGA	NAACAGGATG	CCTATATCCC	CAAAATGAGC	TCCAGGACAC	5880
35	TGATGGGAAT	GATCCCAANG	ATCACCCAC	CTCAGAAAC	GTCTGTGCCA	ANAGACTTCC	5940
	CCAGATAGAA	NCACCTGGAG	AGTGGTTTGA	ACGACTCTCT	TTATGGTTGT	CCAGTTTGCT	6000
	ATGGAATATA	AAGGCATTTA	TTTTTTAAAA	AAGATGATTT	GAACCTGTCT	TTGGCCACAT	6060
	AGGGCCACTT	GGATCCATTT	CCAGGCCCTTA	CTCATATATT	GCCCTTCACT	AAGGGCTTTG	6120
	GCTTTAAGTC	CCAGACTGGT	CTCCCAAGTG	AACCATAAGT	GTTTTGGAGC	TCATCTGGGG	6180
40	TGAGGCATGA	GAATGTTGCC	CCATCTATCC	CTTCAGGAAA	AGGTGCCCTC	CCTCCCTTTC	6240
	TCCTAAAGCC	TGGTCCCAAA	AAAATGTTTT	TGCTCCCAAA	AGTCTAGTAT	GGTCTTTATA	6300
	CACCCANACT	CTTAGTGTTG	GGTCTGCCTT	TGTTTCCCTG	TTAAGGATCT	ATGCANACCT	6360
	CCCGCTTTGG	CTTAGCTAGC	GTGACATTGG	CTATCAATTT	ACAAGACTAA	CTTTTTTTTT	6420
	TTTTTTTTTG	ACTGAGTCTC	CCTCTGTTCAC	CTAGGCTGGA	GTGCACTGGC	ACAATCTTGG	6480
45	CTCGCTGCAA	CCCTTACCCCT	TCACCTCCCA	GGTGGAAAGG	ATTCTCTCTC	CTCAGCTCCC	6540
	CGAGTAGCTG	NCATCTAGAG	GGTGGCCAC	CAAACTCTGG	TATTTTTTTA	TTATATTATT	6600
	TTTTAGTAGA	GATGGGGTTT	CACCATGTTG	GCCAGACTGG	TCTTGAATCT	TTGGCCTCAA	6660
	ATTATCTGCC	CACCTCGGCC	TCCCAAGGTG	CTGGGATTAC	AGGCATGAGC	ACCATGCCCA	6720
	GCTGACAGA	CTAATTTTTT	ATCCCTTGGT	TTATTGGCTT	CAACATCTTC	TGGAAATCAGA	6780
50	GGTGATTTTT	TCTTACCTTG	GATGCCTGAG	ACTAGGGGAG	TATAGAATTC	CAATTTGGTA	6840
	TTAAGGCATC	TTCTCTGCTC	TGATCAGAAG	GGCAGGTTAG	TTGGGAGAGG	TCAGATGGCA	6900
	CAACAGAAAT	CACCTGTGTA	GTAAGGCAAA	GACTTTGAAG	GCATTAGCGT	TTCTCATTTAC	6960
	TTAGTCAAT	AACCTTGAGG	GAATCAATGG	CTTTTTTGCC	GCTCTAOCCT	TTTGTGTATC	7020
	TCCTTGACTT	TTCTTCTCT	GTCTAGTTTC	CTCTGTCTCT	AGTTTATATT	CTATGTTATC	7080
55	AGTCTCTCTT	TCCACAGTAC	AAACATCCAT	CCTTTCTCCT	GTGCAATCT	GTCTCTCCCT	7140
	CTTATTATCT	TTTTTCTCTC	CTCCCTGTCT	AGGCATTGGG	CATGTGCCCT	CATGTGCCCT	7200
	TTCTTAGCCT	GTGATTTTGC	CTTGGGACTG	ATGATAAATT	ATTCCAGAT	TCAAATCAGCC	7260
	CTGCTCCTAC	CCCAAGTCAA	TCAGAAGTAT	GTGTTGGGG	AATCAACCTG	ATCCTGGCCC	7320
	TTCTCTCTTC	TCCATTTTCA	TTGGTAATCC	CCCTCAGCAG	ATCTTTACAA	GCAGTTTCCCT	7380
60	TATAGCTCAT	GTATCTTTAG	GTCTTTGCCT	TCCAAGCACT	GTACAGATAA	CTTTGTGGTT	7440
	CCTTTTTAGT	CTGACATTTT	GTGGAGCAGT	GAAGCGTGCT	CAGAGACATA	ATCAGCTGAA	7500
	GAGAAAAAAT	CCACCCATGG	ATTTATATCA	GCTAAATACT	AATAATTGAT	TTTGTTTGAT	7560
	GTGCCCATAA	TTTTTAAAGC	TGCAATATAA	TATAATGAGG	GACCACAGGT	AATTTCTCCT	7620
	GTCAATTGTT	TGGCTGGAT	GGGGGTGGGG	GAGTAATTGC	TTAAAGTTTT	ACCATTACAC	7680
65	ATTAAACTCT	CTATAATAAT	CTTGTGTTGG	GCTTGCTAAC	TGTTGAGCTG	TTTTAACTAA	7740
	ACTGTTAGGC	AATCGAGTTT	GATTTAAATG	AAAAGATAAT	TTAACAAATC	TATACTATAA	7800
	AAAGAGACAT	TGCTTAATTT	GACATGTATT	TTTTCTTCT	GAGTCACTTA	AACATTTACT	7860
	CTTGACACCA	ACTGTTCAAT	ATACTGAATA	GACAGTCCAT	ATAAGAGAAA	TTAGTGGACC	7920
	TAAAGAAGCC	AGATTGTAGG	TGTTAATTTA	TTAAACAGAA	TTGCAAGGCC	CTTGGAAATG	7980
70	TCACTGCTTG	GCAATACCAT	ATGGCATGCC	AAAAATTTACA	ATGACTTTTC	TTTATAAGTT	8040
	ATCCAAAGG	GATTTGAACA	AGTAAGAGGT	TATGCCAAAA	TGCTCCCAAT	GTATGGTCCCT	8100
	GTAATATATT	CGAGCTTGAA	GCCATGATC	CCTTATGACT	TGTATACAC	TAATGCATGT	8160
	TTTATTGAAT	TTTGCAATTC	CCAGTGTGG	TAACTCTTTA	AAATGTTTTT	GATCACCTTT	8220
	MTGTGCCATT	AAACTTGTAT	AGAAAAATGTT	TTTATGGCCA	TTTTCAAGG	GAGAAAGTTT	8280
75	AAAAAGGAAA	CAGCCCAACC	TTTCTGCCCT	ATAGCTGTAG	TTAGAATTGA	GTACCTGTAG	8340
	CAAAACAGCT	GTAATTGGTG	GTTGTAGTGT	TAGAGGTGTT	AGCTTGCTAG	TGACTAGCTT	8400
	TGGAGAGTAA	ATGCATGGTA	TGTACATCA	CATTTCTTAA	CTCGTTTTAA	CCTCTGAAAA	8460
	GAATATATTC	TCTTTGTAG	TCCTTCTTCC	CACCCCCCTG	CCCTCTCCCT	CTCCCTGCTC	8520
	CCAGTTGTCT	TACAGTTGTA	AATATCTGAT	TTGAGGCCCA	ATAACTCTTG	CCAAGTAAAG	8580
80	TCAGCAACCA	ACAAACAAAC	CAAAATGTGG	GGAAAAAGCA	TTTCTCAACC	ATCTCTCAGC	8640
	AGTTATTGAT	CATTTCTTAA	GGAAACGACAT	TGTGATCAAA	GACTCAACTT	TACGTAAAAA	8700
	TCAGTGGTAA	ATTGGGGTTG	TATTGGCCAT	TGATTACATT	CAGGATTGAA	TAGTTTTTCA	8760
	AATCAGATGT	AATCCAAAGA	CAGTAGGTTAG	TGATGTCCCT	TATCCCTGCA	GCTGTTTTAA	8820
	GATAGAGACT	CTGCTTGACC	GATGACCAAT	AATTATTGTA	AAAAAAGAGA	AAAAAAGAGA	8880
	AAAAATGAGA	GAATTAACAT	AGATATTATA	GAACCTTAGC	CACCTATTTA	GAATAGTTAT	8940
85	AGCCAGAAAA	AAACCAAGG	GCAATGAGTT	AAATGCATTA	CTATCAGTGT	CCTAGGCAAT	9000
	ACCTAACCTA	CTCTGAAAT	GTGATTCAAA	AGCAGTATTT	CAAGAGGCAT	TCTCCTTTTT	9060
	TGGTTTGCTG	ACCCCACTTG	GACTGGTAGG	TTTGGTGAGG	CCCCCATAAA	CCAGCTGGAG	9120

CAGACCCCTT TCATCTCCTG TGCTGTAAAC ACCCCTCTTC CCCCACCCCC TCCGCAATTC 9180
 AATGAGGGCT TCTTGGGTC AGAGGACTTC AAGGTTGTCT AGAGAAGTTT GCCATGTGTG 9240
 TAAGTGCTG TGAAGCTGTGA GTGCTGAAGA TCGCAGCAT TCAATACCAG GCAGCCAAAG 9300
 AGCTGCTCTT GCAATTATTT TGGCTCTCAA GCTCTGTCTT TCATCGCATT CTCATTCTG 9360
 TGTACATTTG CAAGATGTGT GTAATGTCAT TTTCCAAAA TAAATTGTA TTTCAAT

Seq ID NO: 214 Protein sequence:
 Protein Accession #: NP_000546

1 11 21 31 41 51
 MELDPGHFDE RDKTSRMRG SRMGLPSPT HSAHCSFYRT RTLQALSNEK KAKKVRFYRN 60
 GDRYPKGIYV AVSSDRFRSF DALLADLTRS LSDNINLPQG VRYIYIDGS RKIGSMDELE 120
 EGESYVCSSD NFFPKVEYTK NVNPNWSVNV KTSANMKAPQ SLASSNSAQA RENKDFVRPK 180
 LVTTIRSGVK PRKAVRVLLN KTAHSFEQV LTDITEAIKL ETGVVKLYT LDGKQVTCLE 240
 DFFGDDVPI ACQPEKFRYA QDDPSLDENE CRVMKGNPSA TAGPKASPTP QKTSKSPGP 300
 MRRSKSPADS ANGTSSQSL TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DSDSLGDSM

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_130467
 Coding sequence: 312..644

1 11 21 31 41 51
 GGCACGAGGC AGAGCTCTGC AAGGAGAGGT TGTGCTCTCG TTTCTTCCGC CATCTTGGTT 60
 CTTTCCAACA TCTTCGTTCT TCTCTACTGA CCGAGACTCA GCGGTAGGT CTGCAGAGTG 120
 GTCTTCTCGG TAATTTAGTT GTGAGTGAAT GTGTGGAGGA GCCAGCGGGC TTAGGACAGG 180
 TCTTGTGGCA CAGTCCGTGG CTTTGAGGGA AAAGGGCCTC GCGGTGGTCC TCGCCTTCC 240
 CCCAGGTCTG GATGACAGCG CCATGGGCGG GTAATCGTGG CTGGCTGGA ACGAGGGAGG 300
 AAGTGAGAGA TATGAGTGAG CATGTAACAA GATCCCAATC CTCAGAAAGA GGAATGACC 360
 AAGATCTCTC CCAGCCAGTT GGACCTGTGA TTGTCCAGCA GCCACTGAG GAAAAACGTC 420
 AAGAAGAGGA ACCACCAACT GATAATCAGG GTATTGCACC TAGTGGGAG ATCAAAAATG 480
 AAGGAGCACC TGCTGTTCAA GGGACTGATG TGGAGAGCTT TCAACAGGAA CTGGCTCTGC 540
 TTAAGATAGA GGATGCACCT GGAGATGGTC CTGATGTCAG GGAGGGGACT CTGCCACTT 600
 TTGATCCAC TAAAGTCTG GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA 660
 ATGAAGACTG AAACCAAGAA TATGTCTCT ATGCTGGAAA TTGACTGCT AACATTCTCT 720
 TAATAAAGTT TTACAGTTTT CTGCAAAAAA AAAAAAAAAA AAA

Seq ID NO: 216 Protein sequence:
 Protein Accession #: NP_569734

1 11 21 31 41 51
 MSEHVTRSQS SERGNDQESS QPVGFEVIVQ PTEKQRQEEB PPTDNQGIAP SGEIKNEGAP 60
 AVQGTDEEAF QQELALLKIE DAPGDGPDVR EGTLPFTDPT KVLEAGBGQL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: NM_001476.1
 Coding sequence: 82..435

1 11 21 31 41 51
 GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCTGCGGT CCGACTCTT TTTCTCTAC 60
 TGAGATTTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACTATTA TTGGCTTAGA 120
 CCAAGCGCT ATGTACAGCC TCTGAAAGTG ATTGGGCTTA TGCGCCCGA GCAGTTCACT 180
 GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACCA CAACTCAACG TCAGGATCCT 240
 GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
 GCTGATAGCC AGGAACAGG TCAACCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGAT 360
 GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAA CGCTGAAGA AGGTGAAAAG 420
 CAATCACAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCTTA TGTGGAAAT 480
 TTGTCAATTA AAATCTCTCC AATAAAGCTT TACAGCCTTC TGCAAAA

Seq ID NO: 218 Protein sequence:
 Protein Accession #: NP_001467.1

1 11 21 31 41 51
 MSWRGRSTYY WPRPRRYVOP PEVIGPMRPE QPSDEVEPAT PEEGEPATQR QDPAAAQEGE 60
 DEGASAGQGP KPEADSQEQG HPQTGCECED GPDQGEVDPP NPEEVKTPPE GEKQSQC

Seq ID NO: 219 DNA sequence
 Nucleic Acid Accession #: NM_001476
 Coding sequence: 90..3671

1 11 21 31 41 51
 ACAGGGAGC GCAGAGTGAG AACCAACAAC CGAGGCGCGG GGCAGGAGCC CCTGCAGCGG 60
 AGACAGAGAC TGAGCGGCCC GGCACGCCCA TGCGTGCCT CTGGCTGGGC TGCTGCTCT 120
 GCTTCTGCTC CTTCTGCCCC GCAGCCCGGG CCACTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAAATGGAT 240
 TCGCTGCTCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGAGAGAAG TGCAAGAATG 300
 GCTTTTACCG GCACAGAGAA AGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT 360

	CTCTTAGTGC	TCGATGTGAC	AACTCTGGAC	GGTGACGCTG	TAAACAGGCT	GTGACAGGAG	420
	CCAGATGGGA	CCGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAG	480
	ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCCGTG	540
5	ACGCGGGCCG	CTGTGTCTGC	AAGCCAGCTG	TACTGAGAGA	ACGCTGTGAT	AGGTGTGAT	600
	CAGGTTACTA	TAATCTGGAT	GGGGGGAACC	CTGAGGGCTG	TACCCAGTGT	TTCTGCTATG	660
	GGCATTACGC	CAGCTGCCGC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
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	TCACCAAGAC	TTACACATTG	AGGTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTACTGCG	GGAACTCTAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCCCCTG	1200
15	TTCTTGGAGC	CCAGACACCC	TGGGTGAAC	AGTGTATATG	TCCTGTGGGG	TACAAGGGGC	1260
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	GTTATTTCAG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCCGCA	CGACCCCCGC	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTGAGCTGCT	1500
20	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCGGGTG	1560
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	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAGG	AGTTCCGGCT	CTGGGAAGTC	2220
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	CACACTTCAG	CTGGGTGACA	TCCATCCCTC	CAITTCATCT	TCCATCCATC	TTTCCATCCA	4680
	TTACCTCCAT	CCATCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
75	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCAATTTTA	AAAAATAAAT	TTAAACTTAC	AAACTTTGTT	TGTCACAACT	GGTGTATTAT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTG	CTCAACAGAA	CATATGTTGC	AAGACCCCTCC	4920
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Seq ID NO: 220 Protein sequence:
Protein Accession #:NP_005553

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WO 02/086443

PCT/US02/12476

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	HMLTDAGCTQ	DQRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYINLDGGN	180
5	PEGCTQCFCY	GHSASCRSSA	EYSVEKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRLLDPVY	FVAPAKPLGN	QOVSYGQSL	FDYRVDRGGR	HPSAHVDVLE	GAGLRITAPL	300
	MPLGKTLPCG	LTKTTFRLN	EHPSNNWSPO	LSYFERYRL	RNLTLRIRA	TYGEYSTGYI	360
	DNVTILISAR	VSGAPAPWVE	QCICPVGYKG	QPCQDCASGY	KRDSARLOPF	GTICPCNCG	420
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10	CNCPGPGVTG	ARCELADGY	FDPGGEHGP	VRPCQPCQN	NNVPSASGN	CORLTGRCLK	540
	CIHNTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCPHGS	EPVGRSDGT	CVCKPGFGSP	600
	NCEHGAFSCP	ACYNQVKIQM	DQPMQQLQRM	EALISKAQGG	DGVVFDTELE	GRMQQAEQAL	660
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	ADRSYQSLR	LLDSVSRLOQ	VSDQSPQVEE	AKRIKQKADS	LSTLVTRMD	EFKRTQKNLG	900
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	QVDNRKAEAE	EAMKRLSYIS	QRVSDASDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
	IEQBIGSLNL	EANVTADGAL	AMEKGLASLK	SEMRVEGEL	ERKELEPDIN	MDAVQMVITE	1080
20	AQKVDTRAKN	AGVTIQDTLN	TLDGLLHLM	QPLSVDEBGL	VLEQLKSLRA	KTQINSQLRP	1140
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Seq ID NO: 221 DNA sequence
Nucleic Acid Accession #: NM_016529
Coding sequence: 13-1854

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	GCTGATCTCT	CTGAGAAATGA	GTATGAGGAG	TGGCTGAAAG	TCTATCAGGA	AGCCAGCACC	240
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	GCGCTCTCT	TGGAAGTCCG	GAGGAGTTTC	CTGGATTGG	CACCTCTCTG	CAAAGCGGTC	660
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	GCCCAAGTGG	GTGTGGGAAT	CAGTGGGAAT	GAAGGCATGC	AGGCCACCAA	CAACTCGGAT	840
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	TACAACCGGG	TGACCAAGTG	CATCTTGTAC	TGCTTCTATA	AGAAAGTGGT	CCTGTATATT	960
45	ATTGAGCTTT	GTTTGCCTTT	TGTTAATGGA	TTTTCTGGGC	AGATTTTATT	TGAAGCTTGG	1020
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Seq ID NO: 222 Protein sequence:
Protein Accession #: NP_057613

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	KAEIKIWLVT	GDKQETAINI	GYSCLRVSON	MALILLKEDS	LDATRAAITQ	HCTDLGNLLG	180
75	KENDVALIID	GHTLKYALSF	EVRRSFLDLA	LSCKAVICCR	VSPLQKSEIV	DVVKKRVKAI	240
	TLAIGDGAND	VGMQTAHV	VGISGNBGMQ	ATNNSDYAIA	QFSYLEKILL	VHGAWSYNRV	300
	TKCILYCFYK	NVVLIIELW	PAFVNGFSGQ	ILFERWCIGL	YNVIFTALPP	FTLGIFERS	360
	TQESMLRFPQ	LYKITONGEG	FNTKVFNGHC	INALVHSLIL	FWFPMKALEH	DTVFDSGHAT	420
	DYLPVGNIVY	TVVVVTVCLK	AGLETTAWTK	PSHLAVWGS	LTWLVFFGIY	STIWPITPIA	480
80	PDMRGQATMV	LSSAHFWLGL	FLVPTACILIE	DVANRAARHT	CKKTILLEEVQ	ELETCSRVLG	540
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Seq ID NO: 223 DNA sequence
Nucleic Acid Accession #: BC017001
Coding sequence: 1-394

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Protein Accession #: AAH17001.1

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55 Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: NM_021048
Coding sequence: 1..1110

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Seq ID NO: 226 Protein sequence:
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1 11 21 31 41 51
| | | | |
MPAPKQRQC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFP SPSSSSSSSS 60

```

5 SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDBGSS SQKEESPSTL 120
 QVLPDSESLP RSRIDERKVD LVQFLLFKYQ MKEPITKAEI LBSVIKNYED HFPLLPSEAS 180
 ECLMLVFGID VKRVDPTGHS FVLVTSLGLT YDGMLSDVQS MPKTGILILI LSIIFIEGYC 240
 TPSEVIWEAL NMGLYDGMH HLIYGEPRKL LTQDWNQENY LEYRQVPGSD PARYEFLWGP 300
 RAHAERKMS LLKFLAKVNG SDPRSFLWY BEALKDEER AQDRIATDD TTMASASSS 360
 ATGSFSTPE

10 Seq ID NO: 227 DNA sequence
 Nucleic Acid Accession #: NM_005025.1
 Coding sequence: 82-1314

1 11 21 31 41 51
 15 GCGGAGCACA GTCGCGCAG CACAAGCTCC AGCATCCCGT CAGGGGTTGC AGGTGTGTGG 60
 GAGGCTTGAA ACTGTTACAA TATGGCTTTC CTGGACTCTT TCTCTTTGCT GGTCTCTGCA 120
 AGTATGGCTA CAGGGGCCAC TTTCCTTGAG GAAGCCATTG CTGACTTGTC AGTGAATATG 180
 TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAATATATC TCTTCTCTCC ATTGAGTATT 240
 GCTCTTGCAA TGGGAATGAT GGAACCTGGG GCGCAAGGAT CTACCCAGAA AGAATCCGCG 300
 CACTCAATGG GATATGACAG CCTAAAAAAT GGTGAAGAAT TTTCTTTCTT GAAGGAGTTT 360
 20 TCAACATGCG TAACGTCTAA AGAGAGCCAA TATGTGATGA AAATGCGCAA TTCCTTGTGT 420
 GTGCAGAAATG GATTTCATGT CAATGAGGAG TTTTTCAGAA TGATGAAAAA ATATTTTAAT 480
 GCAGCAGTAA ATCATGTGGA CTTCAGTCAA AATGTAGCGG TGGCCAACTA CATCAATAAG 540
 TGGGTGGAGA ATACACAAA CAATCTGGTG AAAGATTGGG TATCCCAAGG GGAATTTGAT 600
 GCTGCCACTT ATCTGGCCCT CATTAATGCT GTCTATTTC AAGGGAACCTG GAAGTCGCGAG 660
 25 TTTAGGCCTG AAAATACTAG AACCTTTTCT TTCCTAAAG ATGATGAAAG TGAAGTCCAA 720
 ATTCCAATGA TGATCAGCA AGGAGAAATTT TATTATGGGG AATTAGTGA TGGCTCCAAT 780
 GAAGCTGGTG GTATCTACCA AGTCTAGAAA ATACCATATG AAGGAGATGA AATAAGCAAT 840
 ATGCTGGTGC TGTCCAGACA GGAAGTTCTT CTGTCTACTC TGGAGCCATT AGTCAAGCA 900
 CAGCTGGTGG AAGAATGGGC AAACCTCTGTG AAGAAGCAAA AAGTAGAAGT ATACCTGCCC 960
 30 AGGTTCACAG TGGAACAGGA AATTGATTTA AAAGATGTTT TGAAGGCTCT TGAATAAAT 1020
 GAAATTTTCA TCAAGATGCG AAATTTGACA GGCCCTCTCTG ATAATAAGGA GATTTTCTT 1080
 TCCAAAGCAA TTCACAGTGC CTCTCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT 1140
 GTCTCAGGAA TGAATGCAAT TAGTAGGATG GCTGTGCTGT ATCCTCAAGT TATTGTGAC 1200
 35 CATCCATTTT TCTTTCTTAT CAGAAAAGG AGAAGTGGTA CAATCTTATT CATGGGACGA 1260
 GTCATGCATC CTGAACAATG GAACACAAGT GGACATGATT TCGAAGAACT TTAAGTTACT 1320
 TTATTTGAAT AACAGGAAA ACAGTAACTA AGCATTAT GTTTGCAACT GGTATATATT 1380
 TAGGATTGTT GTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAAC 1440
 AATATATGTA AATTATAAGT AACTTGTCAA GGAATGTTAT CAGTATTAAG CTAATGGTCC 1500
 40 TGTATATGTA TTGTGTTGT GTGCTGTTGT TAAAAATAA AGTACCTATT GAACATGTG

Seq ID NO: 228 Protein sequence:
 Protein Accession #: NP_005016.1

45 1 11 21 31 41 51
 MAPLGLFSL VLSMATGAT PPEEAIADLS VNMYNRLRAT GEDENILFSP LSIALAMGMM 60
 ELGAQSGTQK EIRHSMGYDS LKNGEEFSFL KEFSNMVTAK ESQYVMKIAN SLFVONGFHV 120
 NEBFLQMKK YFNAAVNHVD FSNVAVANY INKWNENNTN NLVKDLVSPR DFDAATYLAL 180
 50 INAVYFKGNW KSQFRPENTR TFSFTKDDDES EVQIPMMYQQ GEFFYYGEFSD GSNEAGGIYQ 240
 VLEIPVEGDE ISMMLVLSRQ EVPLATLEPL VKAQLVEEWA NSVKKQKVEV YLPRTVEQE 300
 IDLKVLLKAL GITEIFIKDA NLTLGLSDNKE IFLSKAIHKS FLEVNEEGSE AAASVGMIAI 360
 SRMAVLVPQV IVDHPFFPLI RNRRTGTILP MGRVMHPETM NTSCHDFEEL

55 Seq ID NO: 229 DNA sequence
 Nucleic Acid Accession #: NM_003695
 Coding sequence: 12-398

1 11 21 31 41 51
 60 CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGCCAGC CCTGGCTGTG GCTACAGGGC 60
 CAGCCCTTAC CCTGCGCTGC CAGTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG 120
 TCTGCGCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGAGCCCT CTGAGGGGGA 180
 ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCCTG CAAGGCCAGG 240
 TCAGCAGCGG CACGAGCTCC ACCCAGTGTG GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
 65 ACAACGCTGC ACCACCCGCG ACCGCTCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
 TGAGCCTCCT GCGCTCATC TTAGCCCCCA GCGTGTGACC TTCCCCCAG GGAAGGCCCC 420
 TCAATGCCCTT CTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGCAACCG 480
 GGGTGCCAGG AGCCCCAGCG TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
 70 CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
 ACAGAGGATG CAGCCCCAGG CTGCATGGA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
 GATTTCACAC TCCTCTGTT TTGTTGCCGT TTATTTTGTA CTCAAATCTC TACATGGAGA 720
 TAAATGATT AAAC

75 Seq ID NO: 230 Protein sequence:
 Protein Accession #: NP_003686

1 11 21 31 41 51
 80 MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCFA SSRFCCTTNT VEPLRGNLVK 60
 KDCAESCTPS YTLQGVSSG TSSTQCCQED LCKEKLHNA PRTALAHSA LSLGLALSLL 120
 AVILAPSL

85 Seq ID NO: 231 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 126-752

	1	11	21	31	41	51	
5	COGGGCGAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCCTGGAGC	60
	AGGGGCGCAG	GAATTCCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
	AGAAGATGAA	GGAATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCCAGC	ACTTCTGGGA	CGCACAGAGA	CGGTGAAGAT	TCCAAGTTCA	240
	GGAGAAGTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCTCTCTTGA	TGCCCTCCATG	CATTCTCAGC	TCAGAAATCCT	GGATGAGGAG	CATCCCAAGG	360
10	GAAAGTACCA	CATGGCTTGT	AGTGTCTCTG	AGCCCATCCG	GACTACTTCC	AAACACCCAGC	420
	ACCCAGTGGG	CAATGTCTGG	CTTTTTCCT	GTATGACTTT	TTGGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTGTGTG	GATCTTCTGC	CGCACCAGGC	660
15	TCATCCTGTC	CATGCTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAATT	720
	TTCAGGATGG	CTGTATTTCTG	CGGTCAGAAT	GAGAGAGTCA	AGCTGGGCAG	AATCTCTCGC	780
	CAAGAGTTCA	GCCTTCCTTT	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
	TTCAGTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACTGTAGG	AAAAGGGGGC	TTTGGCCCTG	900
	TGACTCAGTT	CCCAATTTTG	GATTGCATAC	TGGAAGAAAG	GCCCAATCTT	TTGCTAGTAA	960
20	ACCAGCAACC	CAGCTGTATA	CAGTGGTGAC	CCAAGCAATG	GATATAAAC	TAAAAATCTG	1020
	AGGGAGGGGA	GAGGTGGNAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGAATCAGG	1080
	TTATTTCTCTG	GGACTTGGCA	AAAACTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
	TCTGGTATTA	ATTTAATCTC	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
	GGAAATTCAG	GTAGCTACCT	CCAGACCGTG	GTGTCTGGCC	TCCATTTTGT	TCTGTCTATC	1260
25	AGCTCTGACT	TACAGCTGCA	GTCACTTTTG	CTATAAGGCA	CTTGGGTAGA	AGGGTGGATG	1320
	GGCTTCACAT	CAATTTTTTT	CTTCTTTTAG	GGTGGGGGAT	TGGTTTGGCT	TTCTTTTGT	1380
	GTGGTTTTTT	TTTTTATTTT	TGTCAAGATT	GATTTTTAGA	TGCAAGGACT	TGAAAAGACC	1440
	CAGAAGGATG	CCACAGTTT	TTCTTGAGG	CCTAGGATTT	TTTATCTGT	CCGAGCAGA	1500
	GGTAATTCCT	CACAACTTAG	TGCACCACTA	GCACCAAGCA	TTTTGAGCAG	AGTAACTCTT	1560
30	TGGGGAGCTT	TGCTTTTGT	TTTGTTTT	ATTCTCTTTC	CTTAGCAGCA	AGSTCTTTTT	1620
	TCCTAGAGAA	TCTACTCGT	TGCAGAACTA	TTGCAACCTC	AGGAGCCCTC	ACTGATTTAG	1680
	TGCTGTGAGC	CTGATATACT	ACTTTGGACT	CTGGAACAG	ATATGGGTTC	TATTCTCTAT	1740
	TTCTACTGTG	TGTGTTTAA	CAACCGTCGG	AGACCAAGATG	ACCTGTTAGA	TGGCTAGTCC	1800
	TGTATAACTC	GACTCTGTAT	GTTTCAATGT	ATGTTACTGC	AATGCTTCAC	CTGCTGTACA	1860
35	GTGTTTGTGA	GATGCTCTTT	GAAGATGGTA	CTTTTATATT	T		

Seq ID NO: 232 Protein sequence:

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MRDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
	LDASMSHSQLR	ILDEEHFKPK	YHGLSALKP	IRTTSKHQHP	VDNAGLPSCM	TFWSLSSLAR	120
	VAHKKGEGLSM	EDVNSLSKHE	SSDVNCRRL	RLWQEELENEV	GPDAASLRV	VWIFCRTRLI	180
45	LSIVCLMITQ	LAPSPGPNPQ	DGCILRSE				

Seq ID NO: 233 DNA sequence

Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
50	TTTTAATGGT	GCTCATATAT	ACTGTATTTT	TTGTGTTTTA	GTTTTACTTA	TTGAGAGTGT	60
	CACAACATGA	ATCACATAAT	CATGATTTTT	TTTTTTTACT	TTTACTCCCC	AAATTAITCA	120
	TGTTTCTTAG	ATCGTAGTCA	TTGAGAAATC	CCAATAACTC	TAAACTTTTG	AGTTATAACG	180
	TAGTAAACTT	CTCTTTCATC	TTTGTGTTAG	CTCTGTAGTC	TTAACCTGGA	TTTTAATTTT	240
55	TTTGTTTCCA	AAGTCACAA	TGAATTTATC	TTAGATACTT	TAAAGCACTG	AATTCAGTTC	300
	TGTTTGACTG	AAAGCAAAAC	AACGTGACAG	TTTATTTTCA	AACACTAACT	TCTGTATATT	360
	TTGTATAGGT	ATATCTTTT	ATTAAATATT	TATTTTGACT	AAGCTTTTCA	AAAATATTG	420
	AAGCTATTTT	AATCATCAAG	TATGGAAGAC	AAATTAATAT	TGCATTTTCC	TATATATGCA	480
60	TATATTATGG	ATTAAACAGA	ATTGTATCAT	TTTTGGCCTA	ATGCTCTGGAT	ATAAAAGATA	540
	ATTAGCTTAC	TATAGTATTA	ATAAATTTT	CAGTTGGTTT	GGGCAAAATT	AAACCTGAAA	600
	AATAGGTTAA	AAAGTAGTTA	CAAAATTAAC	TTACTAATTT	ATACCTGATT	TTTTTTCTTG	660
	AATTAAGTA	CATTTTAAAT	GAGCTTTATA	ATACCTTAAA	AAGTTGGTTC	TAAATTAATA	720
	TATGAAGCT	CTGGCTATCA	TCCTGGGATA	GTAATTTCTA	ATTATATAGT	ATTTCAAAAC	780
	TATATATTTT	TTAGTTCCTT	TGAGATAACT	AATTTCTAAT	TATATATGTT	TCAAAAACCA	840
65	TATCCGTGAT	TTTTTTTAAG	AATTGTTTTA	TAAATAGTTC	ATAAGATACA	AGGTCTGCAT	900
	TAGAAGACCC	ACTCTTACTA	GGTCCCTTAA	GGATCTGCCA	TAGATTTTTT	TTTTTTTTTT	960
	TTTTTTTTTG	GTAGTTTAAA	GCAAGCACTG	ATACCAAGTG	GAGTTGGTCT	TGATCTAGGA	1020
	GATTCTGTTA	AGCATCCAAA	AACAATGCCT	AATTTCAAGT	CTTAGGTTAT	GGCTGTGAC	1080
	TCCAGATAAA	AGATGGAGAA	TACCTCATGT	ACTGTGACTT	GAAAATGAAT	TCTTAAAAAT	1140
70	CTTAGGCTCT	CTCCATGTAT	CTTCTTAAG	GAAAAGTTTC	TGAGTGTGAT	CTCTCTTTTG	1200
	CCATAGTATC	AAGTGGAGGG	TAGTTCAGAA	AAGTTAATAG	GAAATCTTTT	GTGACAGCAG	1260
	ACTATAATAG	AAGTTTGAGT	AATATTTTAA	TAAATTTATA	TAAATCAAA	GATAAAAAATG	1320
	TATCAATGTT	ATCCAATGAT	TTTTATTTAA	AAATTACCTT	ATTATTAGAA	CTGTGCCTAT	1380
	TACATAAAAA	GTGCTCATGT	ATTTGAATTT	TAAATAATTT	ATTTAAATCA	AGACCACCAT	1440
75	AAGTCATTAA	TAAATTTAATA	ATTGTTTTAA	ATCAGTGGTT	TTCAACCCCTC	ACTTCATATT	1500
	AGAATCATCT	GAGGACTTTT	AATATGGAAT	CCACCTCATA	ACAATTAAGT	CTAAATTTCT	1560
	GGAAGATGGA	GCCATGCTTG	TTTTTCCAAA	AGCTCTTTGA	GTGATTTCAA	TTTGTAGTCA	1620
	GAGTTGAAGA	CCACTGCTCT	AAATTAGTGC	AGGAAAAATG	TTTTATTCTT	CCCATGTTAA	1680
	CTTTTAAATC	TAGTAATGTA	CCCAGTTAAG	TTTTGTAGGT	TTAAATTTCA	CTAAAGAAAC	1740
80	TATTTCTTCA	ATAACTAGCA	TTTATTACAT	GAAATTTAAG	AGTTTAAAGT	CCATCAAACT	1800
	AGCCCTTGTG	TAGGATTAAT	ATTCTTCTC	TATAACTTCA	AAATAGATAT	TTCAATCAAA	1860
	CTGTTCAGGT	GAGAAAAACAT	AATGGATTTT	TTTTTTTTTC	CTCTGGAGCT	GCCTGTTCAG	1920
	TGAGATGGAG	GAGGTGGGCA	CATTTAAGGT	CAGTTCACCT	ACCTATGSGT	CAGAGTTCCTG	1980
	ATCATATGGA	AGTTTGGAAA	AGAGAGCTTA	TCACAGGTTT	GTATGCTGGT	GAATGGATAG	2040
85	TTTTTAATTC	CAGTCTCTCA	AAAGAGAATC	AGCTCTCCAG	CAGTTCTAGA	AAAGCTTTGA	2100
	CAATCCCCAA	GGGGCAGTGT	TACCTTACTC	CTTCACTGCT	TCTTAGAAGG	TAGAATTAAG	2160
	TTTCTGGAAT	TGCACCTACA	TGTTTTCTTA	TAAACATCCA	GAATGGGAA	TATTAATTTT	2220

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TCCAGTGGT AGTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCCTTT 2280
 CAATTTTGTG TTGTGTTACT TTTATGTAAA AATTGTATAT GTGAATTACA CAGTCTTAAT 2340
 AAAACCTCAT GCTTTTTCAT TACATCTAAT TTGAACCTCTC AACTTCAGTG CCAGAAAGTGC 2400
 TTTAAAGATG CTTTAATGAA AAGTATTAAG AAAATATATA GATTGTATG TCAGTTTATA 2460
 CTTAGAAAT CCATATATTT GTCATATTTA TTTTGTTAGA AACCTCCTAA TTGGATAACT 2520
 AGATGGTATT TAAATGAAT GCCCAAAAAT ATCTGTATCC TTTGTCCAAA AGTTTATCTG 2580
 TTGGAAGCCG CCAGCCATTG ATGTAGAGAG TTTATAAGAA AATAATTAA AATTGTATGC 2640
 ATTTTATATT ACTATGGTAT CTGTGTACCA TATTCTAAG TATTCAATTAT TAAATTGGTA 2700
 CTTCTTAAAA CCATAACCTG GCTTGCTTTT TAGTGTAAA CACAAAATCC AACATTGTAT 2760
 ATAGAGATTG TTTCTTTATG AAGAAGAGCT GAGTAATTT ATTACCACTG CATCTGCACA 2820
 AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAAACA 2880
 CCACATTTAA CAACCAAGCG AACACTCAGA CTTGGCACTT TCCTACGAAT CCATCTTATA 2940
 TGTGCTGGT ATGCGCTCTG GCATAACTTA CACGAATCGT CCTCCCTACT TGTCTACGCT 3000
 CCTTCATCAA GCCTTGCCA ACACATTCAC CTCTAACTTG TACAACCTTA CCAACTCACC 3060
 ACAACATCTG CAACCTTACC CTATCACTG CCAACCTAAA GACCCCAAC ACAACACAAC 3120
 CCCCACACAC AAAACCACTA AATCATAACC ACCACACACG CCACACACCA CACACCCACC 3180
 CACACACCA CACACCCAG ACCAACACCC CCACCAAAA CAAGCTAACA ACCACAAAAC 3240
 GACAACACAT CACATACACT CACTACCCCC CCATACTCCC ACCACCA

Seq ID NO: 234 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 27-281

1 11 21 31 41 51
 AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCGSTCT 60
 GTCACCCGCG TAGCAGTTAC ATCAGACTGA GACACTTCT GTTTACAGGA GACTATAAAA 120
 TTCTGCCCCG GTGCTCAITT GGGGCTGACG CCATTTTAGG CCTCAGCCCA TCTGCACCCA 180
 GGGCTCTACT GAAACAGTGT GTTGCTCCAC ACCGCTTGT TTTGCTTGT GGGCGGCTCT 240
 CAGGGTTCOG ACCAATCCAA GAGCCTTGCA GAAAGCAITA ACGTGCTTT CTCTTTGGCA 300
 GAGTTTTTCT TTGCTCTGAT CTTGGAGACA TCCCTCTGCC TAGTGGAAAC ATAAGGAATA 360
 CAGAAAGAAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCTATGCACT CAAGAGAAAG 420
 ATGTTGCAGG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCACG 480
 TTTTCTCTC CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAACA GGAATGTTT 540
 ATAAAACTG TTCAGCGGTT CGCCAAACAG AAGTGGTAAA GTAGCAAAA TGGGGATGGA 600
 GATGCCAGGA GGAAAGATGC CAGGGSTAAA GTGGGAAAT GGGAACTGA AGCCAGGAGG 660
 TCAAGCCAA GCAACAGGTG TTTCTTTTT CATCACAGAA CTAAATAGTG GTGCTGAGGA 720
 CTCAAACCCG GGAAGCCCA CTCTAGAAC CATGCTGGTC ATCCATATCC CCAAGGCCCT 780
 GGTGAGAACA CAGCTAAGCA GATGGCTTGC GTCATCAGGA CGTCCATTAC ATCCAAAGGA 840
 AGACAGCTG TGACGTTTCA AAAGCAAAAG TCCCTTACCA GCCAGTGAAG CTACCTGATT 900
 TCTCAGTATC TTACGCCAG TGACACGATC TACCCTCAA ACTTAAAAA AAAAGGGAAA 960
 CATAAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAA TAAGAAAAA 1020
 GGAAAGGCTC CCGTGACTG TTTTATTTT AGGGAACAG AGAGGAAGAA GAATGATTTT 1080
 TCTTTGATG ACTCTATATC CAACTCTGAG GTTTGATTAA AGAAATGACC TTGAACACA 1140
 GCAAGAAAAA ATAAAGACA ATTTCCAGTA AGTATGCCAG TTGCAATTAA TGATTTACTT 1200
 TTTATTTTAA AACTGAATTC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA 1260
 TTTGACCTTG AATAATCTT TACATTGTAA ATTCTTAATG ATCAAAACAA GGTCTCAGT 1320
 GATTAAACA TATTAGTAAT TAATTATTAA AGGAGAATAA TTGCAATAC AACATTCCTA 1380
 AAATCTCAAG GCTTTTAAAG CATTGTGACA AATGACTGGA CATTTTATA ATTTGAAAAA 1440
 AAAAAAAGC CCTCATCTG ATTCTCATTT TCTATTGTG TGCAACAACA AAAAAGGTAT 1500
 GCATTTCTCT TCTCATTTTC CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA 1560
 TCCCATCAA GCCAAGAAA GAAAAGAAA TTGTTCTGTA CAGATATATG ACATTAATAA 1620
 ATAATCCC

Seq ID NO: 235 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MHPLKQREA VCLPRSSYIR LRHFLFTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCV 60
 PHRLVLLVGA LSGFRPIQEP CRKH

Seq ID NO: 236 DNA sequence
 Nucleic Acid Accession #: NM_002075
 Coding sequence: 406..1428

1 11 21 31 41 51
 CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCTGTACCT TTCTCCCOCA 60
 ACAGGATCAG ACCCAGAGGC AGCTGTTTGG GGTTTGTGGA GAAGAAGGAT TATCCAGATC 120
 AGTCTCTTCT AATCTCAGCT CCGCTCTGTA CCTCCCATTA CTCACCAAC CCTCTTCCCC 180
 ACCACCTTGA GCTGAGGAGC ACAGTTTGAG GCCCCCCCAA CCCCCCGCG GTCGGGGCCA 240
 GGCAGGCCCA GGCAGCTTCC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG 300
 CGTGCAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAAACC CGGCGAGGT 360
 CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTGCACTGT CAGCATGGG GGAGATGGAG 420
 CAACTGGCTC AGGAAGCGGA GCAGCTCAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT 480
 GCTGACGTTA CTCGCGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGAG AGTCCAGATG 540
 OGGAGCGGCG GGAAGTTAAG GGGACACCTG GCCAAGATT ACGCCATGCA CTGGGCCACT 600
 GATTCTAAGC TGCTGGTAAG TGCTCGCAA GATGGGAAGC TGATCGTGTG GGACAGTAC 660
 ACCACCAACA AGGTGACGCG CATCCCACTG CGCTCCTCCT GGTTCATGAC CTGTGCCTAT 720
 GCCCATCAG GGAATCTTGT GGCATGTGGG GGGCTGGACA ACATGTGTT CATCTACAAC 780
 CTCAAATCCC GTGAGGGCAA GTCAAGGTC AGCCGGGAGC TTTCTGCTCA CACAGGTAT 840
 CTCTCTGCT GCGCTTCTCT GGATGACAC AATAATTGTA CCAGCTCGGG GGACACCAAG 900
 TGTGCTTGT GGGACATGTA GACTGGGCG CAGAAGACTG TATTGTGGG ACACAGGGT 960
 GACTGCATGA GCTGGCTGT GTCTCTGAC TTCAATCTCT TCAATTGCGG GGCCTGTGAT 1020
 GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGGCCAC 1080

	GAGTGGGACA	TCAACGCCAT	CTGTTCTTC	CCCAATGGAG	AGGCCATCTG	CACGGGCTCG	1140
	GATGAGCTTT	CCTGCGGCTT	GTTTGACCTG	CGGGCAGACC	AGGAGCTGAT	CTGCTTCTCC	1200
	CACGAGAGCA	TCATCTGGGG	CATCACTGCC	GTGGCCTTCT	CCCTCAGTGG	CCGCCTACTA	1260
5	TTGCTGGCT	ACGACGACTT	CAACTGCAAT	GTCTGGGACT	CCATGAAGTC	TGAGCGTGTG	1320
	GGCATCTCT	CTGGCCACGA	TAACAGGGTG	AGCTGCCTGG	GAGTCACAGC	TGACGGGATG	1380
	GCTGTGGCCA	CAGGTTCTCT	GGACAGCTTC	CTCAAAATCT	GGAACTGAGG	AGGCTGGAGA	1440
	AAGGGAAGTG	GAGGGCAGTG	AACACACTCA	GCAGCCCCCT	GCCCGAGCCC	ATCTCATTCA	1500
	GGTGTCTCT	TCTATATTCC	GGGTGCCATT	CCCACTAAGC	TTTCTCTTCT	GAGGGCAGTG	1560
	GGGAGCATGG	GACTGTGCTT	TTGGGAGGCA	GCATCAGGGA	CACAGGGGCA	AAGAACTGCC	1620
10	CCATCTCCTC	CCATGGCCTT	CCCTCCCCAC	AGTCTCTACA	GCCTCTCCCT	TAATGAGCAA	1680
	GGACAACTTG	CCCCCTCCCA	GCCCTTTGCA	GGCCAGCAG	ACTTGAGTCT	GAGGCCCCAG	1740
	GCCCTAGGAT	TCCCTCCCCA	GAGCCACTAC	CTTTGTCCAG	GCCTGGGTGG	TATAGGGCGT	1800
	TTGGCCCTGT	GACTATGGCT	CTGGCACCAC	TAGGGTCTCT	GCCCTCTTCT	TATTCATGCT	1860
15	TTCTCTCTTT	TCTACCTTTT	TTTCTCTCT	AAGACACCTG	CAATAAAGTG	TAGCACCCCTG	1920
	GT						

Seq ID NO: 237 Protein sequence:
Protein Accession #: NP_002066

20	1	11	21	31	41	51	
	MGEMDQLRQE	AEQLKKQIAD	ARKACADVTL	AELVSGLEV	GRVQMRTRT	LRGHLAKIYA	60
	MHWATDSKLL	VSAQDGKLI	VMSYTTNKV	HAIPLRSSW	MTCAVAPSGN	FWACGGLDNM	120
25	CSINLKSRE	GNVKVSRRLS	AHTGYLSCCR	FLDDNNIVTS	SGDTTCALWD	IETGQKQTVF	180
	VGHTGDCMSL	AVSPDFNLFI	SGACDASAKL	WDVREGTCRQ	TFTGHESDIN	AICPPFNGEA	240
	ICTGSDDASC	RLFLRLADQE	LICFSHESII	CGITSVAFSL	SGRLLFAGYD	DFNCNVWDSM	300
	KSERVGILSG	HNDNRVCLGV	TADGMVAATG	SWDSFLKIWN			

Seq ID NO: 238 DNA sequence
Nucleic Acid Accession #: CAT cluster

30	1	11	21	31	41	51	
	TCCCAATGTG	TNGAACCTAC	CATAAATTCT	TTTCTTACNG	GACAACTCTA	TNCTAANCAA	60
35	TACCAATTGG	TTTAAAGGCA	GATAATCCTC	CAAGTTTCTT	AATGATATCT	GAAACTATTA	120
	ACTGATTCTG	TGAATTATGA	AATCTGAAAA	GGAAATTGGAA	GTGTCTAAAA	ATCTATCATT	180
	TGCATTGACC	AGTGTGAAGC	ACAGTGGAA	GAGAATGCGT	GCCCTGACAC	CAAAGAAAAA	240
	TAAGTGACTG	GAAAGCTGAA	GAATCACCGG	CTTCAGTGAC	ATGGAAACCCA	GTGATTGAT	300
40	TTTTGACGAG	TATCGGGTGA	CTTTGAGGTG	GTCAAGAAAC	CACACTTTAA	GAACAATGTC	360
	CAAAAAGGGG	AAAAAAAAGA	GCAACCAAA	AAAAAAATC	CATAAAATTG	CACAGAAGAA	420
	AAGAAAGAAA	AATAAAATAC	ACAATATGGA	CGATGGAGAA	AAACAGTTAC	ATTTCTTTAT	480
	GGATCAAGAA	GTGTTGTGAC	ACATAATCTC	ATTTTGAGAT	ATATAACTAT	TTTTGTCTTT	540
	CAGAAAGTGA	TCAAAATATT	TCAAAATGCT	GTCTTATGAA	ACTACAATAT	TCTCACAGAT	600
45	TAGAAAGTTT	TTTCTGTAAA	AGTCAGATAG	TAAATATTTT	AGGTTTGTGA	GTGTCTTTTG	660
	CAACTACTCA	ACTTCTCTAC	TGTAGCACAA	GAGTAGCTGT	GGTACTGTGC	AAATAAATTG	720
	CTTGTTGTCC	AATAAAGCTT	CATTTACAAA	AACATGCCAT	GGGCCATATT	TGGCCTGTAC	780
	ACTGTTGTTT	GCCAAAGTCT	AATATAGTTG	CTTAGCAAGT	ATTGTGAGCT	ATTTGAGGAA	840
	GACATGAAGG	TCTATTGGGT	TGCTAAAAAG	TATGTAGAAA	TTCAAAGGAA	AATTTAAATT	900
50	TAGGCTAAGT	TATAATACAC	TGTTTAAACA	ATTGTAATAA	GTAAGAGAAA	TTTACAAATA	960
	AAAAATCCAA	ATAAAA					

Seq ID NO: 239 DNA sequence
Nucleic Acid Accession #: NM_001786.1
Coding sequence: 130-1023

55	1	11	21	31	41	51	
	GGGGGGGGGG	GGCACTTGGC	TTCAAAGCTG	GCTCTTGGAA	ATTGAGCGGA	GAGCGACGGG	60
60	GTGTTGTAG	CTGCGCTGCG	GGCGCGCGCG	GAATAATAAG	CCGGGATCTA	CCATACCCAT	120
	TGACTAACTA	TGGAAGATTA	TACCAAAATA	GAGAAAATTG	GAGAAGGTAC	CTATGGAGTT	180
	GTGTATAAGG	GTAGACACAA	AACTACAGGT	CAAGTGGTAG	CCATGAAAAA	AATCAGACTA	240
	GAAAGTGAAG	AGGAAGGGGT	TCTAGTACT	GCAATTGCGG	AAATTTCTCT	ATTAAAGGAA	300
	CTCGTCACT	CAATATAGT	CAGTCTTCAG	GATGTGCTTA	TGCAGGATTC	CAGGTTATAT	360
65	CTCATCTTTG	AGTTCTTCTT	CATGGATCTG	AAGAAATACT	TGGATTCTAT	CCCTCCTGGT	420
	CAGTACATGT	ATTCTTCACT	TGTTAAGAGT	TATTTATACC	AAATCTTACA	GGGGATTGTG	480
	TTTTGTCACT	TAGAAGAGT	TCTTCACAGA	GACTTAAAAAC	CTCAAAATCT	CTTGATTGAT	540
	GACAAAGGAA	CAATTAAGT	GGCTGATTTT	GGCCTTGGCA	GAGCTTTTGG	AATACCTATC	600
	AGAGTATATA	CACATGAGGT	AGTAACACTC	TGGTACAGAT	CTCCAGAAGT	ATTGCTGGGG	660
70	TCAGCTCGTT	ACTCAACTCC	AGTTGACATT	TGGAGTATAG	GCACCATATT	TGCTGAACATA	720
	GCAACTAAGA	AACCACTTTT	CCATGGGGAT	TCAGAAATTG	ATCAACTCTT	CAGGATTITC	780
	AGAGCTTTGG	GCACTCCCAA	TAAATGAAGT	TGGCCAGAGG	TGGAATCTTT	ACAGGACTAT	840
	AAGAATACAT	TTCCCAAAAT	GAAACAGGGA	AGCCTAGCAT	CCCATGTCAA	AAACTTGGAT	900
	GAAATAGGCT	TGGATTGCT	CTCGAAAATG	TTAATCTATG	ATCCAGCCAA	ACGAATTTCT	960
75	GGCAAAATGG	CACATGAATCA	TCCATATTTT	AATGATTGGG	ACAATCAGAT	TAAGAAGATG	1020
	TAGCTTTCTG	ACAAAAAGTT	TCCATATGTT	ATGTCACAG	ATAGTTGTGT	TTTTATTGTT	1080
	AACTCTTGTG	TATTTTGTG	TTATATATAT	TTCTTTGTTA	TCAAACTTCA	GCTGTACTTC	1140
	GTCTTCTAAT	TTCAAAAATA	TAACTTAAAA	ATGTAAATAT	TCTATATGAA	TTTAAATATA	1200
	ATTCTGTAAA	TGTGAAAAAA	AAAAAATAAA	AAAAA			

Seq ID NO: 240 Protein sequence:
Protein Accession #: NP_001777.1

85	1	11	21	31	41	51	
	MEDYTKIEKI	GEGTYGVVYK	GRHKTTGQVV	AMMKIRLESE	EEGVVPSTAIR	EISLLKELRH	60
	PNIVSLQDVL	MQDSRLYLIF	EFLSMDLKKY	LDSIPPQGYM	DSSLVKSYLY	QILQGIVFCH	120

SRRLVRLDLK PQNLLIDDKG TIKLADFLGA RAFGIPIRVY THEVVTLYWR SPEVLLGSAR 180
 YSTPVDIWSI GTIPFLATK KPLFHDSEI DQLFRIFRAL GTPNNEVWPE VESLQDYKNT 240
 FPKWPKGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGRM ALNHPYFNDL DNQIKRM

5

Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_033379.1
 Coding sequence: 132-854

10

1 11 21 31 41 51
 CGCCGCGCGG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTGGCAGAG CGCGCGGCA 60
 GCTTTGCAGA GAGCGCCCTC CAGGGACTAT GCGTGCAGG ACACGGGATC TACCCATACC 120
 ATTGACTAAC TATGGAAGAT TATACCAAAA TAGAGAAAAT TGGAGAAGGT ACCTATGGAG 180
 TTGTGTATTA GGTGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC 240
 TAGAAGATGA AGAGGAAGGG GTTCTAGTA CTGCAATTCT GGAATTTCT CTATTAAAGG 300
 AACTTGGTGA TCCAAATATA GTCACTCTTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT 360
 ATCTCATCTT TGAGTTTCTT TCCATGGATC TGAAGAAATA CTGGATTCT ATCCCTCCTG 420
 GTCAGTACAT GGATCTCTCA CTGTTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG 480
 TATTGCTGGG TGCAGCTCGT TACTCAACTC CAGTTGACAT TTGGAGTATA GGCACCATAT 540
 TTGCTGAATC AGCACTAAG AAACCACTTT TCCATGGGGA TTCAGAAATT GATCAACTCT 600
 TCAGGATTTT GAGGCTTTTG GGCATCCCA ATAATGAAGT GTGGCCAGAA GTGGAATCTT 660
 TACAGGACTA TAAGAATACA TTTCCCAAT GGAACCCAGG AAGCCTAGCA TCCCATGTCA 720
 AAAAATCGGA TGAATATGGC TTGATTGTC TCTGAAAAT GTTAATCTAT GATCCAGCCA 780
 AACGAATTTC TGCAAAAATG GCACTGAATC ATCCATATTT TAATGATTG GACAATCAGA 840
 TTAAGAAGAT GTAGCTTTCT GACAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900
 TTTTATGTGT TAACCTTGT CTATTTTGT CTATATATA TTTCTTTGT ATCAAACTTC 960
 AGCTGTACTT CGTCTCTAA TTTCAAAAAT ATAACCTAAA AATGTAATA TTCTATATGA 1020
 ATTTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAAAA AAAAAA

30

Seq ID NO: 242 Protein sequence:
 Protein Accession #: NP_203698.1

35

1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EGVVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKVVTL WYRSPVLLG 120
 SARYSTPDIW WISGTIFAEL ATKPLFHDG SEIDQLFRIF RALGTPNNEV WPEVBSLQDY 180
 KNTFPKWKPG SLASHVKNLD ENGLDLLSKM LIYDPAKRIS GRMALNHPYP NDLNQNIRKM

40

Seq ID NO: 243 DNA sequence
 Nucleic Acid Accession #: AP101051.1
 Coding sequence: 221-856

45

1 11 21 31 41 51
 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCCGCC CCGGCGCGCG ACCCCAAACC 60
 CGACCCAGAG CTTTCCAGC GCGGGGCGCAG CGAGCAGGGC TCCCGCCCTT AACTTCTCTC 120
 CGGGGGCCCA GCCACCTTCG GAGTCCGGG TTGCCCACTC GCAAACTCTC CGCTTCTGCG 180
 AACTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAAG CGGGGCTGCA 240
 GCTGTGGGCG TTCACTCTCG CCTTCTGCG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300
 GCCCCAGTGG AGGATTACT CCTATGCCG CGACAACATC GTGACGCCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCTT GCGTGTGCGA GAGCAACCGG CAGATCCAGT GCAAACTCTT 420
 TGACTCTCTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG 480
 CATCTCTCTG GGAGGTATAG CAATCTTGT GGCACCGCTT GGCATGAAGT GTATGAAGTG 540
 CTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTCTT 600
 TCTTGCAAGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCATAGAA TCGTTCAAGA 660
 ATCTATGATC AGATGATGCT CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCAC 720
 TGGCTGGGCT GCTGCTCTCT TCTGCTTCT GGGAGGTGCC CTACTTGTCT GTTCTGTCTC 780
 CGAATAAACA ACCTCTTACC CAACCAACAG GCGCTATCCA AAACCTGCAC CTCCAGGCG 840
 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAATCA TGTGAAACA AACCGAAAT 900
 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAAAACAAA CAAACAAACA AAAAAACCAT GTGTTAAAT ACTCAGTGCT 1020
 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCATT GAGTAATCAT ACTCAATGG GGGAGGGGGT GCTCTTAA 1140
 TATATATAGA TATATATATA TACATGTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAT GTATTTAATT 1260
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCTTATAT ACATATGTA 1320
 CAGTCAAAAT TCAATTACTC TTCTTCAITA GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCTTTCAATT CTTATGCGGT GCGCTTTTCA TATACTTATT 1440
 TTATTTTTTA CCATATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTGTG 1500
 TTTCAATGGT CTCTATCTCC TGAATCTAAC ACATTTTATA GCGTACATT TAGTTTCTAA 1560
 AGCCAGAAAG AATTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAA 1620
 GTGATAAAT CTGTTGACC TTCCACACA ATCCCTGTAC TCTGACCCAT AGCACTCTTG 1680
 TTTGCTTTGA AAATATTGT CCAATTGAGT AGCTGCATGC TGTCCGCCA GGTGTTGTAA 1740
 CACAACCTTA TTGATTGAAT TTTTAAGCTA CTTATTCTAT GTTTTATATC CCGCTAAACT 1800
 ACCTTTGTG TCCCATTTCC TTAATTGTAT TGTTTCCCA AGTGTAAAT TCAATGCTTT 1860
 TATATCTTCC TAAATAGGTG TGGTCTGTTT GCTGAAACAA AGTGCTAGAC TTTCTGGAGT 1920
 GATAATCTGG TGACAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTCTTACC 1980
 TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG 2040
 AATATTAAAT AGTTTATATT ACTTCTATT TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
 TTTATTGTCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACAGTAC 2160
 CTTCATGTGA TTCACTGCTC TCCCTCTCTC ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
 ACACATACCT TCATGTGTTT CAGTGCCTTC CTCTCTCTAC CAGTCTATT CCACTGAACA 2280
 AAACCTAGCC ACATACCTTC ATGTGGCTCA GTGCGCTTCT CTCTCTACCA GTCTATTTC 2340
 ATTCTTTCAG CTGTGCTGTA CATGTTTGTG CTCTGTTCCT TTTTAAACA TGCTCTTACT 2400
 TTTCCAGTCT GTACAGAATG CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460

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GCACTGGTGT CTGGAGACCT GGATTGTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
GTGGTTTGTG AATTGAAAAA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAACTGCATA 2700
CGTTTGTGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACCGAAT 2820
AAGATTCTGA GGAAGTCTTA TCCTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
ACAGATGTAA TGGGAAGAAA TAAAGGCTTA CGTGTGGTA AATCCACAG CAAGGGAGAT 2940
TTTTGAATCA TAATAACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTTGC 3000
TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
CTACACAAGG AAGTCAGCC ACCGTGCTTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
TGCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTTAAA ATTTAAATGG CTTTGGCAC 3180
ATACATAGAT CTTCATGATG TGTGAGTGTA ATTCATGTG GATATCAGTT ACCAAACATT 3240
ACAAAAAAT TTTATGGCC AATATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT 3300
TTTGATCTTT TTATATTCTT CTACCAACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
TTATAATGGG AATTGTGATA AAGCATTACT CTTTTCAAT AAATGTGTTT TTAATTTAAA 3420
AAAAAGGAAA AAAAAA AAA

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20 Seq ID NO: 244 Protein sequence:
Protein Accession #: AAD16433.1

25

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1 11 21 31 41 51
| | | | |
MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMEYGL WMSCVSQSTG 60
QIQCKVFDLS LNLSSLTQAT RALMVVGILL GVIAIPVATV GNMCKMCLSD DEVQKMRMAV 120
IGGAIFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALPTGWA AASLCLLGGA 180
LLCCSCPRKT TSYPTRPRYP KPAFSSGKDY V

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30 Seq ID NO: 245 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1 11 21 31 41 51
| | | | |
TTTTTTTTTT TTTTTTTTTT TTTTCAAGG AGAGCACAAG GAACCTTIAT AATGACTTTC 60
TTAATGGTTA AATGCTGTGT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAATCC TTTCTTTGTC TTCACCTAGT 180
TTTTCTTCCT GAGATTAGT TTCTTCATCG TTAACAATGA GGATATTAAT ATGTTTCACA 240
CAGTTGTTAT GAAGAATGCA TATATTAGAA TGCCCTGATG CTCAGCTACT CAGGAGGCTA 300
AGGTGGGGAG GTGCTCAAG CCCAGGAATT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
TTAATAGCCA CTGCACTTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTCGGAGG 420
GTCTACGCC CAGGAGTCT CGCTGATTGC TAGCACAGCA GTCGTGAGATC AAACGTCA

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45 Seq ID NO: 246 DNA sequence
Nucleic Acid Accession #: XM_058553.2
Coding sequence: 897-1400

50
55
60
65
70
75

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1 11 21 31 41 51
| | | | |
AATTTTCAGA AGTTTGTAT GGGGATGGTT TTATATAAAT TCAGGTTTTT CCCACAATAA 60
TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTTC TATAGAAAAG GATTCAAAC 120
GTGAACACAT TTCTCTTTTA ATGTTTCACA TTCCTGTTAC AGATTGTTC TCTGTGACT 180
CTGTTATCCA TAATATGGAC AGTTCTTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAGTATT GCCACTTTAG CACTGAAGAT 300
TGGGATGAGA GAGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCCT 360
GATCATGTTT AAGAAAATGC ATGAAAATGG TGAAGTAGTG TTTCCAAGCA TATTGGAAGG 420
GTTGAGTGTA TACTGTCTGT CAAAGACTTC CAGCAITTC AGGTCTAGA GAGGAACAAG 480
ACTGTAACCC TGCTATCTGT TATTTTAAAG AACCCAGGAG GAAAGCTTTA TAATAGAAC 540
TTATTTCTGT GTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
TTGTCCAGCC CAAGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAG TGATCTGCCT 660
GCCTTTGCCT CTTGAGTAGC TGGGACTACA GGCATGAGCC CCCATGCCTG GCTAAGTTTG 720
TTTTTTTGTG TGTGTTTGTG TTTGTTTTTG GGGGGGGTGT TTTTGTTTTT TGTAGAGACG 780
TAGTCTGTCT TTGTTGCCAG GCTAGTCTCA AACTCCTGGC TTCAAGTGAT CCTCTGCCT 840
CAGCCCTCCA GAGTGCTAGG ATTACAGCAC TTGGATTGAG CTCTTCATT TCCAACATGG 900
AAGAACTTA CACCGACTCC CTGGACCCTG AGAAGCTATT GCAATGCCCC TATGACAAAA 960
ACCATCAAAT CAGGCTTTC AGGTTTCTCT ATCATCTTAT CAAGTCGACA AAGAAATCATC 1020
CTGATGTTGC AAGCAAAATG GCTACTTGTG CCTTCAATGC TCGCCACCAG GTTCTCTGAG 1080
CTGAAATGAT TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAAGATGTTG 1140
TCAACCAAAC CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTGG CAGTGCCCTC 1200
CTTGCGATGA AGACTGGGAT AAAGATTGTG GGGAGCAGAC CAGCACCCCA TTTGTCTGGG 1260
GCACAATCA CTACTCTGAC AACAACAGCC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
ATAACCTGGC TTCAGGCATG CGAGTTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
ACAAATGAAA TGCACAGTAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
GTTGCTCTCT CTCTACCAAG TGGGTTCTCA TTTTCTCTCT AATCTAATTA TAGAATGGTA 1500
AACTCCCTGT GACTTTCCAA ACTGACAAGC ACACTTTTTT CCTCCCCCT TGAATCCTCA 1560
TTTAATGCAA GAACCTCAT ACTCAGAAGC TTCCAAATAA ACCTTTGATA CAGATTG

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80 Seq ID NO: 247 Protein sequence:
Protein Accession #: XP_058553.1

85

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1 11 21 31 41 51
| | | | |
MEETTTDSLD PEKLLQCPYD KKHQIRACRF FYHLIKCRKN HPDVASKLAT CPFNARHQP 60
RABISHISS CDRSCIEQD VVNQTRSLRQ ETLAESTWQC PCDDEDWDKD LWEQTSTPFV 120
WGTHYSDNN SPASNIVTEH KNNLASGMRV FKSLPYVLPW KXNGNAQ

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Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

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1 11 21 31 41 51
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AACTGATTAT GAAACATAAG ATGTTAAITC GGAGCTGCAT TTCCAGCTG GGCCTCTCG 120
10 CGCGCTGGTC CCGGGGGCCT CGCCCCCACC CCGCTGCCCT TCCTCCCGC GTCCGCCCC 180
CATCCTCCAC CCCCCGCGCT GGGCACCOCG CCTCCTTGGC AGCCTCTGGC GGCAGCGCGC 240
TCCACTCGCC TCCCGTGTCT CTCTCGCCCA TGGAAATTAAT TCTGGCTCCA CTGTGTGCTC 300
GGCCAGGTT GGGGAGAGGA CGGAGGGTGG CCGCAGCGGG TTCTGAGTGT AATTACCCAG 360
GAGGGAATGA GCACAGCACC AACTAGAGAG GGGTCAGGG GTGGGGACT CGAGCGAGCA 420
15 GGAAGGAGGC AGCGGCTGGC ACCAGGGCTT TGACTCAACA GAATTGAGAC ACGTTTGTAA 480
TCGCTGGCGT GCCCGCGCCA CAGGATCCCA GCGAAATCA GATTTCCTGG TGAGGTTGCG 540
TGGGTGGATT AATTGTGAAA AAGAACTGCT CTATATCTTG CCATCAAAAA ACTCACGGAG 600
GAGAAGCGCA GTCAATCAAC AGTAACTTA AGAGACCCCC GATGCTCCCC TGGTTAACT 660
TGTATGCTTG AAAATTATCT GAGAGGGAAT AAACATCTTT TCCTCTCTCC CTCTCCAGAA 720
20 GTCCATTGGA ATATTAGGCC CAGGAGTTGC TTTGGGATG GCTGGAAGTG CAATGTCTTC 780
CAAGTTCTTC CTAGTGGCTT TGGCCATATT TTTCTCCTTC GCCCAGGTTG TAATTGAAGC 840
CAATTCTTGG TGGTGGCTAG GTATGAATAA CCCTGTTTCA ATGTGAGAAG TATATATTAT 900
AGGAGCAGAC CCTCTCTGCA GCCAACTGGC AGGACTTTCT CAAGGACAGA AGAACTGTG 960
25 CCACCTTGAT CAGGACCACA TGCACTACAT CGGAGAAGGC GCGAAGCAG GCATCAAGA 1020
ATGCCAGTAT CAATTCCGAC ATCGACGGTG GAACCTGCAG ACTGTGGATA ACACCTCTGT 1080
TTTTGGCAGG GTGATGCAGA TAGGCAGCGC CGAGACGGCC TTCACATAGC CGGTGAGCGC 1140
AGCAGGGGTG GTGAAAGCCA TGAGCCGGGC GTGCCGGGAG GGGAGCTGT CCACCTGCGG 1200
CTGCAGCGCC GCCCGCGGCC CCAAGGACCT GCCCGGGAC TGGCTCTGGG GGGCTGCGG 1260
CGACAACATC GACTATGGCT ACCGCTTTGC CAAGGAGTTC GTGGACGCC GCGAGCGGGA 1320
30 GCGCATCCAC GCGCAAGGCT CCTACGAGAG TGCTCGCATC CTGATGAACC TGCACAACAA 1380
CGAGGCGCGC CGCAGGACGG TGTAACAACCT GGTGATGTG GCGTGAAGT GCCATGGGT 1440
GTCCGCTCA TGTAGCTCTA AGACATGCTG GCTGCAGCTG GCAGACTTCC GCAAGTGGG 1500
TGATGCCCTG AAGGAGAAGT ACGACAGCGC GCGCGCCATG CGGCTCAACA GCCGGGGCAA 1560
35 GTTGTGTACG GTCAACAGCC GCTTCAACTC GCCCACCACA CAAGACCTGG TCTACATCGA 1620
CCCCAGCCCT GACTACTGCG TGCGCAATGA GAGCACCGGC TCGCTGGGCA CGCAGGCGCC 1680
CCTGTGCAAC AAGAGCTCGG AGGGCATGGA TGGCTGCGAG CTCATGTGCT GCGGCGGTG 1740
GTACAGCAGC TTCAAGACCG TGCAAGCGGA GCGCTGCCAC TGCAAGTTCC ACTGGTGTG 1800
CTACGTCAAG TGCAAGAAGT GCAAGGAGAT CGTGGACCAG TTTGTGTGCA AGTAGTGGT 1860
GCCACCCAGC ACTCAGCCCC GCTCCAGGGA CCGCTTATT TATAGAAAGT ACAGTGATT 1920
40 TGGTTTTTGG TTTTATAGAAA TATTTTTTAT TTTTCCCAA GAATTGCAAC CGGAACCAAT 1980
TTTTTCTCTG TTACCATCTA AGAACTCTGT GGTATTATAT TAATTATATA AITATTATT 2040
GGCAATAATG GGGGTGGGAA CCAAGAAAAA TATTTATTTT GTGATCTTT GAAAGGTAA 2100
TACAAGACTT CTTTTGGATA GTATAGAATG AAGGGGAAAA TAACACATAC CCTAAGTTAG 2160
45 CTGTGTGGGA CATGTACAC ATCCAGAAGG TAAAGAAATA CATTTCTTT TTCTCAATA 2220
TGCCATCATA TGGGATGGGT AGGTTCCAGT TGAAGAGGGG TGGTAGAAT CTATTACAA 2280
TTCACTCTCT ATGACCAAAA TGAGTTGTA ATTCTCTGTT GCAAGATAAA AGGTCTTGG 2340
AAAACAAAAC AAAACAAAC ACAATGGAAG GACAAGAATG TCATATCTC AAGGAAAAA 2400
50 CATTTTCAAA ATGATAAATT ACAATGGAAG GACAAGAATG TCATATCTC AAGGAAAAA 2460
GGTATATCAC ATGTCTCAT CTCTCAAAAT ATTCCATTG CAGACAGACC GTCATATTCT 2520
AATAGCTCAT GAAATTTGGG CAGCAGGGAG GAAAGTCCCC AGAAATTAAA AAATTTAAAA 2580
CTCTTATGTC AAGATGTTGA TTTGAAGCTG TTATAAGAAT TGGGATTCCA GATTGTGAAA 2640
AAGACCCCCA ATGATTCTGG ACACATAGAT TTTGTGTTGG GGAGGTTGGC TTGAACATAA 2700
ATGAAATATC CTGTATTTTC TTAGGGATAC TTTGGTTAGTA AATTATAATA GTAGAAATAA 2760
55 TACATGAATC CCATTACAG GTTCTCAGC CCAAGCAACA AGGTAATTGC GTGCCATTCA 2820
GCACTGCAC AGAGCAGACA ACCTATTGTA GGAATAACAG TGAATCCAC CTTCCTCTC 2880
ACACTGAGCC CTCTCTGATT CCTCCGTGTT GTGATGTGAT GCTGGCCACG TTTCCAAAAG 2940
GCAGCTCCAC TGGGTCCTCT TTTGTTGTAG GACAGGAAT GAAACATTAG GAGCTCTGCT 3000
TGGAAAACAG TTCACTACTT AGGGATTITT GTTTCCTAAA ACTTTTATTT TGAGGAGCAG 3060
60 TAGTTTTCTA TGTTTTAAAT ACAGAACTTG GCTAATGGAA TTCACAGAGG TGTTCGACGG 3120
TATCACTGTT ATGATCCTGT GTTTAGATTA TCCAATCATG CTCTCTCTAT TGTACTGCAG 3180
GTGTACCTTA AAATGTTTCC CAGTGTACTT GAACAGTTGC ATTTATAAGG GGGGAAATGT 3240
GGTTTAAATG TGCGTGATAT CTCAAAGTCT TTTGTACATA ACATATATAT ATATATACAT 3300
ATATATAAAT ATAAATATAA ATATATCTCA TTGCAGCCAG TGATTTAGAT TTACAGCTTA 3360
65 CTCTGGGGTT ATCTCTCTGT CTAGAGCATT GTTGTCTTTC ACTGCAGTCC AGTTGGGATT 3420
ATTCCAAAG TTTTGTGAGT CTTGAGCTTG GCGTGTGGCC CCGCTGTGAT CATACCTGTA 3480
GCACGACGAA GCAACCTCGT TTTCTGAGGA GAAGCTTGAG TTTCTGACTC CTGAAATGCG 3540
TGTGTGGGTG AAGATATCTT TTTTCTTTT CTGCTCACC CCTTGTCTC CAACCTCCAT 3600
70 TTTCTGTTAC TTTGTGGAGA GGGCATTACT TGTTCGTTAT AGACATGGAC GTTAAGAGAT 3660
ATTCAAACT CAGAAGCATC AGCAATGTTT CTCTTTTCTT AGTTCAATTCT GCAGAAATGGA 3720
AACCCTAGCC TATTAGAAAT GACAGTACTT ATTAATTGAG TCCCTAAGGA ATATTAGGCC 3780
CACTACATAG ATAGCTTTTT TTTTTTTTTT TTTTTTTTAA TAAGGACACC TCTTTCCAAA 3840
CAGGCCATCA AATATGTTCT TATCTCAGAC TTAGGTTGTT TTAAGGTTT GGAAGAGATC 3900
75 ACATCTTTTC ATACCCCCC TTAGGAGGTT GGGCTTTTCA ATCACTCAG CCACTGTGG 3960
CTCTTAATTT ATTGCATAAT GATATCCACA TCAGCCAACT GTGGCTCTTT AATTATATGC 4020
ATAATGATAT TCACATCCOC TCAGTTGCAG TGAATTGTGA GCAAAAGATC TTGAAAGCAA 4080
AAAGCACTAA TTAGTTTAAA ATGTCACCTT TTTGTTTTTT ATTATACAAA AACCATGAAG 4140
TACTTTTTTT ATTTGCTAAA TCAGATTGTT CCTTTTGTAG GACTCATGTT TATGAAGAGA 4200
80 GTTGAAGTTA ACAAATCCTAG CTTTAAAAAG AAACATTTTA ATGTAAAAATA TTCTACATGT 4260
CAATCAGATA TTAATGATAT CTCTAGCCCT TTAATCTGTA CTTTAAATGT ACATATTCT 4320
GTCTTGGGTG ATTTGTATAT TTCACTGGTT TAAAAACAA ACATGAAAG GCTTATTCCA 4380
AATGAAGAT AGAATATAAA ATAAAACGTT ACTTGTAAAA AAAAAAAA

Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

85
1 11 21 31 41 51
| | | | | |

5 MAGSAMSSKP FLVALAIFFS FAQVVEANS WWSLGMNPFV QMSEVYIIGA QPLCSQLAGL 60
 SQQKGLCHL YQDHQYIGB GAKTGIKECQ YQPHRRWNC STVDNTSVFG RVMQIGSRET 120
 APTYAVSAAG VVMAMSRACR EGELSTCGCS RAARPKDLPR DWLWGGCGDN IDYGYRFAKE 180
 FVDARERERI HAKGSYVESAR ILAMLENNEA GRRTVYNLAD VACKCHGVSG SCSLKTCWLQ 240
 LADPRKVGDA LKSKYDSAAA MRLNSRGLV QVNSRFPNSPT TQDLVYIDPS PDYCVNEST 300
 GSLGTQGRLC NKTSSGMDGC ELACCGRGYD QFKTVQTERC ECKPHWCCTV KCKKCTEIVD 360
 QPVCK

10 Seq ID NO: 250 DNA sequence
 Nucleic Acid Accession #: NM_014058
 Coding sequence: 56..1324

15 1 11 21 31 41 51
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 TGACTTGGAT GTAGACCTCG ACCTTCACAG GACTCTTCAT TGCTGGTTGG CAATGATGTA 60
 TCGGCCAGAT GTGGTGAGGG CTAGGAAAAG AGTTTGTGG GAACCCCTGGG TTATCGGCCT 120
 CGTCATCTTC ATATCCCTGA TTGTCTGGC AGTGTGCATT GGACTCACTG TTCAATTATGT 180
 GAGATATAAT CAAAAGAAGA CCTACAATTA CTATAGCACA TTGTCAATTA CAACTGACAA 240
 ACTATATGCT GAGTTTGGCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT 300
 20 TGAATCAATG GTGAAAAATG CATTTTATAA ATCTCCATTA AGGGAAGAAT TTGTCAAGTC 360
 TCAGGTTATC AAGTTCAGTC AACAGAAGCA TGGAGTGTGG GCTCATATGC TGTGTGATTG 420
 TAGATTTCAC TCTACTGAGG ATCTCGAAGC TGTAGATAAA ATTGTTCAAC TTGTTTACA 480
 TGAAGAGCTG CAAGATGCTG TAGGACCCCC TAAAGTAGAT CCTCACTCAG TTAATAATTAA 540
 AAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTGCGGAA CACGAAGAAG 600
 25 TAAAACCTCA GTTCAGAGTC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG 660
 GCOCTGGGAG GCTAGCCTGC AGTGGGATGG GAGTCATCGC TGTGGAGCAA CCTTAATTAA 720
 TGCCACATGG CTTGTGAGTG CTGCTCACTG TTTTACAACA TATAAGAACCC CTGCCAGATG 780
 GACTGCTTCC TTGGAGTAA CAATAAAACC TTGAAAATG AAACGGGGTC TCCGGAGAAAT 840
 AATTGTCCAT GAAAATACA AACACCCATC ACATGACTAT GATATTTCTC TTGCAGAGCT 900
 30 TTCTAGCCCT GTTCCTTACA CAAATGCAGT ACATAGAGTT TGCTCCCTG ATGCATCCTA 960
 TGAGTTTCAA CCAGGTGATG TGATGTTGT GACAGGATTG GGAGCACTGA AAAATGATGG 1020
 TTACAGTCAA AATCATCTTC GACAAGCACA GGTGACTCTC ATAGACGCTA CAACTTGCAA 1080
 TGAACCTCAA GCTTACAATG ACGCCATAAC TCCTAGAAATG TTATGTGCTG GTCCTTAGA 1140
 AGGAAAAACA GATGCATGCC AGGGTGACTC TGGAGGACCA CTGGTTAGTT CAGATGCTAG 1200
 35 AGATATCTGG TACCTTGCTG GAATAGTGAG CTGGGGAGAT GAATGTGCGA AACCCAACAA 1260
 GCCTGGTGT TATACTAGAG TTACGGCCTT GCGGGACTGG ATTACTTCAA AAACCTGGTAT 1320
 CTAAGAGAGA AAAGCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTGG GGTGTGGAGG 1380
 CCATTTTTAG AGATACAGAA TTGGAGAAGA CTTGCAAAAC AGCTAGATTG GACTGATCTC 1440
 40 AATAAATCTG TTGCTTGATG CAAAAAATA A

Seq ID NO: 251 Protein sequence:
 Protein Accession #: NP_054777

45 1 11 21 31 41 51
 | | | | |
 MYRPDVRAR KRVCEPFWI GLVIFISLIV LAVCIGLTVH YVRYNQKITY NYYSTLSFTT 60
 DKLYAEFGR ASNFTMSQ RLBSMVKNF YKSPLEEFV KSQVIKFSQ KHGVLAHMILL 120
 50 ICRPHSTBDP ETVDRIQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR 180
 RSKTLGQSLR IVGGTEVEEG EWPWQASLQW DGSHRGATL INATWLVSAA HCPITYKNPA 240
 RWTASFVGTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSSPVPYTN AVHERVCLPDA 300
 SYEPQPDVM FVTGPGALKN DGYSQNHRLQ AQVTLIDATT CNEPQAYNDA ITPRMLCAGS 360
 LEGKTDACQG DSGGPLVSSD ARDIWYLAGI VSWGDECAKP NKPGVYTRVT ALRDMITSRT 420
 GI

Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: NM_003504.2
 Coding sequence: 71-1771

60 1 11 21 31 41 51
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 GGCACGAGGC CTCGTGCCGC CGGGCTCTTG GTACCTCAGC GCGAGCGCCA GGCGTCCGGC 60
 CGCGTGGCT ATGTTCTGTG COGATTTCOG CAAAGAGTTC TAGAGGTGG TCCAGAGCCA 120
 GAGGGTCTCT CTCTTCGTGG CCTCGGACGT GATGTCTCTG TGTGCGTGCA AGATCTCTTA 180
 65 GGCTTTGTT CAGGTGACG ACGTGCAATA TACGCTGGTT CCAGTTTCTG GGTGGCAAGA 240
 ACTTGAACT GCATTTCTTG AGCATAAAGA ACAGTTTCAT TATTTTATTC TCATAAACTG 300
 TGGAGCTAAT GTAGACCTAT TGGATATTCT TCAACCTGAT GAAGACACTA TATTTCTTGT 360
 GTGTGACACC CATAGGCCAG TCAATGTCTG CAATGTATAC AAGGATACCC AGATCAAAAT 420
 ACTCATTAAC CAAGATGATG ACCTTGAAGT TCCCGCTAT GAAGACATCT TCAGGGATGA 480
 70 AGAGGAGGAT GAAGAGCATT CAGGAAATGA CAGTGATGGG TCAGAGCCTT CTGAGAAGCG 540
 CACACGGTTA GAAGAGGAGA TAGTGGAGCA AACCATGCGG AGGAGGCAGC GCGAGAGATG 600
 GGAGGCCCGG AGAAGAGACA TCCTCTTTGA CTACGAGCAG TATGAATATC ATGGACATC 660
 GTCAGCCATG GTGATGTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT 720
 GTGGTGGGCC ATCGTTGGAC TAACAGACCA GTGGGTGCAA GACAAGATCA CTCAAATGAA 780
 75 ATACGTGACT GATGTTGGTG TCCTGCAGCG CCACGTTTCC CGCCACAACC ACCGGAACGA 840
 GGATGAGGAG AACACACTCT CGGTGGACTG CACACGGATC TCCTTTGAGT ATGACCTCOG 900
 CCTGGTGCTC TACCAGCACT GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACCGC 960
 AGCCAGGTTT CAGCTGTGGT CTGTGCATGG ACAGAAGCGG CTCAGGAGT TCCTTGCGAG 1020
 CATGGGTCTT CCCTGGAAGC AGGTGAAGCA GAAGTTCAG GCCATGGACA TCTCCTTGAA 1080
 80 GGAGAAATTG CGGGAATGA TTGAAGAGTC TGCAAAATAA TTTGGGATGA AGGACATGCG 1140
 GGTGACAGCT TTCAGCAATC ATTTTGGGTT CAAGCACAAG TTTCTGGCCA GCGACGTGGT 1200
 CTTTGCCACC ATGCTCTTGA TGGAGAGCCC CGAGAAGGAT GGCTCAGGGA CAGATCACTT 1260
 CATCCAGGCT CTCCAGGCC TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA 1320
 ACTGCCCAAG AAGCAGCTGC GAGCCACCCA GCAGACCAAT GCCAGCTGCC TTTGACACCA 1380
 85 CTTGCTATC TCCAGGGGC CTTTCTGTGA CTGCTCTCTC ATGGAGGGCA CTCAGATGAT 1440
 CATGCTGTTC TCTAGGCCGG CATCCCTAAG CTTGCTCAGC AAACACCTGC TCAAGTCTCT 1500
 TGTGTGTTGG ACAAAGAACC GCGCTGCAA ACTGCTGCCC CTGGTGATGG CTGCCCCCTT 1560

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GAGCATGGAG CATGGCACAG TGACCGTGGT GGGCATCCCC CCAGAGACCG ACAGCTCGGA 1620
CAGGAAGAAC TTTTITGGGA GGGGTTTGA GAAGGCAGCG GAAAGCACCA GCTCCCGAT 1680
GCTGCACAC CATTTTGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT 1740
TCTGGACGCA CTTATTTCOC TCTGTCTCTA GGAATTGAT TCTTCCAGAA TGACCTTCTT 1800
ATTTATGTAA CTGGCTTTCA TTTAGATTGT AAGTTATGGA CATGATTGA GATGTAGAAG 1860
CCATTTTITA TTAATAAAAA TGCTTATTTT AGGCTCCGTC CCCAAAAAAA AAAAAAAA 1920
AAAAAAA AA

Seq ID NO: 253 Protein sequence:
Protein Accession #: NP_003495.1

1 11 21 31 41 51
MPVSDFRKEF YEYVQSQRLV LFVADVDAL CACKILQALP QCDHVQYTLV PVSQWQLEET 60
AFLEHKEQPH YFILINCGAN VDLLDILQPD EDTIFFVCDT HRPVNVVNVY NDTQIKLLIK 120
QDDLEVPVAY EDIFRDEED EEHSGNDSG SEPSEKRTLL EEEIVEQTMR RRQRREWEAR 180
RRDILFDYEQ YEYHGTSSAM VMFELAWMLS KDLNDMLWVA IVGLTDQWVQ DKITQMKYVT 240
DVGVLQRHVS RHNHRNDEE NTLSDVCTRI SFPEYDLRLVL YQHNLSLHDSL CMTSYTAARF 300
KLWSVHGQRK LQEFADMDGL PLKQVQKQKQ AMDISLKENL REMIEESANK PGMKDMRVQT 360
FSIHFGPKHK PLASDVVFAT MSLMESPEKD GSGTDEPIQA LDSLRSNLID KLYHGLELAK 420
KQLRATQQTIT ASCLCTNLVI SQGPPLYCSL MEGTPDVMLF SRPASLILLS KHLKSPVCS 480
TKNERCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAPEKAA ESTSSRMLRN 540
HFDLSVIELK AEDRSKPLDA LISLLS

Seq ID NO: 254 DNA sequence
Nucleic Acid Accession #: NM_022337
Coding sequence: 48..683

1 11 21 31 41 51
GGCTGGCTT CCGTGGTCAG GCACGGCAGC TCTGGCCGGC CGCCAGGATG CAGGCCCGC 60
ACAAGGAGCA CCGTGTACAAG TTGCTGGTGA TTGGCGACCT GGGCGTGGGG AAGACCACTA 120
TCATCAAGCG CTACGTGCAC CAGAACTTCT CCTCGCACTA CCGGGCCACA ATCGGCGTGG 180
ACTTCGGCTC CAAGGTGCTC CACTGGGACC CGGAGACTGT GGTGCGCCTG CAGCTCTGGG 240
ATATGCGAGG TCAGAAAGA TTTGGAAACA TGACGAGGGT CTATTACCGA GAAGCTATGG 300
GTGCATTAT TGCTCTOGAT GTCAOCAGGC CAGCCACATT TGAAGCAGTG GCAAAGTGA 360
AAAATGATTG GGAATCCAA TTAAGTCTCC CTAATGGCAA ACCGCTTCA GTGGTTTGT 420
TGGCCAAACA ATGTGACCA GGAAGGATG TGCTCATGAA CAATGGCCTC AAGATGGACC 480
AGTTCGCAAA GGAGCAAGGT TTCTAGGAT GGTGTGAAAC ATCAGCAAAG GAAATATAA 540
ACATTGATGA AGCTCCAGA TGCTGTGTA AACACATACT TGCAATGAG TGTGACCTAA 600
TGAGCTCTAT TGAGCCGGAC GCTGTGAAGC CCCATCTCAC ATCAACCAAG GTTGCCAGCT 660
GCTCTGGCTG TGCCAAATCC TAGTAGGCAC CTTTGTCTGT GTCTGGTAGG AATGACCTCA 720
TTGTCCACA AATGTGCTCT CTATTTTATC CATTTTGGGT AAACGTGAGG ATAGATATAC 780
CACATGTGGC AAGCCAAAGA TCTATGCCTC TGTTTTTCA ATGAGAGAGA AATAGCAAAT 840
GTTCTTTCTA TGCTTTCTCT ACCATCATCA CAGTGTTCAC AAACCTTTGA AAATATTAG 900
TCTGTACAAA ACTTCTGTCA GTAGCTGAC CAAATCTCTG CAGGGCCACA GTGGCAGT 960
TTATTTGCTT CTATTAAATCA GCAAAGGCCT CAAGTCTTAA AATAAAGGG GAGAAGAACA 1020
AACTAGCTGT CAAGTCAAGG ACTGGCTTTC ACCTTGCCCT GGTGTCTTTT TCCAGATTTC 1080
AATATATTCT CTGATGAGCT GACAGGCCTA TTAAGTAGAT GTGATATTTT CTTCCAAGAT 1140
GACCTCCATT CTGGCAGAC CTAAGAGTTG CCTCTGAGTT AGCTCTTTGG AATCGTGAAC 1200
ACAGGTGTGC TATATTGTCC TTGTCTAAC TGTCACTTGC CATGGCCTGA ATGTTGGCTT 1260
AACTGAATAT TGTATGAAAA GACATGCCTC CATATGTGCC TTTCTGTAG CTCTCTTTGA 1320
CTCAAGCTGT GGGGCTCCTC TATACATGCT ATACATGTAA TATATATTAT ATATATTTT 1380
GCAAGTGAAC AATAAACAAT TAAAAATAA AA

Seq ID NO: 255 Protein sequence:
Protein Accession #: NP_071732

1 11 21 31 41 51
MQAPHKEHLY KLLVIGDLGV GKTSIIKRYV HQNFSSHYRA TIGVDPALKV LHWDPETVVR 60
LQLWDIAGQE RFGNMTRVYV REAMGAPIVF DVTRPATFEA VAKWKNLDS KLSLPNGKPV 120
SVVLLANKCD QGKDVLMNNG LKMDQFCKEH GFVGWFETSA KENINIDEAS RCLVKHILAN 180
BCDLMESIEP DVVKPHLTST KVASCSCAK S

Seq ID NO: 256 DNA sequence
Nucleic Acid Accession #: NM_016321
Coding sequence: 25..1464

1 11 21 31 41 51
GGAACGCCC GCTGCCAGCC CGGCCAGGCA CCCCTGCAGC ATGGCCTGGA ACACCAACCT 60
CGCTGGGGG CTGCCGCTCA CCTGCTGCT CCTGCAGGTG ATTATGGTGA TTCTCTTGG 120
GGTGTTCGTG CGCTACGACT TCGAGGCGGA CGCCCACTGG TGCTCAGAGA GGAGCCACAA 180
GAACCTGAGC GACATGGAGA ACGAATCTTA CTATCGCTAC CCAAGCTTCC AGGACGTGCA 240
CGTATGGTTC TTGCTGGGCT TCGGCTTCTT CATGACTTTC CTGCAGCGCT ACGGCTTCTG 300
CGCGTGGGCT TCAACTTCTC TGTGGGAGC CTTCGGCATC CAGTGGGCGC TGCTCATGCA 360
GGGCTGGTTC CACTTCTTAC AAGACCGCTA CATCGTGTG GCGGTGAGGA ACCTCATCAA 420
CGCTGACTTC TGCGTGGCCT CTGTCTGGT GGCCTTTGGG GCAGTTCTGG GTAAAGTCAG 480
CCCATTTCAG CTGCTCATCA TGACTTTCTT CCAAGTGACC CTCTTGTCTG TGAATGAGTT 540
CATCTCTCTT AACCTGCTAA AGGTGAAGGA TGCAGGAGGC TCCATGACCA TCCACACATT 600
TGGCGCTTAC TTTGGGCTCA CAGTGAACCG GATCTCTTAC CGACGCAACC TAGAGCAGAG 660
CAAGGAGAGA CAGAATTCTG TGTACCAATC GGACCTCTTT GCCATGATTG GCACCTCTTT 720
CCTGTGGATG TACTGGCCCA GCTTCAACTC AGCCATATCC TACCATGGGG ACAGCCAGCA 780
CGAGCGGCC ATCAACACCT ACTGCTCTT GGCAGCCTGC GTGCTTACCT CGGTGGCAAT 840

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ATCCAGTGCC CTGCACAAGA AGGGCAAGCT GGACATGGTG CACATCCAGA ATGCCACGCT 900
CGCAGAGGGG GTGGCCGTGG GTACCGCTGC TGAGATGATG CTATGCCTT ACGGTGCCCT 960
CATCATCGGC TTGCTCTGGG GCATCATCTC CACCGTGGT TTTGTATACC TGACCCCAAT 1020
CTTGGAGTCC CGGCTGCACA TCCAGGACAC ATGTGGCATT AACAACTGCG ATGGCAATTCC 1080
TGGCATCATA GGGCGGCATCG TGGGTGCTGT GACAGCGGCC TCCGCCAGCC TTGAAGTCTA 1140
TGGAAAAGAA GGGCTTGTC ATTCCTTTGA CTTTCAAGGT TTCAACGGGG ACTGGACCGC 1200
AAGAACACAG GGAAGATTCC AGATTTATGG TCTCTGGTG ACCCTGGCCA TGGCCCTGAT 1260
GGGTGGCATC ATTTGTGGGC TCATTTTGTG ATTACCATTC TGGGGACAAC CTTCAGATGA 1320
GAATGCTTTT GAGGATGCGG TCTACTGGGA GATGCTGAA GGGAAACAGCA CTGTCTACAT 1380
CCCTGAGGAC CCCACCTTCA AGCCCTCAGG ACCCTCAGTA CCCTCAGTAC CCATGGTGTG 1440
CCCCTACCCC ATGGCTTCTC CGGTACCCCTT GGTACCCCTAG GCTCCACGGG CAGGTGAGGA 1500
GCAGGCTCCA CAGACTSTCC TGGGGCCAG AGGAGCTGGT GCTGACCTAG CTAGGGATGC 1560
AAGAGTGAGC AAGCAGCACC CCCACCTGCT GGCTTGGCCT CAAGGTGCCT CCACCCCTGC 1620
CCTCCCTTTC ATCCAGGGG GTCTGCTGA GAATGGAGAA GGAGAAGCTA CAAAGTGGGC 1680
ATCCAAGCGG GGTTCCTGGT GCAGAAGTTC TGCCTCTGCC TGGGGTCTTG GCCACATTGG 1740
AGAAAAACAG GCTCAAAGTG GGGCTGGGAC CTGTGGGGTG AACCTGAGCT CTCCCAGGAG 1800
ACAACTTAGC TGCCAGTCA CACCTATGAG GCTCTTCTAC CCGGTGCGCT CACCTGGGCC 1860
AGCATCTCCT ATGCTCCCTG GGTCCCCCAG ACCTCTCTGT GTTGTGTGCG TGGCAGCCTC 1920
CAGGAATAAA CATTCTTGTT GTCCCTTGTA AAAAAAAAAA AAAAAAAAAA
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Seq ID NO: 257 Protein sequence:
Protein Accession #: NP_057405

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1 11 21 31 41 51
MAMNTNLNRW LPLTCLLLQV IMVILFGVFV RYDFEADAHW WSETRHKNLS DMENEFYYRY 60
PSFDVHVWV FVGFGLMTF LQRYGPSAVG FNFLAAAFGI QMALLMQGWF HFLQDRYIVV 120
GVENLINADF CVASVAVPAG AVLKGVSPIQ LLIMTFQVIT LEAVNEFILL NLLKVKDAGG 180
SMTIHTPGAY FGLTVTRILY RRLNQSKER QNSVYQSDLP AMIGTLFLWM YWPSFNSAIS 240
YHGDSSQHRRA INTYCSLAAC VLTSAISSA LHKKGKLDNV HIQNATLAGG VAVGTAAEMM 300
LMPYGLALIG FVCGIISTLG FVYLTPFLES RLHIQDTCGI NNHLGIPGII GGIVGAVTAA 360
SASLEVYIKG GLVHSFDPQG FNGDWTARTQ GKPFQIYGLLV TLAMALMGGI IVGLILRLPF 420
WQQPSDENCF EDAVYWEMPE GNSTVYIPED PTFKPSGSPV PSVPMVSLPL MASSVPLVP
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Seq ID NO: 258 DNA sequence
Nucleic Acid Accession #: NM_002358.2
Coding sequence: 75..692

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1 11 21 31 41 51
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TTGTGTCCTT GGGCAGTGGG CTGCAGCTCT CCGGGAGACA GGAATCACC CTGCGCGGGA 120
GCGCGGAATC CGTGGCGGAG TTCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG 180
GCATATATCC ATCTGAAACC TTTACTCGAG TGCAGAAATA CGGACTCACC TTGCTTGTA 240
CTACTGATCT TGAGCTCATA AAATACCTAA ATAATGTGGT GGAACAACTG AAAGATTGGT 300
TATCAAGTGT TTCAGTTTCA AACTGGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG 360
TCCTGGAAGG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGCAC 420
CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA 480
CAGCTACGGT GACATTCTTG CCACTGTGGG AAGTTTCTTG TTCATTTGAT CTGCTGATTT 540
ATACAGACAA AGATTGTGGT GTACCTGAAA AATGGGAAGA GTCCGGACCA CAGTTTATTA 600
CCAATTCTGA GGAAGTCCGC CTTCGTTTCA TTAATACTAC AATCCACAAA GTAAATAGCA 660
TGGTGGCCTA CAAAATTCCT GTCAATGACT GAGGATGACA TGAGGAAAT AATGTAATTG 720
TAATTTTGAA ATGTGGTTTT CCTGAAATCA GGTTCATCTAT AGTTGATATG TTTTATTTC 780
TTGGTTAATT TTTCAATGGA GAAACCAAAA ATGATACTTA CTGAACTGTG TGTAAATTGT 840
CCTTTATTTT TTTGGTACCT ATTTGACTTA CCATGGAGTT AACATCATGA ATTTATTGCA 900
CATTGTTCAA AAGGAACCG GAGGTTTTTT TGTCAACATT GTGATGATA TTCCTTTGAA 960
GATAGTAACCT GTAGATGGAA AAACCTGTGC TATAAAGCTA GATGCTTTCC TAAATCAGAT 1020
GTTTGGTCA AGTAGTTTGA CTCAGTATAG GTAGGGAGAT ATTTAAGTAT AAAATACAAC 1080
AAGGAAGTC TAAATATTCA GAATCTTTGT TAAGGTCCCTG AAAGTAACCT ATAATCTATA 1140
AACAAATGAA TATTGCTGTA TAGCTCCTTT TGACCTTCAT TTCATGTATA GTTTTCCTTA 1200
TTGAATCAGT TTCCAATTAT TTGACTTTAA TTTATGTAAC TTGAACCTAT GAAGCAATGG 1260
ATATTTGTAC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTTT TTCATGTGTT 1320
TTATAAATC AAGTTTAAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGTT TTAATAAAAA 1380
AAAAAAAAAA
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Seq ID NO: 259 Protein sequence:
Protein Accession #: NP_002349.1

70
75

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1 11 21 31 41 51
MALQLSREQG ITLRGSARIV AEFPSFGINS ILYQRGIYPS ETPTRVQKYG LTLVLVTTDL 60
LIKYLNVVVE QLKDWLYKCS VQKLVVVISN IESGEVLERN QFDIECDKTA KDDSAPREKS 120
QKAIQDEIRS VIRQITATVT FLPLLEVSCS FDLILIYTDK LVVPERKWEES GPQFIITNSEE 180
VRLRSPTTTI HKVNSMVAYK IPVND
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Seq ID NO: 260 DNA sequence
Nucleic Acid Accession #: NM_001211
Coding sequence: 43..3195

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1 11 21 31 41 51
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GAAGGGGGTG CTCTGAGTGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA 120
GAAAAATGAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGGG AGCACTGGCA 180
CAAGAATCTG CCTGTACAAA TACTCTTCAG CAGCAGAAAC GGGCATTGTA ATATGAAATT 240
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CGATTTTACA CTGGAATAGA CCTCTGGAT GTTTGGGATA GGTATATCAG CTGGACAGAG 300
 CAGAACTATC CTCAGGTGG GAAAGAGAGT AATATGTCAA CGTTATTAGA AAGAGCTGTA 360
 GAAGCACTAC AAGGAGAAAA ACGATATTAT AGTGATTCCTC GATTTCCTCAA TCTCTGGCTT 420
 AATATTAGGC GTTTATGCAA TGAGCCTTGT GATATGTACA GTTACTTGCA CAACCAAGGG 480
 ATTGGTGTIT CACTTGCTCA GTTCTATATC TCATGGGCAG AAGAATATGA AGCTAGAGAA 540
 AACTTTAGGA AAGCAGATGC GATATTTTAC GAAGGGATTG AACAGAAGGC TGAACCACTA 600
 GAAAGACTAC AGTCCCGACA CCGACAATTG CAAGCTCGAG TGTCTCGGCA AACTCTGTGT 660
 GCACCTTGAG AAGAAGAAGA GGAGGAAGTT TTTGAGTCTT CTGTACCACA ACGAAGCACA 720
 CTAGCTGAAC TAAAGAGCAA AGGGAAGAA ACAGCAAGAG CTCCAATCAT CGGTGTAGGA 780
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 ACAGCTTCC TGATAGCTGT ACCGCTGTG CTTCCTCAT TCACTCCATA TGTGGAAGAG 1080
 ACTGCACAA AGCCAGTTAT GACACCATGT AAAATTGAAC CTAGTATAAA CCACATCCTA 1140
 AGCACCAGAA AGCCTGGAAA GGAAGAAGGA GATCCTCTAC AAAGGGTTCA GAGCCATCAG 1200
 CAAAGCGTCT AGGAGAAGAT AGAGAAGATG ATGTATTGTA AGGAGAAGAT TTATGCAGGA 1260
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 GAAGAGATAG AAGAGAAATC AAAAGAAATC CAACTACTC AGCAAGAAAG AACAGGTGAT 1440
 CAGCAAGAG AGACGATGCC TACAAAGGAG ACACTAAAC TGCAAAATGC TTCGAGTCT 1500
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 GAAACTTAC TTGCGAGAA CATTGGCAG GAACAACTC ATTCTAAAGG TCCAGTGTGA 1620
 CCTTTCTCCA TTTTGTATGA GTTCTTCTT TCAGAAAAGA AGAATAAAG TCCCTCTGCA 1680
 GATCCCCAC GAGTTTATG TCAACGAAGA CCCCTTCAG TTCTCAAAAC CTCAGAAAGC 1740
 ATCACTCAA ATGAAGATGT GTCTCCAGAT GTTGTGATG AATTACAGG AATTGAACCC 1800
 TTGAGCGAG ATGCCATTAT CACAGGCTTC AGAAATGTAA CAATTGTGTC TAACCCAGAA 1860
 GACACTTGT ACTTTGCCAG AGCAGCTCGT TTTGTATCCA CTCCTTTCA TGAGATAATG 1920
 TCTTGAAGG ATCTCCCTTC TGATCTCTAG AGACTGTTAC CGGAAGAAGA TCTAGATGTA 1980
 AAGACCTCT AGGAGCAGCA GACAGCTTGT GGCACATCT ACAGTCAGAC TCTCAGCATC 2040
 AAGAAGCTGA GCCCAATTAT TGAAGACAGT CGTGAAGCCA CACACTCCTC TGGCTTCTCT 2100
 GGTTCCTCTG CCTCGGTTGC AAGCACCTCC TCCATCAAAT GTCTTCAAAT TCCTGAGAAA 2160
 CTAGAACCTA CTAATGAGAC TTCAGAAAAC CCTACTCAGT CACCATGGTG TTCACAGTAT 2220
 CGCAGACAGC TACTGAAGTC CCTACCAGAG TTAAGTGCTC CTGCAGAGTT GTGTATAGAA 2280
 GACAGACCAA TGCTTAAGTT GGAATTTAG AAGGAAATG AATTAGGTAA TGAGGATTAC 2340
 TGCAATTAAC GAGAATACCT AATATGTGAA GATTACAAGT TATTCTGGGT GGCGCCAAGA 2400
 AACTCTGAG AATTACAGT AATAAGGTA TCTTCTCAAC CTGTCCTATG GACTTTTAT 2460
 ATCAACCTCA AGTTAAAGGA ACGTTTAAAT GAAGATTGT ATCATTTTGT CAGCTGTAT 2520
 CAATATCAAG ATGGCTGTAT TGTTTGGCAC CAATATATAA ACTGCTTAC CCTTCAGGAT 2580
 CTCTCCCAAC ACAGTAGAATA TATTACCCAT GAAATAACAG TGTGTATTAT TTATAACCTT 2640
 TTGACAATAG TGGAGATGCT ACACAAAGCA GAAATAGTCC ATGGTGACTT GAGTCCAAGG 2700
 TGTCTGATT TCAGAAACAG ATCCACGAT CCTATGATT GTAACAAGAA CAATCAAGCT 2760
 TTGAAGATAG TGGACTTTTC CTACAGTGT GACCTTAGGG TGCAGCTGGA TGTTTTTACC 2820
 CTCAGCGCTC TCGGACTGT ACAGATCCTG GAAGGACAAA AGATCCTGGC TAACTGTTCT 2880
 TCTCCCTACC AGTGTCTCTG GGTGGTATA GCAGATTAG CACATTACT ATTGTTCAAG 2940
 GAACACTTAC AGGTCTCTG GGTGGGTCC TTCTGGAAC TTAGCCAAA TATTCTGTAG 3000
 CTAAGAGATG GTGAATTGT GGAATTAATC TTTGTGCGGA TTCTGATGC CAATGATGAG 3060
 GCCACAGTGT CTGTCTTGG GGAGCTTGCA GCAGAAATGA ATGGGGTTTT TGACACTACA 3120
 TTCCAAAGTC ACCTGAACAA AGCCTTATG AAGGTAGGGA AGTTAACTAG TCCTGGGGCT 3180
 TTGCTCTTTC ATGTCTTGT GCAATCAAGT CTCACAGATT GCTGCCTCAG AGCAATGGTT 3240
 GTATTGTGGA AACTGAAAC TGTATGTGCT GTAATTAAAT TTAGGACACA TTAGATGCA 3300
 CTACCATTGC TGTCTACTT TTTGGTACAG GTATATTTTG ACGTCACTGA TATTTTTAT 3360
 ACAGTGATAT ACTTACTCAT GGCTTGTCT AACTTTTGTG AAGAACTATT TTATCTAAA 3420
 CAGACTCAT ACAAATGTT ACCTTGTAT TTAACCCATT TGTCTCTACT TTTCCTCTGA 3480
 CTTTCCCAT TTGTAATTG TAAAAATGTC TCTATGATC ACCATGTATT TTGTAATAA 3540
 TAAATAGTA TCTGTTAAAA AAAAAA AAAA AAAA AAAA

Seq ID NO: 261 Protein sequence:
Protein Accession #: NP_001202

1 11 21 31 41 51
 MAAVKKEGGA LSEAMSLBED EWELSKENVQ PLRQGRIMST LQGALAQESA CNNTLQOQKR 60
 AFEYEIFYPT GNDPLDVWDR YISWTBQNYP QGKESNMST LLERAVEALQ GEKRYSDPR 120
 FLNLWLKGR LCNELDMYS YLENQIGIVS LAQFYISWAE EYEARENFRK ADAIPQEGIQ 180
 QKAEPLERLQ SQHRQFQARV SRQTLALEK EEEVEVFESS VPQRSTLAEK KSKGKKTARA 240
 PIIRVGALK APSQNRGLQN PFPQMQMNS RITVFDENAD EASTAELSKP TVQFWIAPPM 300
 PRAKENELQA GPWNTGRSLR HRPRGNTASL IAVPAVLPSF TPYVEETAQQ FVMTPKKIEP 360
 SINHLSTRK PGKEBGDPLO RVQSHQQAEE EKKEKMYCK EKIVAGVGEF SFERIRAEVF 420
 RKKLKEQREA ELLTSAEKRA EMQKQIEEME KKLKEIQTTQ QERTGDQEE TMPTKETTKL 480
 QIASSESQRP GMTLSSSVQC VNCCARETSL AENIQEQPH SKGPSVFPFI FDEPILLSKK 540
 NKSPADPPR VLAQRRLPVL LKTSSESITN EDVSPDVCE FTGIEPLSED AIITGPRNVT 600
 ICPNPEDTCD PARAAFPVST PPHEIMSLKD LPSDPERLLP EEDLDVKTSE DQQTACGTIY 660
 SQTLSIKKLS PIIESREAT HSSGFSGSSA SVASTSSIKC LQIPEKLELT NETSENPTQS 720
 PWCQYRRQL LKSLPELSAS AELCIEDRFM PKLEIEKEIE LGNEDYCIK R EYLICEDYKL 780
 FNVAPRNSAE LTVIKVSSQP VPWDFYINLK LKERLNEFD HPCSCYQYQD GCIVHWHQYIN 840
 CFTLQDLQHE SEYITHEITV LIYNLLTIV EMLHKAEIVH GDLSRCLIL RNRIHDPYDC 900
 NKNQALXIV DFSYSVDLRV QLDVFTLSGF RTVQILEGK ILANCSFPYQ VDLFGIADLA 960
 HLLLFKEHLQ VFWGDSFWKL SQNISSELKDG ELWNKFFVRI LNADEATVS VLGLAAEEN 1020
 GVFDITPQSH LNKALWKVGK LTSPGALLFQ

Seq ID NO: 262 DNA sequence
Nucleic Acid Accession #: NM_003784
Coding sequence: 365..1507

1 11 21 31 41 51
 85

	GTCTACTTAT	CAATAAGCAG	CTGCCTGTGC	AGAGTGCAGG	CTGCACCTTT	GGACAGCCTT	60
	TAAACTGTAA	TTCTCAGAAT	TTTAGAACAA	ATTTTGTCT	AGAAATGCTG	ACTTTGGTTC	120
	ATTAGTAGT	GGTAAACAG	GCTCCCTTGG	AAGCTCTCCT	TCATCACCTT	CCTAAGTGCA	180
5	TGTACAGGGA	AGCTCTCCTT	CATCACCTTC	CYAAGTGCAT	GGGGGAAAT	ACCTAGGGCT	240
	CAACAGTCTT	GAGAAGTGTG	GAAACATTTT	CTTTGTGAGT	GAGAACAGAT	CACCTAGAGA	300
	AAGGAAACCA	GATTCCCATC	ACTGCTTCTG	GGTATCAGAT	GCTAGCGCTG	CACCTCATTT	360
	TGCAATGGCC	TCCTTGTCTG	CAGCAATGCG	AGAGTTTTGC	TTCAACCTGT	TCAGAGAGAT	420
10	GGATGCAAT	CAAGGAAATG	GAAATGTGTT	CTTTCTCTCT	CTGAGCCTCT	TCGCTGCCCT	480
	GGCCCTGGTC	CGCTTGGGCG	CTCAAGATGA	CTCCCTCTCT	CAGATTGATA	AGTTGCTTCA	540
	TGTTAACAAT	GCCTCAGGAT	ATGGAAACTC	TTCTAATAGT	CAGTCAGGGC	TCCAGTCTCA	600
	ACTGAAAACA	GTTTCTTCTG	ATATAAATGC	ATCCCAACAG	GATTATGATC	TCAGCATTGT	660
	GAAATGGGCT	TTTGTGTAAG	AAGTGTATGG	CTTTCATAAG	GACTACATTG	AGTGTGCCGA	720
15	AAAATTATAC	GATGCCAAAG	TGGAGCGAGT	TGACTTTACG	AATCATTTAG	AAGACACTAG	780
	ACGTAAATAT	AATAAGTGGG	TTGAAAATGA	AACACATGGC	AAAATCAAGA	ACGTGATTGG	840
	TGAAGGTGGC	ATAAGCTCAT	CTGCTGTAAT	GGTGCTGGTG	AATGCTGTGT	ACTTCAAAGG	900
	CAAGTGGCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TGCCATTTC	AATCTCCCAA	960
	GTGCTCTGGG	AAGSCAGTCG	CCATGATGCA	TCAGGAACGG	AAGTTCAATT	TGTCTGTTAT	1020
20	TGAGAGCCCA	TCAATGAAGA	TTCTTGAGCT	CAGATACAAT	GGTGGCATAA	ACATGTACGT	1080
	TCTGCTGCCT	GAGAATGACC	TCTCTGAAAT	TGAAAACAAA	CTGACCTTTC	AGAATCTAAT	1140
	GGAAATGGAC	AATCCAAAGC	GAATGACCTC	TAAGTATGTT	GAGGTATTTT	TTCTCAGTTT	1200
	CAAGATAGAG	AAGAATATGC	AAATGAAACA	ATATTGAGA	GCCCTAGGGC	TGAAAGATAT	1260
	CTTTGATGAA	TCCAAGCAG	ATCTCTCTGG	GATTGCTTGG	GGGGGTCTGC	TGTATATATC	1320
25	AAGGATGATG	CACAAATCTT	ACATAGAGGT	CAGTGGAGG	GGCACCGAGG	CTACTGCTGC	1380
	CACAGGAAGT	AATATTGTAG	AAAAGCAACT	CCCTCAGTCC	ACGCTGTTTA	GAGCTGACCA	1440
	CCCATTCTTA	TTTGTATCA	GGAAAGGATG	CATCATCTTA	TTCACTGGCA	AAGTTCTCTG	1500
	CCCTTGAAA	TCGAATTGGT	TTCTGTTATA	GCAGTCCCA	CAACATCAAA	GRACCAACCA	1560
	AAGTCAATAG	ATYTGRTT	AATGGGAAA	ATGTGGTGT	TCCTTTGAGT	TTATTTCTTC	1620
30	CTAACATTGG	TCAGCAGATG	ACACTGGTGA	CTTGACCTTT	CCTAGACACC	TGGTTGATTG	1680
	TCCTGATCCC	TGCTCTTAGC	ATTCTACCAC	CATGTGTCTC	ACCCATTTC	AAITTCATTG	1740
	TCCTTTCTCC	CAGCTCATT	TCTATCATTC	TCCCCCATGA	CCCGTCTGGA	AAITATGGAG	1800
	RGTCCTCAAC	TGGTAAGGAG	AACGTAGAAG	TAGCCCTAGG	GATCCTTTT	GAAACTCTAC	1860
	AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
35	CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TGTTTGACCT	ATGAAGATTT	TAGAGTTTAC	1980
	CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAAAAAATG	TGAAATTGGG	2040
	ATTAGGGACC	TACCAAAATA	TTTCATTAAT	GCCTTCAATT	GACAAATTTT	GGCCTTTCTT	2100
	TGATAAGACA	ATATGTACAT	GTTTCTTCAA	ATATTAAAGA	TCTTTTAACT	GTGGCAGTT	2160
40	GTTATCTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTC	TCTATTATTC	2220
	AGAATAAAGA	AATACAACAT	ACCTGTAAA				

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

45	1	11	21	31	41	51	
	MASLAAANAE	PCPNLFREMD	DNQNGNVFP	SSLSLPAALA	LVLGAQDDG	LSQIDKLLHV	60
	NTASGYGNSS	NSQSGQLSQL	KRVFSDINAS	HKDYDLISVN	GLPAEKVYGF	HKDYIECAER	120
	LYDAKVERVD	PTNHLIEDTR	NINKWVENET	HGKIKNVIGE	GGISSAVMV	LVNAVYFKKG	180
50	WQSAPTKSET	INCHFKSPKC	SGKAVAMMHQ	ERKPNLSVIE	DPSMKILELR	YNGGINMYVL	240
	LPENDLSEIB	NKLTFQNLME	WTNPRMTSK	YVEVFFPQFK	IEKNYEMKQY	LRALGLKDIF	300
	DESKADLSGI	ASGGRIYISR	MMHKSYLEVT	EBGTETAAT	GSNIVERQLP	QSTLFRADHP	360
	FLFVIRKDDI	ILFSGKVSCP					

Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

60	1	11	21	31	41	51	
	AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
	CTCTGGGTCC	TTAATGGCAG	CAGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
	GCTCCTGCTG	TCCGGCTGGT	CCCGGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
65	CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
	GGATGAAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCACAC	CTGTCACTCC	300
	CCTGGGGAAG	AACTAAATG	TCACAACGGC	CTGGAAAGCA	CAGAACCCAG	TACTGAGAGA	360
	GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTGAG	CTGGAGAAAT	ACACACCCAA	420
	GGAAACCCCT	ACCTGTCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
70	TGGATCTTGG	CAGTTCAGTT	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
	AATGTGGACA	ACGGTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAAATGACAA	600
	GGTTGTGGCC	ATGTCTCTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
	CTTCTTGATG	GGCATGGACA	GCACCTTGGA	GCCAAGTGCA	GGAGCACCAC	TCGCCATGTC	720
	CTCAGGCACA	ACCCAATCA	GGGCCACAGC	CACCAACCTC	ATCCTTTGCT	GCCTCCTCAT	780
75	CATCCTCCCC	TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
	AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AACTCGCC	TTCTGTCTGG	900
	CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
	TGGACCCAAAT	AGCTCATTTA	CTGCCTTGAT	TCCTTTTGCC	AACAAATTTA	CCAGCAGTTA	1020
	TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTAACCTGA	TGGAATTCCT	GCACTTAAAG	1080
80	TTCTGGCTGA	CTAAACAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAATCAAA	1140
	GTACTTCTTT	GAATGATGAT	CTCTTCTTGG	CAAAATGATAT	TGTCAGTAAA	ATAATCAAGT	1200
	TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGTCCTGAAA	GAGAAATTTT	AAATATTATTA	1260
	ATAAGAAAAA	ATTATATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
	TTTAAATAAA	GAGTCTATT	TCCCAAAAAA	AAAAA			

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1

1 11 21 31 41 51
 5 MAAAAATKIL LCLPLLLLLLS GWSRAGRADP HSLCYDITVI PKPRPGPRWC AVQGVQVDEKT 60
 FLHYDOGNKT VTPVSPLGKK LNVTTAWKAQ NPVLREVVDI LTEDLRDIQL ENYTPKEPLT 120
 LQARMSCEQK AEGHSSGSWQ PSFDGQIFLL FDSEKRMWTT VHPGARXKKE KWENDKVAM 180
 SPHYFSGDC IGWLEDFLNG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC 240
 FILPGI

10 Seq ID NO: 266 DNA sequence
 Nucleic Acid Accession #: XM_084853.1
 Coding sequence: 127-444

1 11 21 31 41 51
 15 ATTGATGATA TATTAAACGA AATCAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC 60
 GACAAGATCA ACTTACCAGA TTTCTTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT 120
 AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCTAAAGGG 180
 AAAAAGGCCA TTGGAAGAGA GGACTTCTCTG AGACTGCTCG TTAATAAAGG TGAGCATATG 240
 20 ACGGAGGAGG AGATGTTGGA TTGCTTTGCT TCACTGTTTG GCGTGAATCC CGAGGGATGG 300
 AARTCGAGCG CTGCAACCTG CTCGTCAGAA GGTTCAGAAA TTTGCCTTGA AGAAGAACTT 360
 CCAGAGCAAA TCACTGCAGA AATATTGCGG ACTGAAATTC TTGGCTTAAC CATTTTCAGAA 420
 GATTTCGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACAA AGGACTTTGG 480
 GTGTGTGTGC ATGCACATGT GTGTGTTTTC CATGAGGCAC TGCTTTTAT GCATTCCTCT 540
 25 CCCCCCTCTC ATCTTAGAG CATTTAGACA TTAAAGCAAG TTTCTGGTGA GCAATG

30 Seq ID NO: 267 Protein sequence:
 Protein Accession #: XP_084853.1

1 11 21 31 41 51
 30 MSGIHKSEFV LGYTNSKGKK AIRREDPLRL LVTKGEHMT EEMLDCEASL PGLNPEGWKS 60
 EPATCSVKGS EICLEEELPD EITAEIPATE ILGLTISEDG GQDQG

35 Seq ID NO: 268 DNA sequence
 Nucleic Acid Accession #: NM_001898
 Coding sequence: 57-482

1 11 21 31 41 51
 40 GGCTCTCACC CTCTCTCTCT GCAGCTCCAG CTTTGTGCTC TGCCTCTGAG GAGACCATGG 60
 CCAGATATCT GAGTACCCTG CTGCTCTGCG TGGCCACCCT AGCTGTGGCC CTGGCCTGGA 120
 GCCCAAGGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCATATGATG 180
 45 AGTGGGTACA GCGTGCCTTT CACTTCGCGA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
 ACTACTACAG ACGTCCGCTG CGGCTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
 ATTACTTCTT CGAGCTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCAG CCCAACTTGG 360
 ACACCTGTGC CTTCCTATGA CAGCCAGAAC TGCAGAGAA ACAGTTGTGC TCTTTCGAGA 420
 TCTACGAAGT TCCTGGGAG AACAGAAAGT CCGTGGTGAA ATCCAGGTGT CAAGAATCCT 480
 50 AGGGATCTGT GCGAGGCCAT TCGCACCAGC CACCACCACC TCCACCCCCC TGTAGTGCTC 540
 CCACCCCTGG ACTGGTGGCC CCACCCCTGC GGGAGGCGCT CCATGTGCCC TGCGCCAAGA 600
 GACAGACAGA GAAGGCTGCA GGAGTCTCTT GTTGCTCAGC AGGGCGCTCT GCCCTCCTCT 660
 CTTCCTTCTT GCTTCTAATA GCCCTGGTAC ATGGTACACA CCCCCCACC TCCTGCAATT 720
 AACAGTAGC ATGCC

55 Seq ID NO: 269 Protein sequence:
 Protein Accession #: NP_001889.1

1 11 21 31 41 51
 60 MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK 60
 DDYYRRPLRV LRARQQTGGV VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120
 EIYEVFWENR RSLVKSRCQE S

65 Seq ID NO: 270 DNA sequence
 Nucleic Acid Accession #: XM_093210
 Coding sequence: 13-1854

1 11 21 31 41 51
 70 ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCAAC 60
 AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAAG 120
 GGCAGAGGGA ATGGGAGAGG GGCATCTCTC CCCATATCTG AGGTGCGACT GCGGGACGTA 180
 GAGCGGACTG GGCCTTTCCC GTTGGCGGCT GGCTCAATC AGGACTTCTT GCCCAGCTGC 240
 75 GCCTTCAAAA CGGTAAGAGC TGCAACTGAA CGTGTGAGAC ATGGTGCGAG TAGGCTGAGA 300
 GCGCGGGGGA GAGATGCCCA TGAACCTAAG TACCCGGACA CGCCCTCCAC TTCTACCACC 360
 ACGAGTAACA CCGCCCCCAC GGGACCGCTC TCGAGGTCCC CCAAGCCAG GACGCAAGGA 420
 GGAACGCCCC GCGCGCGCGC CAGCAGCGGC GGGCACCAGC CCAATGGCCA GCGAACTCAG 480
 CACTGGCAGT CGGCCCTCTC CACACCGCAG GCGTGCAGTG TGGCGAGCGG AGCCTCCCGG 540
 80 CCGAGGAGCC CAGCTAGGCC GTCAACCCGG TTGCTCCAC GGGGAGGGGC ACCAGGCAAA 600
 CTGCCAAGG CCGCGAGCCC AGGCTCCCTG GCGGAGGCCT CCGCTGGTCC GCGCCAGATC 660
 ATGGCCGCCA CCAGGCTCCC GAGCCATGGC TTCTGTCCG GGAACGGCCC GGCGTCTCG 720
 CTGTCCAGCT AG

85 Seq ID NO: 271 Protein sequence:
 Protein Accession #: XP_093210

1 11 21 31 41 51

5 MLRHGEQKRR RARKKNDPLF TCAFKTVRAA TERVRHGADR LRGGGRDAHE LKYPDTPSTS 60
TTTSNTAPTQ PLRSRSPKPT QGGTPRRRPA AAGTRANGHG TQHMQSALLT PQACSVADGA 120
SRAEDPARPS RRLLEPREGAP GKLPKAPSPG SLAEASAGLL AHVRLQNADA QRVISQALP 180
PNSSVGRKEE RPGAQQORRA PAPMATELST GSRPSSHERR AVNPTPEPPG RTOLEPSRL 240
LPREGAPGKL FKAPSPGSLA EASAGPAQIM AATRLPSRGP LSGNGPASWL SS

10 Seq ID NO: 272 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..732

15 1 11 21 31 41 51
GGATACTGTG TCACTCAAAG TAATGGGAGG GAGAGAGAAC AGGGAGGGTA GGGATGCTTT 60
TGAAAAAGCT TTTTTCCTCA CTTTAACTT GCTTTAGCGT TAAGAGTACT TACCAGCTAA 120
TAATGTGGAG GAAATATATC TTTCTCATG GAGATTACAG AATATATCTA TTCATCTTGA 180
ATACCCACTT GAAGCCTCTG TAGAAAATGTC TCGTCTCCCG GTTGATTTTC TAAAACCTAC 240
ATGATTTTGT CTGTGTTCTG CAGTGAGAAA TTACATCCAT AGCAAAGACA AAAGTCTTTT 300
20 TAAATTAATT TTATTTATCT TTCATATAGT TCTTACAATT TCTAAAAAT TAACACTCAT 360
TTAGTATCAC AATTTATGGG AGAGGGTTTT TTGTATTTTT AAGCATATGT GGCTTATATA 420
AAAATTGCAG AAGTCATAGG ACTGTCATGT ATTGCAGCTC TGAGAACCAA TGCTTGAAC 480
TTAAGCC

25 Seq ID NO: 273 Protein sequence:
Protein Accession #: Eos sequence

30 1 11 21 31 41 51
MGGRENREGR DAPEKAPFFPT FNLL

35 Seq ID NO: 274 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299-961

40 1 11 21 31 41 51
CTCTGAGCTT CTCTGAGCCT TGTITGCTCA TCTGGAAAAA GGGGATTAAA CCATTACCT 60
CATGGAGTTG TGAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCTTG TTCTCACCT GGAGAACTG 180
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTGCAA GCTGCCTCAA 240
CAGGAGGGTG GGGGAACAGC TCAACAAATGG CTGATGGGCG CTCTGTGTGT TGATAGAGAT 300
GGAACTTGGA CTGGAGGGCC TCTCCACGCT GTCCCACTGC CCTGGCCTA GGGGCAGCC 360
45 TGCCCTGTGG CCCACCTTGG CCGCTCTGGC TCTGCTGAGC AGCGTGCAG AGGCCTCCCT 420
GGGCTCCGCG CCGCGCAGCC CTGCCCCCGG CGAAGGCCCG CCGCTGTTC TGCGTCCCG 480
CGCCGCGCAC CTGCGGGGGG GACGCAAGGC CCGCTGTGTC AGTGAAGAG CCGCGGGGCC 540
GCGCGCGCAG CCTTCTCGGC CCGCGCCCCC GCGCCTGCA CCCCCATCT CTCTTCCCG 600
CGGGGGCGCG GCGCGCGCGG CTGGGGGCCC GGGCAGCCCG GCTCGGCAG CGGGGGGCG 660
GGGCTCGCCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTGCGCCTGG GCCACCGCTC 720
50 CGACGAGCTG GTGGCTTTC GCTTCTGCG CCGCTCTGTC CGCGCGCGCG GCTCTCCACA 780
CGACCTCAGC CTGGCCAGCT TACTGGGCGC CGGGGCCCTG CGAACGCCCC CGGGCTCCCG 840
GCCGTCAGC CAGCCCTGCT GCGACCCAC GCGCTAAGAA GCGGTCTCCT TCATGGACGT 900
CAACAGCACC TGGAGAACC GGGACCGCCT CTCGCCACC GCCTGCGGCT GCCTGGGCTG 960
AGGGCTCGCT CCAGGCTTT GCAGACTGGA CCTTACCGG TGCTCTTTC TGCTGGGAC 1020
55 CCTCCGCGAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCT CAAAGCTGAG 1080
AGGCCCTTAC CGGTGGGTGA TGGATATCAT CCCGGAACAG GTGAAGGGAC AACTGACTAG 1140
CAGGCCCGAG GCCTCTACCC TGGGATCCCG AGCCTAAAAG ACACCAAGA CCTCAGTAT 1200
GGAGCCCTTC GACCCCACTT CTCACAGACT CTGGCACTGG CCAGGCTCG AACCTGGGAC 1260
60 CCTCTCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGGCCAGG CCCTGTAGGG 1320
ACAGCATTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCCCTGTG CTGGAACCTG 1380
CCTGTACTCA CTATGGGAG CTGGCCCC

65 Seq ID NO: 275 Protein sequence:
Protein Accession #: NP_003967.1

70 1 11 21 31 41 51
MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSPALP RGGRAARAGG PGSRARAAGA 120
RGCRLRSLV FVRALGLGHR SDELVRFRFC SGSCRARSP HDLSLASLLG AGALRPPPGS 180
RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

75 Seq ID NO: 276 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783-1445

80 1 11 21 31 41 51
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
GGACCCCCAA ATCTGCAGCT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
TGGCTCCCGG CCCTCACTCA CTCTCTCCCG CCCTCGGCCG GGCTCCCGAG CTCTCTACTT 180
CGCGTGTCTA CAACTCAAC TCCCGGTTTC CGTGCCCTCT CACCGCTCGA GTTCTCTACT 240
CTCCATATCC GAGGGGCCCT TCCAGCATC TACCCCTCTC CCAACCTCGG GGGACCTAGC 300
85 CAAGCTAGGG GAGCATGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG 360
CGGGGCAAGG GCGCTCCAG CCCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAAATTGA 420
CACCGAGCGG CTGGCGGCGC GGGCAGGAG CTGCTGAGGG ATGAGATTGG GCCCGGCCCG 480
CAGACAAGGC CCGGGGGCTC CGCCAGCAG AGGTCCCTCG GCGCCAGCC CTGCTGCCA 540

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CCGGGGCTG GAGCCCAACA CCGGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAGAGGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTGTGAGCT TCGGGGGAGA 660
 GCCCAGCACT GGTCCCAGGA AAGGTGCTTA GAAGAACAAG GTGCAGGACC CCGTCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGGCTCCTGT GTGTGTGATAG 780
 AGATGGAACT TGGACTTGA GGCCTCTCCA CGCTGTCCCA CTGCCCTGG CCTAGGCGGC 840
 AGCTGCGCTC GTGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
 CCTTGGGCTC CGCGCCCGC AGCCCTGCC CCGCGAAGG CCCCCCGCT GTCTGGCGT 960
 CCGCGCGCG CACCTGCGC GGGGGACGCA CGGCGCGCTG GTGCAGTGA AGAGCCCGGC 1020
 GGCCTGCGCT GCAGCTTCT CGGCGCGCG CCGCGCGCTG TGCACCCCA TCTGCTCTTC 1080
 CCGCGCGCG CGCGCGCGG CGGCTGGGG GCCCGGGCAG CCGCGCTCG GCAGCGGGG 1140
 CGCGGGCTG CCGCTGCGC TCGCAGCTGG TGGCGGTGG CGGCTCGGC CTGGGCCACC 1200
 GCTCGGACGA GCTGGTGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG CGCGCTCTC 1260
 CACACGACCT CAGCTGGCC AGCCTACTGG GCGCGGGGC CTGCGACCG CCGCGGGCT 1320
 CCGCGCGCT CAGCCAGGCC TGCTGCCGAC CCACGCGCTA CGAAGCGTC TCCTTCATGG 1380
 ACGTCAACAG CACTGGAGA ACCGTGGACC GCGCTCTCGC CACCGCTGC GCGCTGCTGG 1440
 GCTGAGGGCT CGCTCCAGGG CTCTTGACAG TGGACCTTA CCGTGTGGTC TTCTGCGCTG 1500
 GGACCTTCCC GCAGAGTCCC ACTAGCCAGC GCGCTCAGCC AGGGACGAAG GCGTCAAGC 1560
 TGAGAGGCC CTACCGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA 1620
 CTAGAGCCC CAGAGCCCTC ACCCTGGGGA TCCAGCCCTA AAGACACCA GAGACCTCAG 1680
 CTATGGAGCC CTTCGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
 GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
 AGGGACAGCA TTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
 CTGGCTGTGA CTCACTCATG GGAGCTGGCC CC

Seq ID NO: 277 Protein sequence:
Protein Accession #: NP_003967.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ PALNPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP RGGRAARAGG PGSRRARAAGA 120
 RGCLRRLSQLV PVRLALGLHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPVSQPCCRP TRYBAVSFMD VNSTWRTVDR LBAATACGCLG

Seq ID NO: 278 DNA sequence
Nucleic Acid Accession #: NM_057160.1
Coding sequence: 1-714

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1 11 21 31 41 51
 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCGCTCCTTG AGGTCTTCC TCCCCAAGCC 60
 CACCTGGGTT CCGCTTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
 TGGCCCAACC TGGCCGCTCT GGCCTCTGCT AGCAGCGTCG CAGAGGCCTC CCGTGGCTCC 180
 GCGCCCGCA GCGCTGCCCC CCGCGAAGGC CCGCCGCTTG TCCTGGCGTC CCGCGCGCGC 240
 CACCTGCGCG GGGGACGAC GCGCCGCTGG TGCACTGGA GAGCCCGCG GCGCGCGCGC 300
 CAGCCTTCTC GCGCCGCGCC CCGCGCGCTC GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
 CGCGCGCGC GCGCTGGGG CCGCGGACG CCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
 CGCCTGCGCT CCGAGCTGGT GCGGCTGCG CCGCTCGGC TGGCCACCG CTCGACGAG 480
 CTGGTGGGTT TCGCTTCTG CAGCGGCTCC TGCCCGCGCG CCGCTCTTCC ACACGACCTC 540
 AGCCTGGGCA GCGTACTGG GCGCGGGGCC CTGCGACCG CCGCGGGCTC CCGCGCGGTC 600
 AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
 ACCTGGAGAA CCGTGGACCG CCTCTCGCC ACCGCTCGG GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGCG TTTCGAGACT GGACCTTAC CGGTGGCTCT TCCTGCTGG GACCTCCCG 780
 CAGAGTCCCA CTAGCCAGCG GCGTCAAGGC GGGACGAAG CCTCAAAGCT GAGAGGCCCC 840
 TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAG GACAACTGAC TAGCAGCCCC 900
 AGAGCCCTCA CCGTCCGAT CCCAGCCTAA AAGACACAG AGACCTCAGC TATGGAGCCC 960
 TTGGGACCCA CTCTCAACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCGCCCGGCC AGGCCCTGTA GGGACAGCAT 1080
 TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCT GTGCTGGAAC TGGCTGTATC 1140
 TCACTCATGG GAGCTGCCCC C

Seq ID NO: 279 Protein sequence:
Protein Accession #: NP_476501.1

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1 11 21 31 41 51
 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SVAEASLGS 60
 APRSPAPREG PPFVLASPA HLPGGRTARW CSGRRARPPP QPSRPAPPPP APPSALPRGG 120
 RAARAGGPGS RARAAGARG RLRSQLVPR ALGLGHRSD LVRFRFCSGS CRRARSPHDL 180
 SLASLLGAGA LRPPFGSRPV SQPCCRPTRY BAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 280 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29-715

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1 11 21 31 41 51
 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTTGA CTGAGAGGCC TCTCCACGCT 60
 GTCCCACTGC CCGTGGCTTA GCGGCGAGGC TCCACTTGGT CTCTCGGCG AGCCTGCCCT 120
 GTGGCCCAACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCGT CCGTGGGCTC 180
 CGCGCCCGC AGCCTTGGC CCGCGAAGG CCGCCGCTGT GTCTGGCGT CCGCGCGCG 240
 CCACCTGCGG GGGGACGCA CCGCCGCTG GTGCAGTGA AGAGCCCGGC GCGCGCGGCC 300
 GCAGCTTCT CCGCCCGCG CCGCGCGGCC TGACCCCGCA TCTGCTCTTC CCGCGGGGG 360
 CCGCGCGCG GCGGCTGGG GCGCGGCGC CCGCGCTCG GCAGCGGGG GCGGGGCTG 420
 CCGCTCGCG TCGCAGCTGG TGCGGTGGG CCGCTCGGC CTGGGCCACC GCTCGGAGA 480
 CTGCTGGCT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG GCGGCTCTC CACACGACCT 540
 CAGCTGGGCC AGCCTACTGG GCGCGGGGC CTGCGACCG CCGCGGGCT CCGCGCGGCT 600
 CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG 660

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CACCTGGAGA ACCGTGGACC GCGCTCTCCG CACCGCCTGC GCGCTGCTGG GCTGAGGGCT 720
CGCTCCAGGG CTTTGCAGAC TGGACCCCTTA CCGGTGGCTC TTCTGCTGCTG GAGCCCTCCC 780
GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCCC 840
CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
CAGAGCCCTC ACCCTGGCGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
CTTGGAGCCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTGGAACCTG GGACCCCTCC 1020
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140
CTCACTCATG GGAGCTGGCC CC

Seq ID NO: 281 Protein sequence:
Protein Accession #: NP_476431.1

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1 11 21 31 41 51
MELGLOGLST LSHCPWPRRQ APIGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
GPPPVLASPA GHLPGGRTAR WSGRARRPP PQPSRPAPP PAPPSPALPRG GRAARAGGPG 120
SRARAAGARG CRLRSQIVPV RALGLGHERSD ELVRFRCPSG SCRRARSPHD LSLASLLGAG 180
ALRFPFGRSP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 282 DNA sequence
Nucleic Acid Accession #: Eos sequence

25
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1 11 21 31 41 51
CTACTGCACC TGCCCTCTCTG TTCCTTTGGA AATCTCTTAC CTTTCATTAG GGTTCCTTTC 60
ATAGCAATTT CCTTTGGTTT TTAAGACTTC TACATTGCTT TTTCTTTTAT TATCTGTGCT 120
CCGTGAACCT TATGAATGCT GCTTAAAAAT AATGTCAAAA TATGTTTTAG CTGCCTACTC 180
AGGTAAAGTT TTTCTTTGCT CTCATCTTGG TTCCATATA CTATTTTGG TTTTGTGTA 240
GATCTAATCA ATGATCTAGT CAGAAGCTAC TTCCTCTGCT AACAGTGATC ATGTTTATGT 300
GCTAAAAATG AACTTGAAC ACGGAAGTAG TGGTTGGTCC AGTTTGAAG CTCTTATTAG 360
TATTCTTCAT CCTGGCTGTA ATAATAGCCA TTATTGTGA TGCCCTTTGT ATGTAGCAGA 420
CACTCTTAAG GATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA 480
GAATCTCAGG ATACCTACAT TTATCACTTT TTCATATAT ATGTATTCTT TATT

Seq ID NO: 283 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 564-1481

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1 11 21 31 41 51
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CAAGAGGTC AAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAAGATG CCAGGCAAAAC 120
GAAGTGCTAC CAACAACAGC AATGACTGTC CTAAAAGTGC GTTCTGGAT ACACCTGTAA 180
ACTTGGATCA AGTTCCCTCC CCTCTCTCA AAATATATCG ACTTGTGCTG AAAGAAATCA 240
CGACCGATGC TCACAATTCT GACCTCGTAA TTATATAGGG GGTGGTTTGG GTTCTGCGT 300
CTTTCCCTGA TTCACTGGCA GGTAAACATAT TTCATGTACA AAATGAACCT CAACACCACG 360
GCAAAACAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAGTGGCGT 420
GGGAGACAC CGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCTGCCC ACTGAGGAGG 480
AAGGCTGCG TAAAGGAGGC CGGGGCGGAG GAAGCCAAGC TCTGCAGGCC CTGACAAAGT 540
CCTCCCGGCC TCCACGCGTC GCCATGGCAA CGCGGGGTCT GTGCTGGCCG GGATTTGGCC 600
GCCCTGGCGG CGCAGGGCCC GCTGGGAAAG CGCGTCCCC CGCGGGCTCC GCCAGTTTGA 660
ACTTGGCGGG CCAAGATGCG GCGGCGGGGC GCTGGGGGCC TACTTTTCCC TCTTCTAAG 720
COGTTTCTC TGCTGACTGC AGACCCAGGT CTCGGCCCTC CTGGACTCC TGCTCAGTCC 780
CTATGACGCG CGCACGTGGG CAGGGGCTGG AGGTGGTGGC CTCGCCCTCG CCGCGCTGCT 840
CGCTGAGCTG CAGCAATTCC ACCAGTGGC TGTTGTCTCC CCTTGGCCAC CAGAGCTTCC 900
AGTTTGAAGA GGAACGCTGA GACGGGGAAG ATGAGGAAGA CGTGGATGAT GAGGAAGACG 960
TGGATGAAGA TGCCCATGAT TCAGAGGCCA AAGTGGGAG CCTGAGAGGA ATGGAGTTAC 1020
AGGGGTGCGC CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC 1080
GCTTACCAGA AAGCCGCTG ACACCATGGG AGGTGTGGTT TATTGGCAAA GAAAAAGAA 1140
AACGTGACCG GCTGCAACTG AAAGCTCTAG AGGAATTAAA TCAACAATA GAAAAAGAA 1200
AAGAAATGGA AGAAGCTGAA AAAAGAAAGA TAATTGCTGA AGAAAAAGCAC AAGGAATGGG 1260
TTCAGAAAAA GAATGAGCAA AAAAGAAAG AAAGAGAAC AAAAAATTAAT AAAGAAATGG 1320
AGGAAAAAGC AGCAAAAGAA CTGGAGAAAG AATACTTGCA AGAAAAAGCA AAAGAAAAAT 1380
ATCAAGAATG GTTAAAGAAA AAAAATGCTG AAGAAATGTA GAGGAAGAAG AAAGAAAAAG 1440
AAAACACAGC CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAAA AGTTTCAAGA 1500
ATGTTGGGAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA 1560
TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACCCAGCT TTTATAATCC 1620
AATTCGGTG AAACCAATTC ATATGCCACC TCCCAAGAA GCTAAGGATC TATCAGGAAG 1680
GAAGAGTAAA AGAAGCTGTA TAAGTCAGCC ACACAAGTCA TCATCTCTGG TAATTCATAA 1740
AGCCAGGAGC AATCTTGGCC TTGGAATCT GTGCAGAAAT CAAAGATAGC GTATGTGGAA 1800
AATAACATGC TTTTATCTGG AGCTATTAA TTTAAAAATC AGAAATTTGT TTTTACTGCT 1860
CAGTCAATAA CTCACACTTT AATGTGATTA TTGACAAATA GCAATTTTTG CATTTGTATA 1920
TGGAGTCCCT AGAGTTGAGG AAGATATTTT CTGGATTTTG GTTTTTATAA ACTTTTTAAG 1980
GTTGATCTTG GCATGTTGTT TTGCAGAAAT AGTGGCTGAA TATGTAAGAA TTGTGTTTGT 2040
ATTAGCTTG TATTAAAGT ACACCTGAAT ACCAATAAAA CTAACAATT TTCTTG

Seq ID NO: 284 Protein sequence:
Protein Accession #: Eos sequence

80
85
1 11 21 31 41 51
MATRGLCWPG LAGLARAGPA GKARPRGSA SLNLAGQWMA AGRWGPPTFP SYAGFSADCR 60
PRSRPSSDSC SVPMTGARQ GLEVVRSPP PLPLSCSNST RSLLSPLGHQ SFQFDEDDGD 120
GEDEEDVDE EDVDEDAHDS EAKVASLRGM ELQGCSTQV ESENQBEQK QVRLPESRLT 180
PWEVWFIGKE KEERDLRLQK ALEELNQOLE KRKEMEEREK RKI LAEEKHK EHVQKQNEQK 240
RKERBQKINK EMEKAAKEL EKEYLQEKAK EKYQSWLEKK NARECERJCK EKQKNSILKY 300

RRKRX

Seq ID NO: 285 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1-1746

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	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGOC	AAGCCTGGGG	TGCAGGGTTG	60
10	GOCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCAAC	120
	GGGGCAGCA	TTGTGGCGGT	GCCCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTGG	GCATCAACGC	CTGGGGCCTT	CCGAAACCTG	300
	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCTCT	360
15	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAGCT	GTTCGAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACAC	480
	CTGGAAATCA	TCCCTGACGG	AGCCTTGGAC	CACCTGGTAG	GACTCAAGAA	GCTCAATCTG	540
	GGCAGAATA	GCCTCAACCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCTCGCG	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGCACTTT	TGATGGGCTT	660
20	GTAAACCTGC	AGGAACCTGG	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCAACACCT	CCAGAGACTC	TACCTGTCCA	ACAACCATAT	CTCCAGCTGC	780
	CCACCCAGTA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTGGGG	CCCATGCCCA	ACCTGGGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCGGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
25	GTCTCGATTG	TTAGCCGCAA	TCAGATCAGC	TTCACTCTCC	CGGGTGGCTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCATGCG	AGGACCTGGA	CGGGAAATGT	1080
	TTCCGATGTT	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTGCACAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCCAG	1200
	CTGGAGAACT	TGCCCTCTCG	CATCTTCGAT	CACCTGGGGA	AACGTGTGTA	GCTCGCGCTG	1260
30	TATGACAATC	CTGGAGGTGG	TGACTCAGAC	ATCCTTCCCG	TCGGCAACTG	GCTCTGCTCT	1320
	AACCAAGCTA	GGTATGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCCAAG	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTCTGTTC	CAAGGCTCCA	TGTCCCTGAG	1440
	GTGCTAGTTC	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCACTGA	GCTAACCAAG	CCTGTGGGAG	ACTACACTGA	TCTGACTACC	1560
35	ATTCAAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCCAAGG	CGGGCTGGCC	1620
	ATTGCGCCCA	TGTAAATGGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGGCTCGCG	1680
	TGTTGCTGCT	GCAAGAGAGG	GAGCCAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGCTGCG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
40	CTAGATAAAG	GTGTGCTCAC	CTCTTCTGTA	CTTGCTGTAT	TCTCCGCTAG	AGAAGCAGGT	1920
	CGTGCGGAGC	CTTCTCAACA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCCGA	TTCAATACCC	TGGGCTTCTT	TGGAGAGGGC	TCTTCTCCCA	AATCTCCCTC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGGG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCCTGTCT	ACTTCGTGGG	AATAGTTTCT	CGCTGAGATA	GCCCTCTCTG	2160
45	CCTAAGTATT	ATGTAAAGTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTGTTGT	CTATGGCTTG	2220
	ACCCAGCATG	TCCCTCAAAA	TGAAGTTTCT	CCCTTGAATT	TTCTGCTCCT	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAGAAA	GACTTCAAAC	CATTAACTCG	GTTTCTTAAG	AGCCGTCAAT	2340
	CAGCCTGGTT	TTGGGATGCG	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAAG	CGCCTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAATA	GGAGAAACAA	2460
50	CCCCAGCACA	CTGAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACTTTGCTT	2520
	TGAAAAGTTT	AGCCCTTTAA	GGAAATGAAAT	CATGTAGAAAT	TTTGGACTTC	TAAAAACATT	2580
	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCCCTGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTGTTGTTTA	AAATTTTATA	TGAAGCATG	TGAAGTGTAC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCAAAA	ACTGAAACATA	CCTGTGTAAT	2760
55	CAGCATCTAG	CCAGACGCCG	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCAGAA	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGAACCT	CCCCCATGAA	GCCAGGACGG	2880
	TCCCCCACA	GTGACCTGTG	GCAAAGGCCC	CGTGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCTTGAA	CAGGAGATTT	TATTATATCT	GGAGACCTCG	3000
	AGAGACCTCG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
60	GTCCGTGCGG	CCACACCCCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
	TCCGCTGCGA	GCCTTCTATG	GAOGTGATAT	GCCTGTATCT	GTTTATAATT	TTCAATCTTC	3180
	ACTTAGGGGA	AGTGAATTCG	CTCAGAGATG	AGATCCCTTA	ATTGAAAAAG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTCTGG	3360
65	GTCTGGGGGC	TCCTCTGAGC	TCCTCTGGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCCAGGSTTA	TTCTCTCTCT	CGAGTCAACG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
	CTGCTATACA	CATATTACAA	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	CTGGCCCACT	TTACAGTGAA	ATGGAGAATT	TCAGTCTCTC	ACGTCTGCCC	3600
70	AGGAAGAAAC	TTCACTGAC	TCCACGGGGA	TCTGGAATTC	CACGACCAAT	CCGATCGGGC	3660
	TCTTATTAGC	TCCCCCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TCGGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTTGGA	TCTGGAATTC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGG	TGCTGACCA	TTTCCCTTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CATAGTGACA	CTTGTAGCT	TTTCAACCTC	TGTCCCAAGG	AATCTAGGAG	3960
75	AGATGAGGGC	CGTCAGATGC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCAATTCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAAAC	GGAGGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCCTCT	GATGGTGGCC	TGCTGTGCCT	GGTGCCAAAC	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTGGTCCCAT	AGACCTGTGG	4200
	GGTGCTCTCG	TGAGTGGGCT	CCAGATGTCT	TTGTGCTATG	GCACAGTGGG	GCCAGGGCTG	4260
80	GAGGAGGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCCTA	4320
	GGTATTCTCG	GCAGTAGCCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCAGAT	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
85	TACTAGAAAA	GTCTAGTGGG	GTCTCTTTTC	CAACAGGATG	ATGCATTGTC	TCAATTCTCA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAGTTTT	4680
	CCTCTCTGTT	TACAGCTCTT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGAGGTTA	4740

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Seq ID NO: 286 Protein sequence:
Protein Accession #: NP_570843.1

1 11 21 31 41 51
MPLKEYLLLL VGCQAWGAGL AYHGPCSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL 120
FOGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAPD HLVLGLTKLNL 180
GRNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMCTPDGL VNLQELALQQ NQIGLLSPGL 240
PHNNHNLQRL YLSNNHISQL PPSIFMQLPQ LNLRLTLFGNS LKELSLGIFG PMPNLRLEML 300
YDNHISSELD NVFSNLRQLQ VLILSRNQIS FISPGAFNPL TELRELSLHT NALQDLGNV 360
FRMLANLQNI SLQNNRLRLQ PGNIFANVNG LMAIQLQNNQ LENLFLGIFD HLGKLCLERL 420
YDNFWRCDSD ILPLRNWLLL NQPRLGTDIV PFCFSPANVR GQSLIINNV VAVPSVHVPE 480
VPSYPETPMY PDTPSYPDIT SVSSTTELTS PVEDYDILT IQVTDDRVSVM GMTQAQSGLA 540
IAAIVIGIVA LACSLAACVG CCCCCKRSQA VLMQNKAPNE C

Seq ID NO: 287 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 1..954

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Seq ID NO: 288 Protein sequence:
Protein Accession #: NP_002353.1

1 11 21 31 41 51
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GAGGCCCTGG GCCTGGTGGG TGCACAGGCT CCTACTACTG AGGAGCAGGA GGCTGCTGTC 120
TCCTCTCTCT CTCTCTCTGT CCCTGGCACC CTGGAGGAAG TGCCCTGCTGC TGAGTCAGCA 180
GGTCTCTCCC AGAGTCTCTC GSGAGCCTCT GCCTTACCCA CTACCATCAG CTTCACTTGC 240
TGGAGGCAAC CCAATGAGGG TTCCAGCAGC CAAGAAGAGG AGGGGCCAAG CACCTGCGCT 300
GACGCAAGCT CCTTGTTCGG AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT 360
CTGCTCCGCA AGTATCGAGC CAAGGAGCTG GTCACAAAGG CAGAAATGCT GGAGAGAGTC 420
ATCAAAAATT ACAAGCGCTG CTCTCTCTGT ATCTTCGGCA AAGCCTCCGA GTCCCTGAAG 480
ATGATCTTTG GCATTGACGT GAAGGAAGTG GACCCCGCCA GCAACACCTA CACCCCTGTC 540
ACCTGCTGGG GCCTTCTCTA TGATGGCCTG CTGGGTAATA ATCAGATCTT TCCCAAGACA 600
GGCCTTCTGA TAATCGTCTT GGGCACAAAT GCAATGGAGG GCGACAGCGC CTCTGAGGAG 660
GAAATCTGGG AGGAGCTGGG TGTGATGGG GTGTATGATG GGAGGGAGCA CACTGTCTAT 720
GGGGAGCCCA GGAACCTGCT CACCCAAGAT TGGGTGCAGG AAAACTACCT GGAGTACCGG 780
CAGGTACCCG CAGTAATCT TGCGCGCTAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT 840
GAAACAGCAT ATGTGAAAGT CCTGGAGCAT GTGTGCAGG TCAATGCAAG AGTTCGCATT 900
GCCTACCCAT CCCTGCGTGA AGCAGCTTTG TTAGAGGAGG AAGAGGGAGT CTGA

Seq ID NO: 289 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 46..1344

65
70
75
80
85

Seq ID NO: 289 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 46..1344

1 11 21 31 41 51
MSSEKQSQC KPEGVEAQE EALGLVGAQA PTTEEQEAHV SSSSPLVPGT LEEVPAESA 60
GPPQSPQAS ALPTTISFTC WRQPNEGSSS QEEZGPSTSP DAESLPREAL SNKVDELHP 120
LLRKYRAKEL VTKAENLERV IKNYKRCPPV IFGKASESLK MIPGIDVKEV DPASNTYTLV 180
TCLGLSYDGL LGNNQIFPKT GLLIIVLGTI AMEGDSASEB BIWEELGVMG VYDGREHTVY 240
GEPRKLLTQD WQENYLEYR QVPGSNPARY EFLWGPRLA ETSYVKVLEH VVRVNRVRI 300
AYPSLREAAAL LEEBEGV

Seq ID NO: 289 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 46..1344

1 11 21 31 41 51
CGGCGGCGCG GCCTTGGTTG GGTCCCACT GCTCTCGGG GCGCATGGA CGAGGCGGTG 60
GGGCACTGA AGCAGCGCT TCCCTGTGTG GCGGAGTCG CACGCTCCA CGTGGAGGTG 120
CATCAGGCGG GCAGCAGCAC TGCAAGAGAA GAAGACATAA ACCTGAGTGT TAGAAAGCTA 180
CTCAACAGAC ATAATATTGT GTTGGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT 240
TTGACAGAA ATGTGCAGTC TGTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA 300
CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACTTCACA TTTTCCAGCT GAATGAAGAT 360
GGCCCATGCA GTGAAATCT CGAGGAAGAG ACAGAAAACA TAATTGCAGC AAATCACTGG 420
GTTCTACCTG CAGCTGAATT CCATGGGCTT TGGGACAGCT TGGTATACGA TGTGGAAGTC 480
AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTGAGACAA GAACGTCAAC 540

5 AGCAAOCTCA TCACCTGGAA CCGGGTGGTG CTGCTCCAGC GTCCTCTGCG CACTGGAAAA 600
 ACATCCCTGT GTAAAGCGTT AGCCCAAGAA TTGACAAATTA GACTTTCAAG CAGGTACCGA 660
 TATGGCCAAAT TAATTGAAAT AAACAGCCAC AGGCTCTTTT CTAAGTGGTT TTCGGAAAGT 720
 10 GGCAAGCTGG TAACCAAGAT GTTTCAGAAG ATTCAGGATT TGATTGATGA TAAAGACGCC 780
 CTGGTGTGCG TGCTGATTGA TGAGGTGGAG AGTCTCACAG CCGCCCGAAA TGCCCTGAGG 840
 GCGGGCACCG AGCCATCAGA TGCCATCCGC GTGGTCAATG CTGTCTTGAC CCAAATTGAT 900
 CAGATTAAAA GGCAATCCAA TGTGTGATT CTGACCACTT CTAACATCAC CGAGAAGATC 960
 GAGGTGGCCT TCGTGGACAG GGCTGACATC AAGCAGTACA TTGGGCCACC CTCTGCAGCA 1020
 15 GCCATCTTCA AATCTACCT CTCTGTGTTG GAAGAACTGA TGAAGTGTCA GATCATATAC 1080
 CCTCGCCAGC AGCTGCTGAC CCTCGAGAG CTAGAGATGA TTGGCTTCAT TGAAAAACAC 1140
 GTGTCAAAAT TGAGCCTTCT TTTGAATGAC ATTTCAAGGA AGAGCGAGGG CCTCAGCGGC 1200
 CGGGTCTCGA GAAAACTCCC CTCTCTGGCT CATGCGCTGT ATGTCCAGGC CCCCACCGTC 1260
 ACCATAGAGG GGTTCCTCCA GGCCCTGTCT CTGGCAGTGG ACAAGCAGTT TGAAGAGAGA 1320
 20 AAGAAGCTTG CAGCTTACAT CTGATCCTGG GCTTCCCAT CTGGTCTTT TCCCATGGAG 1380
 AACACACAAC CAGTAAGTGA GGTGCCCCA CACAGCGCTC TCCCAGGGA TCCCTTCTGC 1440
 AAACCAACG TTACTTAGAC TGCAAGCTAG AAAGCCACCA AGGCCAGGCT TTGTTAAAG 1500
 AAGTGATTC TATTTATGTT GTTTTAAAT GCATACTGAG AGACAAACAT CTGTCTATT 1560
 TCACTGTTG TAAAGATAA TTCAGATTGT TTGTCTCCT GTGAAGAAC ATCGAAACCT 1620
 25 GTTGTGTTCC AGCCACCCC CAGTGGATGG GATGCATAAT GCCAGCAAGT TTTGTTTAA 1680
 AGCAAAAAAG GAGATTAAAT GCAGGTGTTA TAGAAGCCAG AAGAGAACT GTGTCAACCT 1740
 AAAGAAGCAT ATAATCATAG CATTAAAAAT GCACACATTA CTCCAGGTGG AAGGTGGCAA 1800
 TTGCTTCTG ATATCAGCTC GTTTGATTGA GTGCAAAAAT GTTTTCAAGA CTATTTAATG 1860
 GATGTAAAAA AGCCTATTTC TACATTATAC CAACTGAGAA AAAAATGGTC GGTAAAGTGT 1920
 30 TCCTTCATAA TAAATAATCA AGACATGCTC CCAATTGCGA GAAAAGTGCA GACTCTGAGT 1980
 GTTCAGGGA AACACATGCT GGACATCCCT TGTAAACCCG TATGGGCGCC CCTGCATTGC 2040
 TGGGATGTTT CTGCCACGG TTTTGTGTTG GCAATAACGT TATCACATTT CTAATGAGGA 2100
 TTCACTTAA TATAATATAA AATAAATAGG TCAGTTACTG GTCTCTTCT GCGAATGTT 2160
 ATGTTTGTCT TTTATCTCAC AGTAAATAA ATATAATTA AAA

Seq ID NO: 290 Protein sequence:
 Protein Accession #: NP_004228

35 1 11 21 31 41 51
 MDEAVGLKQ ALPCAESPT VEVVHQHRS STAKKEDINL SVRKLNRHN IVPDYTWTE 60
 FDEPFLTRNV QSVSIIIDTEL KVKDSQPIDL SACTVALHIF QLNEDGPSSE NLEETENII 120
 AANEHWLPAA EFEGLMDSLV YDVEVKSHLL DYVMTLLFS DENVNSNLI WNRVLLHGP 180
 PGTKTSLCK ALAQKLTIRL SSRVRYQLI EINSLSLFSK WFSSEGLVT KMFQKIQDLI 240
 40 DDKDALVFLV IDEVESLTA RMACRAGTEP SDAIRVNVAV LTQIDQIKRH SNVVILITSN 300
 ITEKIDVAFV DRADIKQYIG PPSAAAIKFI YLSLEELMK CQIIYPRQQL LTLRELEMIG 360
 FIENNVSKLS LLNDISRKS EGLSGRVLRL LFPLAHLVY QAPTVTIEGF LQALSLAVDK 420
 QFERKKLAA YI

45 Seq ID NO: 291 DNA sequence
 Nucleic Acid Accession #: NM_002658.1
 Coding sequence: 77-1372

50 1 11 21 31 41 51
 GTCCCGCAG CGCGCTCGCG CCTCCTGCC GCAGGCCACC GAGGCGCGCG CCGCTAGCG 60
 CCCCGACCTC GCCACCATGA GAGCCCTGCT GCGCGCGCTG CTCTCTGCG TCCCTGGTCT 120
 GAGCGACTCC AAAGCGAGCA ATGAACCTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
 TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCAAA 240
 55 GAAATTOGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
 TCACCTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
 CTCTGCCACT GTCCCTCAGC AAACGTACCA TGCCCAAGA TCTGATGCTC TTCAGCTGGG 420
 CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
 GCAGGTGGGC CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
 60 AAAGCCCTCC TCTCTCCAG AAGAATTAAA ATTTCACTGT GGCCAAAAGA CTCTGAGGCC 600
 CGCCTTTAAG ATTATTTGGG GAGAATTAC CACCATOGAG AACAGCCCTT GGTTTGCGGC 660
 CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
 CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCAATTGAT TACCCAAAAG AGGAGGACTA 780
 CATCGTCTAC CTGGTGTGCT CAAGGCTTAA CTCCAACAGC CAAGGGGAGA TGAAGTTTGA 840
 65 GGTGGAAGAC CTCACTCTAC ACAAGGACTA CAGCGCTGAC ACCTTGCTC ACCACAACGA 900
 CATTGCTTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCGGACTAT 960
 ACAGACCATC TGCCCTGCCCT CGATGTATAA CGATCCCCAG TTTGGCACA GCTGTGAGAT 1020
 CACTGGCTTT GGAAGAGAGA ATTCTACCGA CTATCTCTAT CCGAGCAGC TGAAGATGAC 1080
 TGTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
 70 CACCACAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCCCT GCCAGGGAGA 1200
 CTGAGGGGGA CCCCTGCTCT GTTCCCTCCA AGGCCGCGATG ACTTTGACTG GAATTGTGAG 1260
 CTGGGGCGGT GGAATGTGCC TGAAGGACAA GGCAGGCGTC TACAGGAG TCTCACACTT 1320
 CTTACCCCTG ATCCGCACTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
 AGGGAGGAAA CGGSCACCA CCGCTTTCTT GCTGGTTGTC ATTTTGTGAG TAGAGTCATC 1440
 75 TCCATCAGT GTAAAGAGAG ACTGGGAGGA TAGGCTCTGC ACAGATGGAT TTGCTGTGG 1500
 CACCACAGG GTGAAGGACA ATAGCTTTAC CCTCACGGAT AGGCCCTGGGT GCTGGCTGCC 1560
 CAGACCTCT GGGCAGGATG GAGGGGTGGT CCGTCACTCA CATGTTACTG ACCAGCAACT 1620
 TGTCTTTTTT TGGACTGAAG CCTGCAGGAG TTAAGAAAGG CAGGGCATCT CCGTGTGATG 1680
 GGCTCGAAGG GAGAGCGAGC TCCCGGACG GGTGGGCATT TGTGAGGCC ATGTTGTAGA 1740
 80 AATGAATAAT TTCCCAATTA GGAAGGTGTA GCAGCTGAGG TCTCTGAGG GAGCTTAGCC 1800
 AATGTGGGAG CAGCGGTTTG GGGAGCAGAG ACACATAACGA CTTGAGGCA GGGCTCTGAT 1860
 ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGACACT TGTGTGTGG 1920
 GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCTCT 1980
 85 AAACGTGTGT GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGCTCACT 2040
 CTGGGCGCTC TTGGGTCGCC CACGTGACAG TGCCCTGGGA TGTACTTATT CTGCAGCATG 2100
 ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
 ATCCCTTCTT TTAGGCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAAG ACCACTCTCT 2220
 ACACCTGAATA TTTATATTTT ACTATTTTAA TTTATATTTT TGTAAATTTA AATAAAGTG 2280

ATCAATAAAA TGTGATTTTT CTGA

Seq ID NO: 292 Protein sequence:
Protein Accession #: NP_002649.1

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1	11	21	31	41	51	
MRALLARLLL	CVLVVS DSKG	SNELHQVPSN	CDCLNGGTCV	SNKYPSNIHW	CNCPKKGFGQ	60
HCEIDKSTKC	YEGNGHFYRG	KASTDTMGRP	CLPWNSATVL	QQTYHAHRSD	ALQLGLGKEN	120
YCRNPDNRRR	PWCYQVQGLK	PLVQECMVHD	CADGKKPSSP	PEELKPFQCG	KTLRPRFKII	180
GGEFTTIIENQ	PWFAAIYRRH	RGGSVTYVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVYLG	240
RSRLNSNTQG	EMKFEVENLI	LHKDYSADTL	AHNDIALALK	IRSKEGRCQA	PSRTIQTICL	300
PSMYNDPQFG	TSCEITGFGK	ENSTDVLYPE	QLKMTVVKLI	SHRECCQPHY	YGEVTTKML	360
CAADPQWKTD	SCQGDSSGGL	VCSLQGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHPLPWIR	420
SHTKRENGLA	L					

Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_001498
Coding sequence: 93..2006

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GGCAGGAGGC	TGAGTGTCCG	TCTCGCGCCC	GGAAGCGGGC	GACCGCCGTC	AGCCCGGAGG	60
AGGAGGAGGA	GGAGGGGAGG	GAGGGGGCGG	CCATGGGGCT	GCTGTCCAG	GGCTCGCCGC	120
TGAGCTGGGA	GGAAACCAAG	CGCCATGCCG	ACCAAGTGGG	GCGGCAAGGG	ATCCTCCAGT	180
TCCTGCACAT	CTACCACGCC	GTCAAGGACC	GSCACAAGGA	CGTTCTCAAG	TGGGGCGATG	240
AGGTGGAATA	CATGTTGGTA	TCTTTTGATC	ATGAAAATAA	AAAAGTCCGG	TGTGTCCTGT	300
CTGGGGAGAA	AGTTCTTGAA	ACTCTGCAAG	AGAAGGGGGA	AAGGACAAAC	CCAAACCATC	360
CTACCCCTTG	GAGACCAGAG	TATGGGAGTT	ACATGATTGA	AGGGACACCA	GGACAGCCCT	420
ACGGAGGAAC	AATGTCCGAG	TTCAATACAG	TTGAGGCCAA	CATGCGAAAA	CGCCGGAAGG	480
AGGCTACTTC	TATATTAGAA	GAAATACAGG	CTCTTTGCAC	AATAACTTCA	TTCCCAGAT	540
TAGGCTGTCC	TGGGTTTACA	CTGCCCCGAG	TCAAACCCAA	CCCAGTGGAA	GGAGGAGCTT	600
CCAAGTCCCT	CTTCTTTCCA	GATGAAGCAA	TAAACAGCA	CCCTCGCTTC	AGTACCTTAA	660
CAAGAAATAT	CCGACATAGG	AGAGGAGAAA	AGGTTGTGAT	CAATGTACCA	ATATTTAAGG	720
ACAAGAATAC	ACCATCTCCA	TTTATAGAAA	CATTACTGTA	GGATGATGAA	GCTTCAAGGG	780
CTTCTAAGCC	GGATCATATT	TACATGGATG	CCATGGGATT	TGGAATGGGC	AATTGCTGTC	840
TCCAGGTGAC	ATTCCAAGCC	TGCAGTATAT	CTGAGGCCAG	ATACCTTTAT	GATCAGTTGG	900
CTACTACTCG	TCCAATTGTT	ATGGCTTTGA	GTGCTGCATC	TCCCTTTTAC	CGAGGCTATG	960
TGTGAGACAT	TGATTGTCCG	TGGGGAGTGA	TTTCTGCATC	TGTAGATGAT	AGAACTCGGG	1020
AGGAGCGAGG	ACTGGAGCCA	TTGAAGAACA	ATAACTATAG	GATCAGTAAA	TCCCGATATG	1080
ACTCAATAGA	CAGCTATTTA	TCTAAGTGTG	GTGAGAAAATA	TAATGACATC	GACTTGACGA	1140
TAGATAAAGA	GATCTACGAA	CAGCTGTTGC	AGGAAGGCAT	TGATCATCTC	CTGGCCCAGC	1200
ATGTTGCTCA	TCTCTTTATT	AGAGACCCAC	TGACACTGTT	TGAAGAGAAA	ATACACCTGG	1260
ATGATGCTAA	TGAGCTGAGC	CATTTTGAGA	ATATTGAGT	CACAAATTGG	CAGACAATGA	1320
GATTTAAGCC	CCCTCTCCCA	AACCTCAGCA	TTGGATGGAG	AGTAGAATTT	CGACCCATGG	1380
AGGTGCAATT	AACAGACTTT	GAGAACTCTG	OCTATGTGGT	GTTTGTGGTA	CTGCTCAGCA	1440
GAGTGATCCT	TTCTTACAAA	TTGGATTTC	TCAATCCACT	GTCAAAGGTT	GATGAGAAAC	1500
TGAAGTAGAG	ACAGAAAAGA	GATGCTGCTC	TGCAGGGAAT	GTTTTATTTC	AGGAAAGATA	1560
TTTGCAAGG	TGCAATGCGA	GTGGTGGATG	GTTGTGGCAA	GGCCCAAGAC	AGCAGCGAGC	1620
TCGCTCAGAG	GGAGTACACC	CTCATGAGCA	TAGACACCAT	CATCAATGGG	AAGGAAGGTG	1680
TGTTTCTCTG	ACTGATCCCA	ATTCTGAACT	CTTACCTTGA	AAACATGGAA	GTGGATGTGG	1740
ACACCAGATG	TAGTATTCTG	AACTACCTAA	AGCTAATTAA	GAAGAGAGCA	TCTGGAGAAC	1800
TAATGACAGT	TGCCAGATGG	ATGAGGGAGT	TTATCGCAAA	CCATCCTGAC	TACAAGCAAG	1860
ACAGTGTGAT	AACTGATGAA	ATGAATTATA	GCCTTATTTT	GAAAGTGAAC	CAAAATTGCA	1920
ATGAATTATG	TGAATGCCCA	GAGTTACTTG	GATCAGCAAT	TAGGAAAGTA	AAATATAGTG	1980
GAGTAAAAAC	TGACTCATCC	AACTAGACAT	TCTACAGAAA	GAAAAATGCA	TTATTGACGA	2040
ACTGGCTACA	GTACCATGCC	TCTCAGCCCG	TGTGTATAAT	ATGAAGACCA	AATGATAGAA	2100
CTGTACTGTT	TTCTGGGCCA	GTGAGCCAGA	AATTGATTAA	GGCTTTCTTT	GGTAGGTAAA	2160
TCTAGAGTTT	ATACAGTCTA	CATGTACATA	GTAAGATATT	TTTGATTAA	AATGATTTT	2220
AATAACATAT	CTAAAGTCAT	CATGAACCTG	CTTGATACAT	TTTAAATTCT	TACTCTGGAG	2280
CAACCTACTG	TCTAAGCAGT	TTTGTAATG	TACTGGTAAT	TGTACAATAC	TTGCATTCCA	2340
GAGTTAAAT	GTTTACTGTA	AATTTTGT	CTTTTAAAGA	CTACCTGGGA	CCTGATTAT	2400
TGAAATTTT	CTCTTAAAA	ACATTTCTC	TCGTTAATTT	TCCTTTGTCA	TTTCTTTGT	2460
TGTCTACATT	AAATCACTTG	AATCCATTGA	AAGTGCCTCA	AGGGTAATCT	TGGGTTTCTA	2520
GCACCTTATC	TATGATGTTT	CTTTTGCAAT	TGGAATAATC	ACTTGGTCAC	CTTGCCCA	2580
GCTTTCCCT	CTGAATAAAT	ACCATTGAA	CTCTGAAAA	AAAAAAAAA	AAAA	

Seq ID NO: 294 Protein sequence:
Protein Accession #: NP_001489

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85

1	11	21	31	41	51	
MGLLSQGSPL	SWEETKRHAD	HVRRHGILQF	LHIYHAVKDR	HKDVLKNGDE	VEYMLVSFDH	60
ENKKVRLVLS	GEKVLETLQE	KGERTNPNHP	TLWRPEYGSY	MIEGTGPGPY	GGTMSFPNTV	120
EAMRRRRKE	ATSILEENQA	LCTITSFPL	GCPCGFTLPEV	KFNPEVGGAS	KSLFFPDBAI	180
NKHPFSTLT	BNTRHRRGEK	VVINVPFKD	KNTPSPIET	FTEDDEASRA	SKPDHIYMDA	240
MFGMGNCCCL	QVTFQACSSIS	EARLYLDQLA	TICPIVMALS	AASPFYRGYV	SDIDCRWGI	300
SASVDDRTRE	ERGLEPLKNN	NYRISKSRD	SIDSYLSKCG	EKYNDIDLT	DKEIYEQLLQ	360
EGIDHLLAQH	VAHLFIRDPL	TLFEERHLD	DANESDHFN	IQSTINWQTM	FKPPFPNSDI	420
GWRVEFRPME	VQLTDFENSA	YVVPVLLTR	VILSYKLDPL	IPLSKVDENN	KVAQRDAVL	480
QGMFYFRKDI	CKGNAVVDG	CGKAQNSTEL	AAEYETLMSI	DTIINGKEGV	FPGLIPIILNS	540
YLENMEVDVD	TRCSILNLYLK	LIIKGRASGEL	MTVARWMEP	IANEPDYKQD	SVITDEMNYNS	600
LILKCNQLAN	ELCECPPELLG	SAFRKVKYSG	SKTDSSN			

Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
      CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
10     GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTGCTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
15     TTCAGCAAGG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACAGAGAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGAACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
20     AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGCATAATC TCGTTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCTGGCAT ATGTTACCGA ATCAAATAGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCATTATAT 1020
      TTGAAAGGAT AACTTGTGTT TTGGTTATTT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
25     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
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Seq ID NO: 296 Protein sequence:
Protein Accession #: Eos sequence

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKILMT 60
      GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SPSGDDLECR ETASSPKSQR 120
      EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDPVKH 180
35     LKKKLKRLMI
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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
      CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
      GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTGCTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAG ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
      TTCAGCAAGG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACAGAGAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGAACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
      AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGCATAATC TCAATTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCTGGCAT ATGTTACCGA ATCAACTGGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCGTTTATAT 1020
      TTGAAAGGAT AACTTGTGTT TTGGTTATTT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
      TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
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Seq ID NO: 298 Protein sequence:
Protein Accession #: Eos sequence

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65     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKILMT 60
      GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SPSGDDLECR ETASSPKSQQ 120
      EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDPVKH 180
70     LKKKLKRLMI
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Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
      CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
      GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTGCTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
      TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCAGTGGT 480
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TCAGCAAGA TAGGATGAT CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGGCC 600
AACAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TGCCTGGAC 660
AAAAATATGA AAAATCTTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTGTGCCCTG GAGGATTATC 840
ACACCCCAAA TGCATAATCT CATTAAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCGAA TCAACTGGCC 960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTATT 1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 300 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKAKKLMAT 60
GHAIPPSQLD SQIDDDFTGFS KDRMMQKPGS NAPVGGNVTS SFGSDDLPCR ETASSPKSQQ 120
EINADIKRKL VKELRCVQKQ YEKIFEMLEG VQGTAVRKR FFSIIKEAA RCMRRDPVKH 180
LKKLKRMI

Seq ID NO: 301 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-812

1 11 21 31 41 51
| | | | |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCTCTCC ATCCCCCTTG 60
GGCCAAACCG GATCGGTGCT TCTGGTGAGA CGCTCCCCCA TGCACATCAC TCCAGGTGC 120
CCTAGGGGGC ACATTTCCTC CACTCCCGAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
GGGAGGGGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTGATATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
TCAGCAAGA TGGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA 540
CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAGGCC 600
AACAGAAAT TAATGCTGAT ATAAAATGTC AAGTAGTGAA GGAAATCOGA TGCCTGGAC 660
AATATGAAA AATCTTGAAG ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC 720
GATTTTTTGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGCAGAGAC TTTGTTAAGC 780
ACCTTAAAGA GAAACTGAAA CGTATGATTT GAGAATACTT GTCCCTGGAG GATTATCACA 840
CCCCAAATGC ATAATCTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT GCTGTTTCT 900
ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC 960
CAGAGGCTAA GAAATTTCTG TTAGTAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTGTA 1020
AAGGATAACT TGTGTTTGG TTATTTTGTA TTCCCACTG TCGTGGTAGA TATTATTAAAC 1080
CCATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA

Seq ID NO: 302 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKEKLMAT 60
GHAIPPSQLD SQIDDDFTGFS KDRMMQKPGS NAPVGGNVTS NFSGDDLECR GIASSPKSQQ 120
EINADIKQV VKELRCVQKQ EKIPEMLEGV QGPTAVRKR FFSIIKEAAR CMRRDPVKH 180
KKKLKRMI

Seq ID NO: 303 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

1 11 21 31 41 51
| | | | |
AGTGTTCGGC TGGGACAGGC ACGCTGTGGC TGGCTACTTC CCTTCTCTCC ATCCCCCTTG 60
GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCA TGCACATCAC TCCAGATGC 120
CCTAGGGGGC ACATTTCCTC CACTCCCGAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
GGGAGGGGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTGATATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
TCAGCAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGGCC 600
AACAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TGCCTGGAC 660
AAAAATATGA AAAATCTTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTGTGCCCTG GAGGATTATC 840
ACACCCCAAA TGCATAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCGAA TCAACTGGCC 960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTATT 1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 304 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
MTDKTEKIVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKAKKLMT 60
GHAIFPSQLD SQIDDPFGPS KDRMMQKPGS NAPVGGNVTS SFGSDLECR BTASSPKSQ 120
5 EINHADIKRL VKELRCVQK YEKIFEMLEG VQGPFAVRKR FFSIIKEAA RCMRRDFVKH 180
LKKKLRMI

Seq ID NO: 305 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 87-689

1 11 21 31 41 51
CGTGGAGGCA GCTAGCGGGA GGCTGGGAG CGCTGAGCG CGCGTGTGC CCTGCGCTGC 60
15 CCAGACTAGC GAACAATACA GTCAGGATGG CTAAAGTGTA CCCCAGAAA CCAAGGGCA 120
AGATGTCCCG TTAGCTCTTC TTTGTGCAGA CATGCAGAGA AGAACATAAG AAGAAAAACC 180
CAGAGGTCCC TGTCATTTT GCGGAATTT CCAAGAAAGT CTCTGAGAGG TGGAAGACGA 240
TGTCGGGAA AGAGAAATCT AAATTGTATG AAATGGCAAA GSCAGATAAA GTGCGCTATG 300
20 ATCGGGAAT GAAGGATTAT GGACAGCTA AGGAGAGCAA GAAGAAGAAG GATCCTAATG 360
CTCCAAAGG GGCACCGTCT GGATTCTTCC TGTTCTGTTC AGAATTCGCG CCCAAGATCA 420
AATCCACAAA CCCCAGCATC TCTATTGGAG ACGTGGCAAA AAAGCTGGGT GAGATGTGGA 480
ATAATTATAA TGACAGTGA AAGCAGCCTT ACATCACTAA GCGCGCAAG GTGAAGGAGA 540
AGTATGAGAA CGATGTGTCT GACTATAAGT CGAAAGGAAA GTTTGATGGT GCAAAGGGTC 600
CTGCTAAAGT TGCCCGGAAA AAGGTGGAAG AGGAAGATGA AGAAGAGGAG GAGGAAGAAG 660
25 AGGAGGAGGA GAGGAGGAG GATGAATAAA GAAACTGTTC ATCTGTCTCC TTGTGAATAC 720
TTAGAGTAGG GGAGCGCGCT AATTGACACA TCTCTTATTT GAGAAGTGTG TGTGTCCCTC 780
ATTAGTTTAA ATTACAAAAT TTGATCACGA TCATATTGTA GTCTCTCAA GTGCTCTAGA 840
AATTGTCACT GGTTTACATG AAGTGGCCAT GSGTGTCTGG AGCACCTGTA AACTGTATCA 900
AAGTTGTACA TATTTCCAAA CATTTTAAAA ATGAAAAGGC ACTCTGTGTG TCTCCTCACT 960
30 CTGTGCACT CTGTGTGTG GTGACAAGGC ATTTAAAGAT GTTCTGCGCA TTTTCTTTT 1020
ATTGTAAAGG TGGTGGTAAC TATGTTTAT GGCTAGAAAT CCTGAGTTT CAACGTGATA 1080
TATCTATAGT TTGTAAAAAG AACAAACAA CCGAGACAAA CCTGTGATGC TCTTGTCTOG 1140
GGGTGAGGCG TGTGGGAAG ATGCTTTTG GGAGAGGCTG TAGCTCAGGG CGTGCACGTG 1200
GAGGCTGGAC CTGTGTGACT TGCAGGGGGC ATCCATTAG CTTCAGGTG TCTTGTTTCT 1260
35 GTATATAGT ACATAGCATT CTGCTGCCAT CTTAGCTGTG GACAAAGGGG GGTGAGCTGG 1320
CATGAGAAAT TTTTTTTTTT TAAGTGGCGT AGTTTAAAA CTGTTGTGTT TTAACAAAC 1380
TATAGAACTC TTCATGTGCA GCAAAGCAA GAGTCACTGC ATCAATGAAA GTTCAAGAAC 1440
CTCCTGTACT TAAACAGAT TCGCAACGTT CTGTATTATT TTTGTATGT TTAGAATGCT 1500
GAAATGTGTT TGAAGTTAAA TAAACAGTAT TACATTTTAA AAACCTCTCT CTATTATAAC 1560
40 AGTCAATTTT TGACTCACAG CAGTGAACAA ACCCCCACTC CATTGTATTT GGAGACTGGC 1620
CTCCCTATAA ATGTGGTAGC TTCTTTTAT ACTCAGTGGC CAGCTCACT AGGGCTGAGA 1680
TGAAGGAGAG GGTACTTGA AGCTACTGTG TGATTTTGTT TGTGTCTGAG TGGCAATCAG 1740
ATGAAGTCTG GAGGAGTTAG GAGAACGACA TAGGCAAGGT TCAGCAGCCT TCCAAGGTAT 1800
AGGAAGGTGG GTGATTAGGA CTGAGGCTAT CTAGGTTTAA CTTTGTGCC ACCTCCACCC 1860
45 CCTATTTTGT TGGGCCAAAT GCATTGCTAA ACAGCAATTT CAGAGTGTAT GGTGTGTCAA 1920
AAATTAAAGC CTTATTGTTT TTCTCTTCA CCCCACCCC CGTGTCTCCT GGCACATATC 1980
ACATTATTGG TGGTGCCCAA CATTTGGGTT CTTGAGCCTG CTGCTGTCTT CCTGGATGCC 2040
AGTGAGGGTA TGTGGGATGG GGTGGTGGGG TAGGGGACGG TATCCTTTT TTGCTCTAC 2100
TTGGAACAC CAAACACCCC AAGGAAGATG ATAGGCTCCA TCTTGGGCCA CTGAGCTAT 2160
50 AGGCGAGGCT AATGGAATCA ACCATTTCTG AGCACTAAAT GTATCATGAA AAGTTGAATG 2220
GCCTGCTCAT AAGTTTAGCT CATTCAGTGG AAATGTAGAT TGATGTTCAA TGTAAACTG 2280
GAAGGAGCTT GGTTTGTGTG TCAGTGGTTA TATTAGTGGG TAGTGTAAAC TTTTATCCAG 2340
GTTGGGTGTA GGGGAGATGG CCACAGTAGC AAGTGGTGAC ACTAAATACC ATTTTGAAGG 2400
CTGATGTGTA TATACATATT TACTGTCCGT AGCAATGAAG GATACAGTAC TGTGTTGTGG 2460
55 GTGAGTGTGG TATTGTCCTA GCATTAAAT TTGGGTGTGT ATGTTTGAAG CATGAAACA 2520
CGCAGGAGTG TTTTGTGTCT ATTAATTTTA AGAGAAAGCA GCTTTTCTT AAAATTCACT 2580
GTTGAGAAAC TTGCATGTCT GGAGGCGGTG TCCTCTCCGC CCTGTGCGGT CCTGGATGAG 2640
TACGAGTTAT GGTACAGGTC ACAGCCTGAT CTCTTATGTG TPCATAGCCA TCGCTCTCC 2700
CATCAGAACT GTTGTCTCTG AATGTGTCTC TCTAGTTCTA GAAATGACC ACTAATTAA 2760
60 AAAACTCGGT TGTGAGTTT GCCCAGAGGC ACTTGTTCCT GAAATTCGCC TCTGCTTCA 2820
GCCATGTCTT TGTCACTTGG CATCTAAGC TAAAGCTTTA GCTTCCCAAT TCGTATGTG 2880
CTAGGCCAAG ATTCGGGAGC TGTGTCAGC CTCGTCAAAT ATGGAAGAGA AACCACTGC 2940
GGTCAAAAGG GAGTGATTG TTAAGTGGTG CGCGTCTATC TCATAACTAG ATGTACCAAC 3000
CAGGGAAGGG CCAAGGATGG AAGGGGTAA CTTTGTGTCT TCCAAAGTAG CTAAGCAGAA 3060
65 GTGGGGGAGC AGTTTAGCCA GATGATCTTT GATTAGGCAA ACATTGAGTT TTAAGAGGCG 3120
TGTCAGTTG AGGCCACTTG GTCCATTAGC TGGGGCAGCA AGATCACTAC TCAACGTTT 3180
CACACTGTGG CAAGATTGCT CTCTAGTGG AATAATGCCC TAGTTCTCT GAGATGATGT 3240
AAGTGGCATG ATGTTACCTA AGGCTTAGGC TTAGCTTGAT TTCTGGGCC ACTGTCTGTG 3300
70 TTCTTAAGT GCCAACCTGT TGCTTTTTC TTTTTCCTC CCCATTTAAA AGGATAGTAC 3360
CTACTCCCTC TAACCACTCT ACCCACTTCT TGAATGACAT TTTATCTCTC GGAAGAAACA 3420
AGGCTGTGAT GTAGTGACTA TTGTCTGTGT CTCTGTGTGT TGTCTGTCTT TGTCACAAT 3480
GTATTGAGG AGTTGAGTG CATTCATTT CTGTAATAAA G

Seq ID NO: 306 Protein sequence:

Protein Accession #: NP_005333.1

1 11 21 31 41 51
MAKGDPIKPK GKMSAYAFV QTCREHKKK NPEVPVNFAB FSKKCSERWK TMSGKEKSKP 60
80 DEMAKADKVR YDREMKDYGF AKGGKKKKDF NAPKRPPSGF FLPCSEFRPK IKSTNPGISI 120
GDVAKKLGM WNNLNDSEK PYITKAAKLK EYKEDVDADV KSKGKFDGAK GPAKVARKKV 180
EEEEEEEEEE EEEEEEREDE

Seq ID NO: 307 DNA sequence

Nucleic Acid Accession #: NM_022342

Coding sequence: 1..2178

	1	11	21	31	41	51	
	ATGGGTACTA	GGAAAAAAGT	TCATGCATTT	GTCCGTGTCA	AACCCACCGA	TGACTTTGCT	60
5	CATGAAATGA	TCAGATACGG	AGATGACAAA	AGAAGCATTG	ATATTCACCT	AAAAAAGAC	120
	ATTCGGAGAG	GAGTTGTCAA	TAACCAACAG	ACAGACTGGT	CGTTTAAGTT	GGATGGAGTT	180
	TTCCAGATG	CCTCCAGGA	CTTGGTTTAT	GAGACAGTTG	CRAAGGATGT	GGTTTCTCAG	240
	CCCTCCGATG	GCTATAATGG	CACCATCATG	TGTTATGGGC	AGACGGGAGC	TGGCAAGACA	300
	ACACCATGA	TGGGGGCAAC	TGAGAAATAC	AAGCACCGGG	GGATCCTCCC	TGTCGCCCTG	360
10	AGCAGGTTT	TTAGGATGAT	CGAAGAACGC	CCCACACATG	CCATCACTGT	GCGTGTTC	420
	ACTTGGAAA	TCTATAATGA	GAGCCTGTTT	GATCTCCTGT	CCACTCTGCC	CTATGTTGGA	480
	CCTCAGTCA	CACCAATGAC	CATCGTGGAA	AACCCCTCAAG	GAGTCTTCAT	TAAGGGCTTG	540
	CAGTTACCC	TCACAAGTCA	GGAGGAGGAT	GCATTACGCC	TCCTTTTGA	GGGTGAGACC	600
	ACAGGATTA	TAGCCTCCCA	CACATATGAAC	AAAAACTCTT	CCAGATCACA	CTGCATTTTC	660
15	CCATCTACT	TAGAGGCCCA	TTCCCGGACC	TTATCAGAGG	AAAAGTACAT	CACCTTCCAA	720
	TTAACTTGG	TGGATCTGGC	AGGCTCAGAG	AGGCTGGGGA	AGTCTGGGTC	TGAGGGCCAA	780
	TCCTGAAGG	AAGCCACCTA	CATCAACAAA	TCGCTCTCAT	TCCTGGAGCA	GGCCATCATT	840
	CCCTTGGGG	ACCAGAAGCG	GGACCAATC	CCCTTGGGC	AGTGAAGCT	CACCCAOGCT	900
	TGAAGGACT	CGTTAGGGGG	AAACTGCAAT	ATGCTCCTCG	TGACAAACAT	CTATGGAGAA	960
20	CTGCCCAAG	TAGAAGAAAC	GCTATCTTCA	CTGAGATTTC	CCAGCAGGAT	GAAGCTAGTC	1020
	CCACTGAGC	CTGCCATCAA	TGAAAAGTAT	GATGCTGAGA	GAATGGTCAA	GAACCTGGAG	1080
	AGGAAGTAT	CACCTACTCA	GCAGGAGCTG	GCTATCCATG	ACAGCCTGAC	CAACCGCAC	1140
	TTGTGACCT	ATGACCCCAT	GGATGAAATC	CAGATTGCTG	AGATCAACTC	CCAGGTGGCG	1200
	GGTACCTGG	AGGGGACATC	GGAGAGATC	GACATAATCA	GCCTTAGACA	GATCAAGGAG	1260
25	TGTTCAACC	AGTTCCGGGT	GGTCTGAGC	CAACAGGAAC	AGGAAGTGGG	GTCCACTTTG	1320
	GCAGGAAGT	ACACCTCAT	TGACAGGAAT	GACTTTGCG	CCATTTCTGC	TATCCAGAAG	1380
	CGGGGCTTG	TGGATGTTGA	TGGCCACCTA	GTGGGTGAGC	CTGAAGGACA	AAACTTTGGA	1440
	TCGGAGTCG	CCCTTTTCTC	TACCAAACTT	GGGAAGAAAG	CCAAGTCCAA	GAAGACATTC	1500
	AAGAGCCAC	TCAGGCCCGA	CACCCACCCC	TCCAAACCAG	TGGCCTTTGA	GGAGTTTAA	1560
30	ATGAGCAAG	GTAGTGAAGT	CAACCGAATT	TTCAAGAAA	ACAAATCCAT	CTTGAATGAA	1620
	GGAGGAAAG	GGGCCAGCGA	GACCAACAG	CACATCAATG	CCATCAAGCG	GGAGATTGAT	1680
	TGACCAAGG	AGGCCCTGGA	TTTCCAGAAG	TCACTACGGG	AGAAGCAAGG	CAAGTACGAA	1740
	ACAAGGGGC	TGATGATCAT	CGATGAGGAA	GAATTCCTGC	TGATCTCAA	GCTCAAAGAC	1800
	TCAAGAAGC	AGTACCCGAG	CGAGTACCAG	GACCTGCGTG	ACCTCAGGGC	TGAGATCCAG	1860
35	ATTGCCAGG	ACCTAGTGGG	TCAGTGTGCG	CACCGCCTGC	TCATGGAATT	TGACATCTGG	1920
	ACAATGAGT	CCTTTGTGAT	CCCTGAGGAC	ATGCAGATGG	CACTGAAGCC	AGGCGGCAGC	1980
	TCGGGACAG	GCATGGTCCC	TGTGAACAGG	ATTGTGCTC	TGGGAGAAGA	TGACCAAGGAC	2040
	AATTACAGC	AGCTGCAGCA	GAGGGTGCTT	CCTGAGGGCC	CTGATTCCAT	CTCCTTCTAC	2100
40	ATGCCAAGG	TCAAGATAGA	GCAGAAGCAT	AATTACTTGA	AAACCATGAT	GGGCTCCAG	2160
	AGGCACATA	GAATAATG					

Seq ID NO: 308 Protein sequence:
Protein Accession #: NP_071737

	1	11	21	31	41	51	
	MGRKKVHAF	VRVKPTDDFA	HEMIRYGDDE	RSIDHLLKDD	IRRGVVNNQQ	TDWSFKLDGV	60
	LHDASQDLVY	ETVAKDVVSQ	ALDGYNGTIM	CYGGTGAGKT	YTMGATENY	KHRGILPRAL	120
50	QOVFRMIEER	PTHAITVRVS	YLEIYNESLF	DLSTLPYVG	PSVTPMTIVE	NPQGVFIKGL	180
	SVHLTSQEDD	APSLFPEGET	NRILASHTMN	RNSRSHCIF	TIYLEAHSRT	LSEKYITSK	240
	INLVDLAGEE	RLRGSSEBQ	VLKEATYINK	SLSFLEQAI	ALGDQKRDEI	PFRQCKLTHA	300
	LKDSLGGNCN	MVLVTNIYGE	AAQLEETLSS	LRFASRMKLV	TTEPAINEKY	DAERMVINLE	360
	KELALLKQEL	AIHDSLTNRT	FVTYDPMDEI	QIABINSQVR	RYLEGTLDDEI	DIISLRQIKE	420
55	VFNQFRVVLG	QQQGEVESTL	RRKYTLIDRN	DFAAISAIQK	AGLVDVDGHL	VGEPEGQNFQ	480
	LGVAPFSTFP	GKAKSKKTF	KEPLRPDTPP	SKPVAPEEFK	NEQGSSEINRI	PKENKSLINE	540
	RRKRASSETQ	HINAIRREID	VTKEALNFQK	SLRKEQKQYE	NKGLMIIDEE	EPLILKLKLD	600
	LKKQYRSEYQ	DLRLDLRAEQ	YCQHLVDQCR	HRLLMEDPIW	YNESFVIPED	MQMALRPGGS	660
	IRPMVFPVNR	IVSLGEDDDQ	KFSQLQQRVL	PEGPDSISFY	NAKVKIEQKH	NYLRTMMGLQ	720
60	QAHRK						

Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
65	TTTTTTTTTT	TTTTTTTAA	TGCCTGCTGT	CATGCTCTGT	CTACCAGGGT	GAATTTCCAA	60
	AAATTTCTGC	ATAGCAATTT	TAGCCAAAAC	TATATATGTT	CTGGGGAGGA	TAGGCATAGG	120
	CACATTGAAG	ACCAAAGGAA	AGAGTGAAGA	AGTGTAGTTG	GSTCAITGTT	AATGGATGTT	180
70	TAGATTGTCA	AGAAAAGTGG	GCCAGAGGCC	CCACCTCACA	CTAGGACGGC	AATTGCCTCT	240
	CATTAGTATC	TCAGGCACCA	TGGGTCTTAT	TTGGTGTGAT	AAGAAACACC	CTCAACAAAG	300
	TAATGAACCC	TCAGCCTCCA	GCTTCTCTTC	TTGGGATTC	TTCTTAGGGC	CTCCTTTTTC	360
	CTTTTATGTT	TCCAGTACCC	TGAATTTCTT	ATTCCCATCC	CCCATTAATA	TCTGCTTCAA	420
	AGAAAAACA	AGAAGGACAC	ATTCACTTTA	AGATCCAAAT	GAATGATAAG	AGCTTAAAC	480
75	ATTATACCTA	TCAGTATTAT	TTGCATTTTT	ATAGAAACCA	AAACCATATT	TCAACAA	

Seq ID NO: 310 DNA sequence
Nucleic Acid Accession #: NM_018622.2
Coding sequence: 1-1140

	1	11	21	31	41	51	
80	ATGGGTGGC	GAGGCTGGGC	GCAGAGAGGC	TGGGGCTGCG	GCCAGGCGTG	GGGTGCGTGG	60
	GTGGGGCGGC	GCAGCTGCCA	GGAGCTCACT	GCGGTCTTAA	CCCCGCCGCA	GCTCCTCGGA	120
	CGCAGGTTTA	ACTTCTTTAT	TCAACAAAAA	TGGCGATTCA	GAAAGCACC	CAGGAAGGTT	180
85	GAACCTCGAA	GATCAGACCC	AGGCACAAGT	GGTGAAGCAT	ACAAGAGAAG	TGCTTTGATT	240
	CCTCCTGTGG	AAGAAACAGT	CTTTTATCCT	TCTCCCTATC	CTATAAGGAG	TCTCATAAAA	300
	CCTTTATTTT	TTACTGTTGG	GTITACAGGC	TGTGCATTGG	GATCAGCTGC	TATTTGGCAA	360

5 TATGAATCAC TGAAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTTG 420
 GATAGCATAA GACCACAAA AGAAGGAGAC TTCAGAAAAG AGATTAAACA GTGGTGAAT 480
 AACCTAAGTG ATGGCCACGG GACTGTGACA GGTATTATAG CTGCAATGT CCTGTATTTC 540
 TGTTTATGGA GAGTACCTTC TCTGCAGCGG ACAATGATCA GATATTTTCA ATCGAATCCA 600
 GCCTCAAAGG TCCTTTGTTC TCCAATGTTG CTGTCAACAT TCAGTCACTT CTCCTTATTT 660
 CACATGGCAG CAAATATGTA TGTTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG 720
 GGTCAAGAGC AGTTTATGGC AGTGTACCTA TCTGCAGGTG TTATTTCCAA TTTTGTCACT 780
 TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGCCATC 840
 10 ATGACAGTCC TCGCAGCTGT CTGCACTAAG ATCCCAAGAG GGAGGCTTGC CATTATTTTC 900
 CTTCGATGT TCACTGTCAC AGCAGGGAAT GCCCTGAAAG CCATTATCGC CATGGATACA 960
 GCAGGAATGA TCCTGGGATG GAAATTTTTT GATCATGCGG CACATCTTGG GGGAGCTCTT 1020
 TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACTGATTT GGAAGAACAG GGAGCCGCTA 1080
 GTGAAATCT GGCATGAAAT AAGGACTAAT GGCCCCAAAA AAGGAGGTGG CTCTAAGTAA

15

Seq ID NO: 311 Protein sequence:
Protein Accession #: NP_061092.2

20 1 11 21 31 41 51
 MAMRWQAQRG WGCGQAWGAS VGGRSCEELT AVLTPPQLLG RRPNFFIQKQ CGFRKAPRKV 60
 EPRRSDPGTS GEAYKRSALI PPVEETVPYF SPYPPIRSLIK PLPPTVGFVG CAFGSAALWQ 120
 YESLKRVRQS YFDGIKADWL DSIRPQKEGD FRKEINKMWN NLSGQRTVT GILANVLVP 180
 25 CLWRVPSLQR TMIRYPTSNP ASKVLCSFML LSTPSHSLF HMAANMYVLW SPSSIVNII 240
 GQBFMAVYL SAGVIANFVS YLGKVAATGRY GPSLGAAGAI MTLVAAVCTK IPEGLALIF 300
 LPMEFTTAGN ALKALIAMDT AGMILGWKFP DHAAHLGGAL FGIWVVTYGH ELIWKREPL 360
 VKIWHBIRTN GPKKGGGSK

30

Seq ID NO: 312 DNA sequence
Nucleic Acid Accession #: NM_000625
Coding sequence: 195..3656

35 1 11 21 31 41 51
 CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG 60
 CACAGTCTCT TCTCTGGTGT GACTGTCTTT ACCCGGGGGA GGCAGTGCAG CCAGCTGCAA 120
 GCCCCACAGT GAAGAACATC TGAGCTCAAA TCCAGATAAG TGACATAAGT GACCTGCTTT 180
 40 GTAAAGCCAT AGAGATGGCC TGTCTTGGGA AATTCTCTGT CAAGACCAAA TTCCACCAGT 240
 ATGCAATGAA TGGCGAAAAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT 300
 CCACTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT 360
 CCGCGCAGCC CTTCTGGGAG ACGGAAAGA AGTCTCCAGA ATCTCTGGTC AAGCTGGATG 420
 CAACCCCAAT GTCTCCCTCA CGGCATGTGA GGATCAAAAA CTGGGCGCAG GGGATGACTT 480
 45 TCCAGACAC ACTTCAACAT AAGGCCAAAG GGATTTTAAC TTGCAGGTCC AAATCTTGCC 540
 TGGGGTCCAT TAGTACTCCO AAAAGTTTGA CCAGAGGACC CAGGGACAAG OCTACCCCTC 600
 CAGATGAGCT TCTACCTCAA GCTATCGAAT TTGTCAACCA ATATTACGGC TCCCTCAAAG 660
 AGGCAAAAT AGAGAAACAT CTGGCCAGGG TGGAAAGCGT AACAAAGGAG ATAGAAACAA 720
 CAGTAACCTA CCAACTGACG GGAGATGAGC TCATCTTCGC CACCAAGCAG GCCTGGGCGA 780
 50 ATGCCCCCAG CTGCATTGGG AGGATCCAGT GGTCCAACT GCAGGTCTTC GATGCCCGCA 840
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 55 AACTTAACAG GGAAGGGCTG GGGTGTGAAA AAGAAGATT TATGAAACC ATTGGTAATT 3300
 TTTATTTTGT ATTTTGGGA CTGCACTATC CTGTTCAAGA AGACATGTGA ACTTGGTTCA 3360
 GTCCAAATGG GGAATTTGAT AAACAGTGC TCTCCATTAG AAATATGGTG CAAGCCACAT 3420
 ATGTAATTTT AAATATTCTA GTAGCCACAT TAATAAAGTN AAAAGAAACA AAAAAAATA 3480
 AA

60 Seq ID NO: 317 Protein sequence:
 Protein Accession #: NP_004464

1 11 21 31 41 51
 65 FKHLTHYROI DTRANSCRIP TIONFACTOR TTFMTAESGP PPPQPEVLAT VKEERGETAA 60
 GAGVPGEATG RGAGRRRRKR PLQRKPPYS YIALIAMAIA HAPERRLTLG GIYKFITERP 120
 PFFRDNPKNW QNSIRENLTL NDCFLKIPRE AGRPGKGNVW ALDPNADMF ESGSPLRRRK 180
 RPKRSLDSTY PAYMEDAAAA AAAAAAATA AAAAAIIFGA VPAARPPYPG AVYAGYAPPS 240
 70 LAAPPPVYYP AASPGPCRVF GLVPERPLSP ELGPAPSGPG GSCAFASAGA PATTTGYQPA 300
 GCTGARFANP SAYAAAYAGP DGAYPQAGS AIFAAAGRLA GPASPPAGGS SGGVETTVDF 360
 YGRTPSQQPG ALGACNPPGG QLGASAGAY HARHAAAYPG GIDRPFVSAM

75 Seq ID NO: 318 DNA sequence
 Nucleic Acid Accession #: NM_005688
 Coding sequence: 126..4439

1 11 21 31 41 51
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 AGAAGATGAA GGATATCGAC ATAGGAAAG AGTATATCAT CCGCAGTCTT GGGTATAGAA 180
 GTGTGAGGGA GAGAACAGC ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA 240
 85 GGAGAACTCG ACCGTTGGAA TGCCAAAGAT CCTTGGAAAC AGCAGCCCGA GCCGAGGGCC 300
 TCTCTCTTGA TGCCCTCCATG CATTCTCAGC TCAGAACTCT GGATGAGGAG CATCCCAAG 360
 GAAAGTACCA TCATGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACAGC 420
 ACCCAGTGA CAATGCTGGG CTTTTTCTCT GTATGACTTT TTCGTGGCTT TCTTCTCTG 480

	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
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	AAGTGTGGCC	AGAGCGTGCT	TCCCTGCGAA	GGGTGTGTGT	GATCTTCTGC	CGCACCCAGGC	660
5	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCCAGCCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTIAGT	GCTGGGGCTC	CTCCTGACGG	AAATCGTGGG	GTCTTGGTGG	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGGGGGG	GGCCATCCTA	ACCATGGCAT	900
	TTAAGAGAGT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
10	TTTGTCCAA	CGATGGGCAG	AGAAATGTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCAATG	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCCCTGG	ATCAGCTGTT	TTTATCCTCT	TTTATCCAGC	AATGATGTTT	GCATCAOCCG	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CGGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
15	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTGCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTTGGGTGTG	GCTCCCATTT	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTCATAT	GACCCCTGGG	TTCGATCTGA	CAGCAGCACA	GGCTTTTACA	GTGGTGACAG	1440
	TCCTCAATTG	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTTCACTAAG	TCCCTCTCAG	1500
	AAGCCTCACT	GGCTGTGTAC	AGATTTAAGA	GTTTGTCTCT	AATGGAAGAG	GTTCACATGA	1560
20	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAATAATGCC	ACCTTGGCAT	1620
	GGGACTCTCT	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGGCGTGGCT	GGCAGAGGCT	AAAGGCCACC	TCTCTCTGGA	CAGTGAAGAG	CGGCCAGTGC	1800
	CGAAGAGAGA	AGAAGGCCAG	CACATCCACC	TGGGCCACCT	GGCTTACAG	AGGACACTGC	1860
25	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACCTGGTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCATC	TCAGCCATTT	TAGGCCAGAT	GACGCTCTTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAA	CTGTGTCTGA	2100
	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGAGATTG	2160
30	GAGAGCGAGG	AGCCAACTCT	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GGCCGGGCTC	2220
	TGTATAGTGA	CAGGAGCATC	TACATCTCTG	ACGACCCCTC	CAGTGCCCTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGTCTTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
35	CCATTTTAA	TAACCTGTGT	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCAAGTG	TTTACAGGAAG	AAGTCAACAAG	ACAAGGGTCC	TAAACACGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAGTGCC	CTGTGAGTGA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCCTGGTTAT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCCTC	AGCACTGGT	2760
40	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAAACCCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGCT	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCATG	CTGATCTCTG	AAGCCATTGG	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGGG	AGCTTCTCCG	CGGCTGCAAT	ACGAGCTTTT	CGGAAGGATC	CTTCCGAAGC	3000
	CTATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
45	TGGATGAAGT	TGACGTGGCG	CTGCCGTTCG	AGGCCGAGAT	GTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCTCTGT	CATCTCTTTT	TCAGTCTCTG	ACATTTCTCT	CAGGGTCTCT	ATTCCGGAGC	3240
	TGAAGGCTCT	GGACAATATC	ACGCACTCAC	CTTTCTCTCT	CCACATCAGG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTCCTGCAG	AGATAACAGG	3360
50	AGCTGCTGGA	TGACAACCAA	GCTCCTTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACACC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCAAGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAAAGGGGCT	GTTCAGATTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTACCTT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAAGCACCT	GCCGAATTTA	3660
55	AGAACAAAGC	TCCCTCCCCC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGG	3720
	AGATGAGGTA	CGGAGAAAAA	CTCCCTCTTG	TCCTAAAGAA	AGTATCTCTC	ACGATCAAAC	3780
	CTAAGAGGAA	GATTGGCAAT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
	CCCTCTTCGG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGGCGAC	CTCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCGGTGTC	3960
60	TGTTCAAGTG	CACCTGTGAG	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAAGCCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTGA	AGTATGGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGACAGCT	4260
65	GTACCATGCT	GACCATTGCC	CATCGCTCTG	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCC	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAAOGACA	4380
	GTTCGGGATT	CTATGCCATG	TTTGTGCTG	CAGAGAACAA	GGTCTCTGTC	AAGGGCTGAC	4440
	TCCCTCCCTGT	TGACGAAGTC	TCITTTCTTT	AGAGCATTGC	CATTCCCTGTC	CTGGGGGGGG	4500
	CCCTCTCTGA	CGTCCCTCTA	CGAAACCTTT	GCCTTTCTCG	ATTTTATCTT	TGCGACAGCA	4560
70	GTTCGGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAAATA	AGCACTGTGC	TATTAACAGT	GCATATTCTT	TTCTATCATT	TTTGTACAGT	4860
75	TGCTGTACT	AGAGATCTGG	TTTGTCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTCTT	4920
	CTCTAGCTGG	TGGTTTCAGG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGGC	CTCCGACAGC	CCCTCTGCTC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGACG	AGCGCGGTGA	GTCTCAGGGG	CTCTGCTCTT	5100
	CTGTCTCTGT	GTCATTTACT	GTTCGTGTCA	GGAGAGCAGC	GGGGGGAAGC	CCAGGCCCTT	5160
80	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTGC	TCTTCTTTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCACTGCC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
	GTGGTTTCCA	AGCCCTGGAG	CCAACTGCTG	CTTTTGTAGG	TGGCACTTTT	TCATTTGCTT	5400
	ATTCCACAC	CTCCACAGTT	CAGTGGCAGG	GCTCAGGATT	TGCTGGGTCT	GTTTTCTCTT	5460
	CTCACCGCAG	TGCTGCGACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
85	CAGCTCTTGC	TAACTCAGTG	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	GCTGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAAACCCC	TTTGTGCTGT	5640
	GGGGCTGGTA	GCTCAGGTGG	GGGTGGTCA	TGCTGTCTAT	AGTTGAATGG	TCAGCGTTGC	5700

ATGTCGTGAC CAACATAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
CAAAATCTG AAAAAATGAA TAAAAATTATT TTGGATTGTT TAAAAAATAA AAAAAAATAA 5820
AAAAAATAA AAAAAAATAA

5

Seq ID NO: 319 Protein sequence:
Protein Accession #: NP_005679

10 1 11 21 31 41 51
MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKPRR TRPLECQDAL ETAARAEGLS 60
LDASMHSQLR ILDEEHFKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCN TFSWLSLAR 120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQELNEV GPDAAASLRRV VNIPTCTRLI 180
LSIVCLMITQ LAGPSGPAPM VKHLETTQA TESNLQYSL LVLGLLLTEI VRWSLALTN 240
15 ALNYRTGVRL RGAILTMAPK KILKLNKIE KSLGELINIC SMDGQRMPEA AAVGSLLAGG 300
PVVAAILGMYI NVVILGPTGF LGSADVILFY PAMMFASRLT AYFRRCVAA TDERVQKME 360
VLTVIKFIKM YAWKAPSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VLAHVVTFSV 420
HMTLGFDLTA AQAPTIVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEVEVMIK 480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTZHQ 540
20 VLAQYKGLL LDSDERPSP EEEGKHILG HLRLQRTLHS IDLEIQEGKL VGIQSVGSG 600
KTSLSAILG QMTLLBGSIA ISGTFAYVAQ QAWILNATLE DNILFGKEYD EERYNSVLNS 660
CCLRPDLAIL YANRFLRIGE RANLSSGGOR QRISLARALY SDRSTIYLD PLSALDAHV 720
NHIFNSAIRK HLKSKTVLTV THQLQYLVD DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
FNNLLGGETP FVEINSKKEK SSSQKKSQDK GPKTGSVKKE KAVKPEBQQL VQLEEKQGS 840
25 VPWSVYGVYI QAAGPLAPL VIMALFPLNV GSTAFSTNWL SYWIKQSGSN TTVTRGNETS 900
VSDSMKDNPH MOYFASIDAL SMAMVLILKA IRGVVVFVGT LRASSRLHDE LFRILRLSPM 960
KFFDTPTTGR ILNRFPSKMD EVDVRLFPQA EMFIQNVILV PFCVMIAGV FFWFLVAVGP 1020
LVILPSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLEHYQEL 1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HQQIPPAYAG LAISYAVQLT 1140
30 GLPQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWQPE GEVTFENAE 1200
RYRENPLVLV KKVSFITKPK EKIGIVGRGT SGKSSSLGMA FBLVELSGGC IKIDGVRISD 1260
IGLADLRSLK SIIPQEPVLP SGTVRNLDL PNFQYTEDQIW DALERTHMEK CIAQLPLKLE 1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAPADCT 1380
35 MLTIAHRLHT VLGSRLIMVL AQGVVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKG

Seq ID NO: 320 DNA sequence
Nucleic Acid Accession #: AK022089.1
Coding sequence: 181-1488

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45 CCCCACCCCC ACCCTCAGAT CACTTTAAGA TAATTTCTTT ATTGTTTTCG CCGACAGACC 180
ATGCTCCCTT TTGGAAGAAA CTGCTAAAG ACTCGGCATA AAAACAGATC TCCAACTAAA 240
GACATGAGTT CAGAAGAGAA GGAAATTTGT GTTTGGGTTT GCCAAGAAGA GAAGCTTGTC 300
TGTTGGGCTGA CTAAACGCAC CACCTCTGCT GATGTCATCC AGGCTTTGCT TGAGGAACAT 360
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50 GAGAAGTCGA GAGCTCCGA AAGGTTCTT CCTCCACTAA CTAGAATCCT GAAGCTTTGG 480
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55 GTACAGGAAA CTTTCCGAAA ACTGGCTAAA ATTAAGCAGG ACACAGTTTC TCATGATCGA 720
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60 AGCGAAGTTG ATGGAATTGA ACAGCTGGAA GAACGACTGA AATATTACCG AATACCTATT 1020
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GATGCGGAAG GGGAGCTGCG AAGTGAACGT GAAAGCTCTA ATTTAGAGAG TGTTAAGTGT 1140
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65 GCCAAGGAA TCAATCTACT TCACATTAGC AACAAAGATG GGTGCCAGTT AAAGGAAAAC 1320
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GTATTTAGCA ATTACACAAA TGACACAGAC TCGGACACTG GTATCAGTTC TAACCAAGT 1440
CAGGACTCCG AAACAACAGT AGGAGATGTG GTGCTGTTGT CAACATAGTT CCAATGGCTC 1500
70 CTTTCTGACC TGCTTTTCA TTTTAATGTT TGTTTAATTT AATAGGAAAC CTCATTTTAA 1560
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GAAATGTGTT GTTCTG

Seq ID NO: 321 Protein sequence:
Protein Accession #: NP_005438.1

75 1 11 21 31 41 51
MAPFGRNLLK TRHKNRSPTR DMDSEEBIV VWVCQEEKLV CGLTKRTTSA DVIQALLEEH 60
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80 LPVPLWRTAE AKLVONTKEL WELSPANMYK TLPPDKQKRI VRKTFRLAK IKQDVTSHDR 180
DNMBTLVHLI ISQHTTHQQ VKRMKELDLE IEKCEAKFHL DRVENDGENY VQDAYLMPFS 240
SEVEQNLDIQ YEENQTLDEL SESDGIQBLE ERLKYRILI DKLSASIEKE VKSCIDINE 300
DABGEAASEL ESSNLESVKC DLEKSMKAGL KHSLSLGIQ KEIKYSDSLI QMKAKYEYEL 360
AKEFNSLHIS NKDGCQLKEEN RAKESEVPSS NGBIPPTQR VPSNYTNDTD SDTGISSNHS 420
85 QDSETTVGDV VLLST

Seq ID NO: 322 DNA sequence
Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

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	CTGGTGGTGG	TAGTGGGCGT	TTATATTTCG	GTTCCTTTTC	ATTCATTCTC	AAATCTCTTA	240
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10	AGAGCAAGAG	GAGGACATGG	AGATGAAGAA	GAAGATTAA	CTGGAGTTAA	GGACAGATC	360
	CCCGGAGGAG	GTGACAGAGT	TAGTCCTTGA	TAAATGCTTG	TGTGTCAATG	GGGAAATTGA	420
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	TTGCTGGCC	CGGCTTCCCA	GCTTAAATAA	ACTTCGAAAA	TTGGAGCTTA	GTGATAATAT	540
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	TGTTGAAGAG	GCGGAAGAAG	AGGAAGAAGA	GGAAGAAGGA	GCTCTCGAG	GCGAGAAGAG	1080
	GAAACGAGAT	GCTGAAGAGC	ATGGAGAGGA	AGAAGATGAC	TAGATCATTC	TAAGACCAGA	1140
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	TTGCCCTATC	ATTCCTAATA	AGAACTAGTC	TGTTAATGAT	CATATTGTAT	GTAGAGAAAA	1320
	ATTTTCAATG	CTGCCCATTG	TGGAATTCCT	TAGCAATTTA	TTTAGACTTA	ATTTTTTAAA	1380
	TTCAAGCTTA	CTGTATTAGT	CATTTTATAG	CCATAATTA	AACATGATCA	CTTTTAAACA	1440
	GGTGTAGTAT	GGTGCATTTT	ATTCCTTATT	TATAGATTAA	CTGAAATTAC	AGTTTGCAT	1500
30	AATATAAAT	GACAAATAGT	TCTTGAGTGG	TAAAGTGGTT	ATTTTTTTAG	AGGTGATCCA	1560
	GGAATCTTTA	GTTTGAAGGC	AGTTACCTTT	TTTTTTTTTT	TTTTTTTTTG	ACTAAGAGTG	1620
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	TAGTGGTAC	TGATAAGATT	TTATTTTGA	AGGAAAAATT	GCTTATACTA	AGTCCAGAGA	1800
35	CATGAGGTG	AGCCCTTTTG	TCAGGCTGCA	AATCATGACA	TGCCGATGGT	TGTTTATTTT	1860
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40	TCTCCTTACC	ATAAATGTTT	CTTGGTTGAC	AACATCTAAG	ACAATATTAG	TGGGATGAAG	2160
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	TAAATGACAT	TAAATGGAAT	ATACTAGGCA	GCTGGAAGAG	TATTTGAAGC	TAAATTGACA	2400
45	TTAAATTAAC	GATTTGTTT	CAAGTGGATG	TCCATTAAAA	GTAGAAAAAT	ATTTGGGATA	2460
	AGTGAGTGTG	TGTTTCTCTA	CATGGCTACT	AAATAAAATA	TAAATGATAT	ACAAGTATAT	2520
	CTCCTCTTTT	GCTATGGAGG	CTCCATGTTT	AAGGCAATGG	CTTTTAAAT	CTTGGCTATC	2580
	TAAAAATTTT	TCCCTTGTGT	TGAAATATTT	GTAAGTTTTT	AAGAAAGTTAG	TGTCAGCAAA	2640
	TTAATGGAAG	TTATGCTTCT	ATACTGGGAC	ATATTTAAAT	ACTGAGTATA	GTACTGCTGC	2700
50	TACTGCTTCT	ACAAATGATA	ATGATGACT	TGGTGTTTTA	AAGTAAAAAT	TATGATGTTA	2760
	CTGTGGAGA	AACATAAAAT	GTGTACAAAC	TGACCGAAAG	AAAACCCCTG	GGGATAAGTT	2820
	TAGTGAGGGG	ATTGGAATCC	CCAAAAAGAT	AACATTTTTC	TTCTGCTTTT	AAAAACTGAA	2880
	ATTCCTGTGT	CTAGTCTCTA	ACAATTTCTA	TTACATACTA	TGCCAGATTA	CAAAATCTTT	2940
	ATTTTAAATA	TGAAATCTAT	ATATTGACTT	TCTTATCAAT	CATCTTACTG	TGCAATCAAA	3000
55	ATTAGATAC	TTTGGTTTGA	AAACAACACT	TAGAGCCTCC	AGATAACTTT	TAAGACTTAT	3060
	TTAGCTTTGT	GGGTGTGATT	TTTATGCAAA	TAAATGAGGG	TGGGTTTAT	ATTTTGTAGA	3120
	AGTTTTCGGT	CCTATTTTAA	TGCTCTTTGT	ATGGCAGTAT	GTATATATTG	TGTTAAGTTC	3180
	CTCAAGAATC	TCTTAAAAAA	CTTTGAAGTT	AATACTTTTG	TGCAACTGTG	TTTTGAATAA	3240
60	AGCCATGACA	GTGTTAAAAA	CAAAAC				

Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

	1	11	21	31	41	51	
65	MEMKKKINLE	LRNRSPEEVT	ELVLNCLCV	NGEIEGLNDT	FKLEFLSMA	NVELSSLARL	60
	PSLNKLRLKE	LSDNIISSGL	EVLAKECPNL	TYLNLGSKNI	KDLSTVEALQ	NLKNLKSIDL	120
	FNCEITNLED	YRSIFELLQ	QITYLDGFDQ	KDNEAPDSEE	EDDEDGEDDD	EEEEENBAGP	180
	PEGYEEEEEE	EEDEDEDEDE	DEDEAGSELS	EGEESEVLSY	LMKEEIQDEE	DDDDYVEBGE	240
70	EEEEEEBGL	RGEKRKRDAE	DDGEEEDD				

Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224..2722

	1	11	21	31	41	51	
75	TCCTCTGCGT	CCCGCCCGCG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGGCGC	60
	GCCCGAGCCC	GAGCCCGCGG	CCCGGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGGCGCA	120
80	CCATGGCGCG	CGAGCCGGCG	TGACCGGCTC	CGCCCGCGGC	CGCCCCCGAG	CTAGCCCGGC	180
	GCTCTCGCGG	GCCACACGGA	GCGCGCGCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGCGAG	240
	CAGCTCGCGG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCCT	GCGGCCCCCA	300
	ACGCGGCCCC	GCGGGCTCGG	TGCTTGCCAG	CGCCCGCGGC	CGCACGCGCG	CCTGCGGCTC	360
	GCTTCTGCTC	CTTCTCTGCT	TGCTCTGCTC	CGCCGCTCTG	TCCCGGCCCC	GCGGCTGGGG	420
85	GGCTGCTGCG	CCAGAGCGTC	GCATTTGGAA	TGAAACTGCA	GAAAAAATTT	TGGGAGTCTC	480
	GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
	AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600

	AAGSCCTTAT	CAGGTCCTTG	ACACAAAGGG	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
	CCATCTGGCC	CAGGCAAGCT	TCGAGATTTA	AGCCTTGGCC	TCCAAATTCA	TTCTTGACCT	720
	CATACCTGAAC	AATGCTTTTGT	TGCTGTTCTGA	TATGTGGTAG	ATTCACTACG	AAGATGGGAA	780
5	ACCACAGTAC	TCTAAGGGTG	GAGAGCATCG	TTACTACCAT	GGAGACATCA	GAGGCGCTCA	840
	AGACTCCAG	GTGGCTCTGT	CAACCTGCCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
	CTTGTGTGAT	ATGATAGAGC	CATAGAGCTG	GGTTCATGAT	GAGAAAAGCA	CAGGTGACC	960
	ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAAAATGAAG	ATTCTCACTAT	1020
	GGAAAGAGGT	GACCAAGTGG	CCTTTCTCTC	TGGAATACAG	TGGTGAAGAA	GAAGGAAGAG	1080
10	AGCAGTGAAT	CGCATCACTG	GTATATTGTA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
	TAATGATCAC	AAAACTGATG	AGAAGCATGG	CTCTCTCAT	GCACATACCA	CAAGCTTTGC	1200
	AAAGTCGGT	GTCAACCTTG	TGGATTCTAT	TTACAGAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
	CTGTGGGCT	GTAGAGACCT	GGACTGAGAA	GCAGCATAGT	GACATACCA	CCAACTCTGT	1320
	GCAGATGCTC	CATGAGTTCT	CAAAATACCG	GCAGCCGATT	AAGCAGCATG	CTGATGCTGT	1380
15	GCACCTCATC	TGCGGGTGCA	CATTCTACTA	TAAAGAGAGT	AGTCTGAGTT	AGTTTGGAGG	1440
	TGTCGTGTTT	CGCACAAGAG	GAGTGTGGTG	GAAGAAGTAT	GGTCTCCAA	TCCGAGTGGC	1500
	ACAAGTATTA	TGCGAGAGCC	TGGCTCAAAA	CTTGTGGAAT	CAATGGGAAC	CTCTAGCAG	1560
	AAAGCCAAA	TGTGACTGCA	CAGAACTCTG	GGGTGGCTGC	ATCATGGAGG	AAACCAAGGGT	1620
	GTCCCAITCT	CGAAAAITTT	CAAAGTCGAG	CATTTGGAG	TATAGAGACT	TTTTACAGAG	1680
20	AGGAGGTTGA	GGTCGCCTTT	TCAACAGGCC	AACAAGAGTA	TTTGAAGCCA	CGGAACTGTG	1740
	AAATGGATAC	TGCGAAGCTG	TGGAGGAGTG	TGATTTGGT	TTTCATGTG	AATGCTATGG	1800
	ATTATGCTGT	AAGAATATGT	CCCTCTCCAA	CGGGGCTCAC	TGCGAGCAGG	GGGCTCCGCT	1860
	TAAACAATAC	CTAGTCTTCT	TTACAGACAAG	AGGGTATGAA	TGCGGGGCTG	CTGTGAAGCT	1920
	GTGTGATATT	ACTGAATATT	GTACTTGAGA	CTGTGTCAG	TGCCCCACCA	ATCTTCAATA	1980
25	GCAGAGCGGA	TACATGTGCA	ATCAAAATCA	CGGCGCTGTC	TACAAATGGG	ATGCGCAAGC	2040
	CAGAGACAAC	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
	CTATGAAAG	CTGAATACAG	AAGGCACATG	GAGGGGAAAC	TGCGGGAGG	ATTGGAGACCT	2160
	GTGGATTTCAG	TGCAGCAAA	ATGATGTGTT	TGTGGGATT	TTACTCTGTA	CCCATCTTAC	2220
	TGAGACTCCA	CGTATTGGCT	AACCTCAGGG	TGAGATCAAT	CCAACTTCCT	CTTACCATCA	2280
30	AGGCGGGGT	ATTGACTGCA	GTGGTGCCCA	TGTGATTTTA	GATGATGATA	CGGATGTGGG	2340
	CTATGTAGAA	GATGGAACGC	CATGTGGCC	GTCATATGAT	TGTTAGATG	GGAGATGCTT	2400
	ACAAATTCAA	GGCTTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AGATGCTGCT	2460
	AGGCAATGGG	TGTTGTAGTA	ATGAAGCCAC	TGTCATTGTT	GATTTCACCT	GGGCAGGGAC	2520
	AGATTGTGAGT	ATCGCGGATC	CAGTATGAGAA	CTCTCAOCCG	CCCAAGGATG	AAGGACCCAA	2580
35	GGGCTCTAGT	GCACCAATC	TCATATAAGG	CCTCATAGCT	GGTGCCATCT	TGTTAGCAGC	2640
	TATTTGCTTT	GGGGGCCACG	GCTGGGGATT	CAAAAATGTC	AAGAAGAGAA	GCTGTGATCT	2700
	TACTGACCAA	GGCCCCATCT	GAACTCAGCT	CGCTGAGTGT	ACACCGCCTT	GCATCTGTTG	2760
	ATTCTGGGTA	TGACATACTC	GCAGCAGTGT	TACTGGAACT	ATTAAAGTTG	TAAACAAAC	2820
	CTTTGGGTTG	TATGACTACT	GGAGCTAAAG	TGTGGGTGAC	AAGGATGGGG	TAAAGAGAAA	2880
40	CTGPTCTCTT	TGGAATAAAT	GTCAAAGAAC	ACCTTTCACC	ACCTGTCAAT	AAACGGGGGA	2940
	GGGGGCCAAA	GACCATGCTA	TAAAGAAAGC	TGTTCCAGAA	CTCTTTTTTT	TCCCTAATGG	3000
	ACGAPAGCA	AACACATGCA	AAAAAATTA	ATGCAATAAA	GGAACTCATTA	AAAA	

[illegible]

	Seq ID NO: 326 DNA sequence									
	Nucleic Acid Accession #: AK074418.1									
	Coding sequence: 244-1515									
	1	11	21	31	41	51				
70	CTTCTCCAA	GACGGCGCGG	CATGCTCTCC	TCCTCTGCCA	GTCCTCTCCA	CCACTCTCTA				60
	ACCTGAGAGC	CTGTGGAATC	TGCCCGTCTC	CCCTCTCTCA	TCAGACACAC	CTGCCTAGGA				120
	AACAGATGGA	AAATGATGAG	GACCGGTGAG	TGACTTGCTG	CTAAAGTTTA	TACCAAGATC				180
	AAATGACAGA	GCTGGAGTGT	TGCTGTGCTG	GGAAGGAGCT	TCGGAAGTCT	TCTAAGGAGA				240
	GTCATGGCGT	ATTACGAGGA	GCCTTCAAGT	GAGACATGCA	TCATCAAGTT	CAAAGAGACG				300
	GATCTTACCA	CTTTGCGGGA	TCACTTGCGT	AGCATGCGCC	GGAGCTTTAA	GGATGAGACA				360
75	TTCCCGCAG	CAGATTCTTC	CATAGGCCAG	AGAGCTGCTC	AGGAAAAAGC	CCCTCCAAAT				420
	TGTATATGGA	AGCGGCCACA	GGATCTACCA	GGGGGTCCTC	CTCACTTCAT	CCCTGGATAGT				480
	ATAGACGAT	TTGACTTCCA	ACAAGGAGGC	CAGCTGACTC	GCTGGTTGCT	GCGACGACTG				540
	GGATCGTTGA	CTCAGACATC	ACAGTACAGG	CAGAGAATCC	TGATGGTCCA	AAGCTTTTCA				600
	CACCAAGTAT	CTGGCATTTT	CGTTTTCCGG	TTCTGGCAAT	GTCGCCAAGT	GCTGGGAAGT				660
80	GTGATGTGAT	ACCGCCTAAC	TGTCCAGGGA	GATAAATGCT	CTTTTGTGGT	TCCTGCGCAC				720
	CAAAACCAAG	AGTTTGTAGC	CTGCGTGCTG	GAGAAGGCGT	ATGCGAAGCT	GCTCGGATCC				780
	TATTCGAGT	TGCACTATGG	CTTCTCGAG	GATGCCCTGG	TGGACCTCAC	AGGAGCGGTG				840
	ATCACCAACA	TCCATTCTGA	CTCTTCCGCT	GTCGACCTGG	TGAAGGCAGT	GAAGACACAG				900
	ACCAAGCCAG	GCTCCTCTGC	AACCTTGTCG	ACTTCCAAGT	GGCCACAGA	TACAGCACAG				960
85	GGGATGGAGA	TATGGGCTGGT	GAGTCTCCAT	CTCTACACTG	TGACTGGGGC	TAGACAGATT				1020
	CAATACCGAA	GGGGCGTGGG	AGAAATTTAT	TCCCTTGTGA	ACCCCTGGGG	CTGGGGCGAG				1080
	ACCGAATGGA	GAGGGCGTGA	GAGTATGGG	CTTCAGAGAT	GGGAGGAAAC	CTGTGATGAT				1140

	CGGAAAGCC	AGCTACATA	GAACGGGAA	GATGGCGAGT	TTTGATGTC	GTGTCAAGAT	1200
	TTCCAACAGA	AATTCATCGC	CATGTTTATA	TGTAGCGAAA	TTCCAATTAC	CCTGGACCAT	1260
	GGAAACACAC	TCCACGAAGG	ATGGTCCCAA	ATAATGTGTA	GGAAAGCAAGT	GATTCTAGGA	1320
5	AACACTGCAG	GAGGACCTCG	GAATGATGCT	CAATTCAACT	TCTCTGTGCA	AGAGCCAATG	1380
	GAAGGCACCA	ATGTTGTCGT	GTGGGTCA	GTGTCTGTCA	CACCATCAAA	TTTGAAGCA	1440
	GAAGATGCAA	AATTTCCACT	CGATTTCCAA	GTGATTCTGG	CTGGCTCACA	GAAACACTGT	1500
	CCAAAGCTCA	AATAATAAAT	TCCGCGCAA	CTTCACCATG	ACTTACCATC	TGAGCCCTGG	1560
	GAATCATGTT	GTGGTTGCAC	AGACACGGAG	AAAATCAGCG	GAGTTCCTTG	TCOGAATCTT	1620
10	CCTGAAAATG	CCAGACAGTG	ACAGGCACCT	GAGCAGCCAT	TTCAACCTCA	GAATGAAGGG	1680
	AAGCCCTTCA	GAACATGGCT	CCCAACAAAG	CATTTTCAAC	AGATATGCTC	AGCAGGTATG	1740
	GTACCTAGCA	CCCAGSGGCG	TTACGTGGGA	TTGGAGAAAG	GGGACCTGAG	GGAGGGACAG	1800
	CCCTCACAGG	CCCTTACTGG	GATGCAGAGA	GGAGAAGTGA	CTTGATGGAC	TATTTTACCT	1860
	GCCTCTCTTC	CTGGATCGTC	TCCAGAACTG	CTGTGGCTGC	CAAGCTCGGT	AGAGACGTGG	1920
	CGCCCCACCC	AGTCTCATCC	GGGGGACTTC	AAGCTGGAAT	GCAGAGCTTA	GAAAGGGAGG	1980
15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
	ACCCCGTGAA	ACCTTTCTCT	CTCTACTTCG	GCCACCTCCC	ACCAACCTGG	CATCGTTTCT	2100
	CCCGGGAGCT	AGCCAGCTTC	AGAAAGCACA	TACAGCATCC	TTGCTGCCAA	ACCACCTATG	2160
	TGCACACAGG	ATTTCTCTAA	TGGCTTAATA	AACCTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
20	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCTCT	TACCGTTAAA	AAAAAATAAA	2280
	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA				

Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

25	1	11	21	31	41	51	
	MAYYQEPSVE	TSIIKFKDQD	FTTLRDHCLS	MGRTFKDETF	PAADSSIGQK	LLQEKRLSNV	60
	IWKRPQDLPG	GPPHFIILDDI	SRFDIQQGGG	ADCFPLAALG	SLTQNPQYRQ	KILMVQSFSS	120
	QYAGIFRFRF	WQCQWVEVV	IDDLRPVQGD	KCLFVRPRHQ	NQEFNPLCLE	KAYAKLLGSY	180
30	SDLHYGFLED	ALVDLTGGVI	TNIHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
	MENGLVSLHA	YTVTGABDIQ	YRRGWEEIIS	LWNPWGWGET	EWGRWSDGSS	QEWEEETCDPR	300
	KSQLEKKRED	GEPFMSQDFF	QQKFIAMFIC	SEIPITLDHG	NTLHBSWSQI	MFRKQVILGN	360
	TAGGPRNDQA	PNFSVQEPME	GTNVVVVCTV	AVTPSNLKA	DAKFPLDFQV	ILAGSQKHCP	420
35	KLK						

Seq ID NO: 328 DNA sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74-2788

40	1	11	21	31	41	51	
	GTGGGTACAG	TGAACCACTT	TTGGGCGGAA	ACCTGGTGTG	TGCTGTAGTG	GCGGAGAGGA	60
	TCGTGGTACT	GCTATGGCGG	AATCATCGGA	ATCCTTCACC	ATGGCATCCA	GCCCGGCCCA	120
45	GCGTCGGCGA	GGCAATGATC	CTCTCACCTC	CAGCCCTGGC	CGAAGCTCCC	GGCGTACTGA	180
	TGCCCTCACC	TCCAGCCCTG	GCGGTGACCT	TCCACCAATT	GAGGATGAGT	CCGAGGGGCT	240
	CCTAGGCACA	GAGGGGCCCC	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGAGATGGG	300
	CATGGAAAGG	GACTACCGCG	CCATCCACGA	GCTGGACGCC	TATGAGGCGG	AGGAGCTGGC	360
	TCTGGATGAT	GAGGACGTAG	AGGAGCTGAC	GGCCAGTCAG	AGGGAGGCAG	CAGAGCGGGC	420
50	CATGGGCGAG	CGTGACCGGG	AGGCTGGCGG	GGGCTGGGCG	CGCATGCGCC	GTGGGCTCCT	480
	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCCTGCCCGC	AAGCGCGGCC	AGGTGGAGGG	540
	GGCCACGGAG	GACGGCGAGG	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	ACCTGGAGGA	600
	TCTCAAGAGC	CATCTGTGTC	GCGAGTGGGT	GAGCATGGCG	GGCCCCGGCG	TGGAGATCCA	660
	CCACCGCTTC	AAGAACCTTC	TGCGCACTCA	CGTCGACAGC	CACGCGCCCA	ACGTCTTCNA	720
55	GGAGCGCATC	AGCGAGCATG	GCAAGAGAGG	CCGTGAGAGC	CTGGTGGTGA	ACTATGAGGA	780
	CTTGGCAGCC	AGGAGGACCG	TGCTGGCCTA	CTTCTGCTCT	GAGGCAACCG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGAGT	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCATCTC	CCACCTGCGT	CTGGTGGAGG	AGCTGCGCTC	960
	GCTGAGGCG	CTGCATCTGA	ACCAGCTGAT	CCGCACCACT	GGGGTGGTGA	CCAGCTGCAC	1020
60	TGGGTCCTCG	CCCTCAGCTCA	GCAATGTCAA	GTACCACTGC	AACAAGTGCA	ATTTGTCTCT	1080
	GGGTCTCTTC	TGCCAGTCCC	AGAAACGAGG	GGTGAACCA	GGCTCCTGTC	CTGAGTGCCA	1140
	GTGGGCGGCG	CCCTTGTAGG	TCAACATGGA	GGAGACCATC	TATCAGAACT	ACCAGCGTAT	1200
	CCGAATCCAG	GAGAGTCCAG	GCAAAAGTGG	GGCTGGCGGG	CTGCCCGGCT	CCAAGGACGC	1260
	CATTCTCCTC	GCAGATCTGG	TGGACAGCTG	CAAGCCAGGA	GACGAGATAG	AGCTGACTGG	1320
65	CATCTATCAC	AACAACATATG	ATGGCTCCCT	CAACACTGCC	AATGGCTTCC	CTGTCTTTGC	1380
	CACGTGTCAT	CTAGCCCAAC	ACGTGGCCAA	GAAGGACAA	AAGGTTGCTG	TAGGGGAAC	1440
	GACCGATGAA	GATGTGAAGA	TGATCACTAG	CCTCTCCAAG	GATCAGCAGA	TCGGAGAGAA	1500
	GATCTTTGCC	AGCATGTGCT	CTTCCATCTA	TGGTCATGAA	GACATCAAGA	GAGGCTGGGC	1560
70	TCTGGCCCTG	TTGCGAGGGG	AGCCCAAAAA	CCGAGGTGGC	AAGCAAGAGG	TACGTGGTGA	1620
	TATCAACGTC	CTCTTGTGGG	GAGACCTGGG	CACAGCGAAG	TGCGAGTTTC	TCAAGTATAT	1680
	TGAGAAAGTG	TCCAGCCGAG	CCATCTTCAC	CACCTGGCCG	GGGGCGTCCG	CTGTGGGCTT	1740
	CACGGGCTAT	GTCCAGCGGC	ACCTGTTCAG	CAGGAGTGGG	ACCTTGGAGG	CTGGGGCCCT	1800
	GGTCTGGGCT	GACCGAGGAG	TGTGTCTCAT	TGATGAATTT	GACAAAGATG	ATGACCAGGA	1860
	CAGAACCAGC	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
75	CGTCACCTCC	CTGCAGGCTC	GCTGCAOGGT	CATTGCTGCC	GCCAAACCCA	TAGGAGGGCG	1980
	CTACGACCCC	TGGCTGACTT	TCTCTGAGAA	CGTGGAACTC	ACAGAGCCCA	TCACTCTCAG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGAGC	AGATGCTGGC	2100
	CGCTCTCGTG	GTGGGACGCC	ACGTGAGACA	CCACCCAGC	AACAGGAGG	AGGAGGGGCT	2160
	GGCCAATGGC	AGCGCTGCTG	AGCCCGCCAT	GCCCAACAG	TATGGCGTGG	AGCCCTGCTC	2220
80	CCAGGAGGTC	CTGAAGAAGT	ACATCATCTA	CGCCAAGGAG	AGGGTCCACC	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAGAT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	GACAGGCAGC	ATCCCAATTA	CGTGGCGGCA	CATGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CCACGCGCGC	ATCCATCTGC	GGGACTATGT	GATGAAAGAC	GACGTCAACA	TGGCCATCCG	2460
	CGTGATGCTG	GAGAGCTTCA	TAGACACACA	GAAGTTGAGC	GTGATGCGCA	GCATGCGCAA	2520
85	GACTTTTGCC	CGCTACTCTT	CATTCCGGCG	TGACAACAAT	GAGCTGTTGC	TCTTCACTAT	2580
	GAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TGACGCAAC	CGCTTTGGGG	CCAGCAGGGA	2640
	CACTATTGAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

	CCTCTCTGCA	TTTTATGACA	GTGAGCTCTT	CAGGATGAAC	AAGTTCAGCC	ACGACCTGAA	2760
	AAGGAAAATG	ATCTGCGAGC	AGTTCTGAGG	COCTATGCCA	TCCATAAGGA	TTCTTGGGA	2820
	TTCTGGTTTG	GGGTGGTCAG	TGCCCTCTGT	GCTTTATGGA	CACAAAACCA	GAGCACTTGA	2880
5	TGAACCTGGG	GTACTAGGGT	CAGGGCTTAT	AGCAGGATGT	CTGGCTGCAC	CTGGCATGAC	2940
	TGTTTGTGTT	TCCAGAGCTG	CTTTGTGCTT	CTCAOCTTTG	GGTGGGATGC	CTTGCCAGTG	3000
	TGCTCTACTT	GTTTGTCTGAA	CATCTTGCCA	CCTCOGATGT	CTTTGTCTCC	ACTCAGTACC	3060
	TTGGATCAGA	GCTGCTGAGT	TCAGGATGCC	TGCGTGTGST	TTAGGTGTTA	GCCTTCTTAC	3120
	ATGGATGTCA	GGAGAGCTGC	TGCCCTCTTG	GGGTGAGTTG	CGTATTTCAGG	CTGCTTTTGC	3180
10	TGCCTTTGGC	CAGAGAGCTG	GTGGAAGATG	TTTGTAAATG	TTTTCAGTCT	CCTGCAGGTT	3240
	TCTGTGCCCC	TGTGGTGGAA	GAGGGCAGGA	CAGTGCCAGC	GCAGCGTTCT	GGGCTCTTCA	3300
	GTCGACGGGG	TGGGATGTGA	GTCAATGCGA	TTATCCACTC	GCCACAGTTA	TCAGCTGCCA	3360
	TTGCTCCCTG	TCTGTTTCCC	CACTCTCTTA	TTTGTGCAAT	CGGTTTGGTT	TCTGTAGTTT	3420
	TAAATTTTAA	TAAAGTTGAA	TAAATATATA	AAAAAAAAAA	AAAAAA		

15 Seq ID NO: 329 Protein sequence:
Protein Accession #: AAH17490.1

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20	MAESSESFTM	ASSPAQRRRG	NDPLTSSPGR	SSRRTDALTS	SPGRDLPPFE	DSEGLLGTE	60
	GPLEEEDGE	ELIGDGMERD	YRAIPELDAY	EAEGLALDDE	DVEELTASQR	EAAERAMRQR	120
	DREAGRGLGR	MRRGLLYDSD	EEDDERPARK	RQOVERATED	GDEDEEMIES	IENLEDLKGH	180
	SVREWVSMAG	PRLEIHHPRK	NFLRTHVDSH	GHNVFKERIS	DMCKENRESL	VVNYEDLAAR	240
	EEVLAYFLPE	APAEQLQIFD	EAALEVVLAM	YPKYDRITNH	IEVRIHSLPL	VEELRSLRQL	300
25	HLNQLITSG	VVTSTCTVLP	QLSMVKYNCN	KCNFVLGPFC	QSQNQEVKPG	SCPEQCSAGP	360
	FEVNMETIY	QNYQRIQIE	SPGKVAAGRL	PRSKDAILLA	DLVDSCKPGD	EIELTGIYHN	420
	NYDGLSLATN	GPPVFPATVIL	ANHVAKKDNK	VAVGELTDED	VKMITSLSKD	QOIGEKIPAS	480
	IAPSIYGHED	IKRGLALALF	GGEPKNPGGK	HKVRGDINVL	LCQDPGTAKS	QPLKYIEKVS	540
	SRAIFTTGGG	ASAVGLTAYV	QRHPVSREWT	LEAGALVLAD	RGVCLIDREF	KMNDQDRTSI	600
30	HEAMEQQSIS	ISKAGIVTSL	QARCTVIAAA	NPIGGRYDPS	LTFSENVDLT	EPIISRPDIL	660
	CVVRDVTDPV	QDEMLARFVV	GSHVRHHPSN	KEEGLANGS	AAEPAMPNTY	GVEPLPQEVN	720
	KKYIYAKER	VEPKLNQMDQ	DKVAKMYSDL	RKESMATGSI	PITVRHIESM	IRMAEAHARI	780
	HLRDYVIEDD	VNMAIRVMLE	SFIDTQKFSV	MRSMRKTFAR	YLSFRDRDNE	LLLFILKQLV	840
35	ABQVTYQRNR	FGAQDQDTEV	PEKDLVDKAR	QINIHNLASF	YDSELEFRMKN	FSDHLKRXMI	900
	LQQF						

40 Seq ID NO: 330 DNA sequence
Nucleic Acid Accession #: M17254
Coding sequence: 257-1645

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	CGGGTGCAC	TAACTCCCTC	GGCGCGGACG	GGCGCGCTAA	CCTCTCGGTT	ATTCCAGGAT	120
45	CTTTGGAGAC	CAGAGGAAAG	COGTGTGAC	CAAAAGCAAG	ACAAATGACT	CACAGAGAAA	180
	AAAGATGGCA	GAAACCAAGG	CAACTAAAGC	CGTCAGGTTC	TGAACAGCTG	GTAGATGGGC	240
	TGGCTTACTG	AAGGACATGA	TTGAGACTGT	CCCGGACCCA	GCAGCTCATA	TCAAGGAAGC	300
	CTTATCAGTT	GTGAGTGAGG	ACCACTCGTT	GTTTGAAGTT	GCCTACGGAA	CGCCACACCT	360
	GGCTAAGACA	GAGATGACCG	CGTCTCTCTC	CAGCGACTAT	GGACAGACTT	CCAAGATGAG	420
50	CCCAOCCGTC	CCTCAGCAGG	ATTGGCTGTC	TCAACCCCCA	GCCAGGGTCA	CCATCAAAAT	480
	GGAAATGAAC	CCTAGCCAGG	TGAATGGCTC	AAGGAATCTT	CCTGATGAAT	GCAGTGTGGC	540
	CAAAAGCGGG	AAGATGGTGG	GCAGCCGAGA	CACCGTTGGG	ATGAACCTAG	GCAGCTACAT	600
	GGAGGAGAAG	CACATGCCAC	CCCCAAACAT	GACCACGAAC	GAGCGCAGAG	TTATCGTGCC	660
	AGCAGATCCT	ACCTGTAGGA	GTACAGACCA	TGTGCGGCAG	TGGCTGGAGT	GGGCGGTGAA	720
55	AGAATATGGC	CTCCAGACG	TCAACATCTT	GTTATTCCAG	AACATCGATG	GGAAGGAAC	780
	GTGCAAGATG	ACCAAGGACG	ACTTCCAGAG	GCTCACCCCC	AGCTACAACG	CCGACATCCT	840
	TCTCTCACAT	TCCCATACC	TCAGAGAGAC	TCTCTTCCCA	CATTGACTTT	CAGATGATGT	900
	TGATAAAGCC	TTACAAAAC	CTCCACGGTT	AATGCATGCT	AGAAACACAG	ATTTACCATA	960
	TGAGCCCCCC	AGGAGATCAG	CCTGGACCGG	TCACGGCCAC	CCCACGCCCC	AGTCGAAAGC	1020
60	TGCTCAACCA	TCTCTTCCCA	CAGTGCCCAA	AACTGAAGAC	CAGCGTCTCT	AGTTAGATCC	1080
	TTATCAGATT	CTTGGACCAA	CAAGTAGCCG	CCTTGCAAA	CCAGGCAGTG	GCCAGATCCA	1140
	GCTTTGGCAG	TTCCTCTGCG	AGCTCCTGTC	GGACAGCTCC	AACTCCAGTG	GCATCACCTG	1200
	GGAAAGGCACC	AACGGGGAGT	TCAAGATGAC	GGATCCCGAC	GAGGTGGCCC	GGCGCTGGGG	1260
	AGAGCGGAAG	AGCAAAACCA	ACATGAAC	CGATAAGCTC	AGCCGCGCCC	TCCGTTACTA	1320
65	CTATGACAAG	AACATCATGA	CCAAGGTCCA	TGGGAAGCGC	TACGCTTACA	AGTTGACTTT	1380
	CCAAGGATC	GCCCAAGCCC	TCCAGCCCCA	CCCCCGGAG	TCACTCTCTG	ACAAGTACCC	1440
	CTCAGACCTC	CCGTACATGG	GCTCCTATCA	CGCCACCCCA	CAGAAGATGA	ACTTTGTGGC	1500
	GCCCCACCTC	CCAGCCCTCC	CGTGACATC	TTCCAGTTTT	TTTGTGCCCC	CAAAACCCATA	1560
	CTGGAATTCA	CCAAGTGGGG	GTATATACCC	CAACACTAGG	CTCCCCACCA	GCCATATGCC	1620
70	TTCTCATCTG	GGCACTTACT	ACTAAAGACC	TGGCGGAGGC	TTTTCCCATC	AGCGTGCATT	1680
	CACCAAGCCA	TGCGCCACAA	CTCTATCGGA	GAAATGAAT	CAAAAGTGCC	TCAAGAGGAA	1740
	TGAAAAAAGC	TTTACTGGGG	CTGGGGAAGG	AAGCGGGGGA	AGAGATCCAA	AGACTCTTGG	1800
	GAGGAGGTTA	CTGAAGTCTT	ACTACAGAAA	TGAGGAGGAT	GCTAAAAATG	TACAGGAATAT	1860
	GGACATATCA	TCTGTGGACT	GACCTTGTA	AAGACAGTGT	ATGTAGAAGC	ATGAAGTCTT	1920
75	AAGGACAAAG	TGCCAAAGAA	AGTGGTCTTA	AGAAATGTAT	AAACTTTAGA	GTAGAGTTTG	1980
	AATCCCACTA	ATGCAAACTG	GGATGAAACT	AAAGCAATAG	AAACAAACAC	GTTTTCAGCT	2040
	AACATACCTT	TTATAATGCC	ATTTTAAGGA	AAACTACCTG	TATTTAAAAA	TAGTTTCATA	2100
	TCAAAAACAA	GAGAAAAGAC	ACGAGAGAGA	CTGTGGCCCA	TCAACAGACG	TTGATATGCA	2160
	ACTGCAATGC	ATGTGCTGTT	TTGGTTGAAA	TCAAAATACAT	TCCGTTGAT	GGACAGCTGT	2220
80	CAGCTTTCTC	AAACTGTGAA	GATGACCCAA	AGTTTCCAAC	TCCCTTACAG	TATTACCGGG	2280
	ACTATGAATC	AAAAGGTGGG	ACTGAGGATG	TGTATAGAGT	GAGCGTGTGA	TTGTAGACAG	2340
	AGGGGTGAAG	AAGGAGGAGG	AAGAGGCAGA	GAAGGAGGAG	ACCAGGCTGG	GAAAGAAACT	2400
	TCTCAAGCAA	TGAAGACTGG	ACTCAGGACA	TTTGGGGACT	GTGTACAATG	AGTTATGGAG	2460
	ACTCGAGGGT	TCATGCAGTC	AGTGTATATC	CAAAACCCAGT	GTTAGAGAGAA	AGGACACAGC	2520
85	GTAATGGAGA	AAGGGAAGTA	GTAGAAATTA	GAAACAAAAA	TGCGCATCTC	TTTCTTTGTT	2580
	TGTCAAATGA	AAATTTTAAC	TGGAATTGTC	TGATATTAA	GAGAAACATT	CAGGACCTCA	2640
	TCATTATGTG	GGGCGTTTGT	TCTCCACAGG	GTCAGGTAAG	AGATGGCCTT	CTTGCTGCC	2700

5

ACAATCAGAA ATCAGCAGG CATTTTGGGT AGGCGGCCCT CAGTTTTCCT TTGAGTCGG 2760
AACGCTGTGC GTTTGTGAGA ATGAAGTATA CAAGTCAATG TTTTTCCTCC TTTTATATA 2820
ATAATTATAT AACTTATGCA TTTATACACT ACGAGTTGAT CTGGCCAGC CAAGACACA 2880
CGACAAAAGA GACAAATCGAT ATAATGTGGC CTTGAATTTT AACTCTGTAT GCTTAATGTT 2940
TACAATATGA AGTTATTAGT TCTTAGAATG CAGAATGTAT GTAATAAAT AAGCTGGCC 3000
TAGCATGGCA AATCAGATT ATACAGAGT CTGCATTGTC ACTTTTTTTA GTGACTAAAG 3060
TTGCTTAATG AAAACATGTG CTGAATGTTG TGGATTGTTG GTTATAATTT ACTTTGTCCA 3120
GGAACCTGTG CAGGAGGAG CCAAGGAAAT AGGATGTTG GCACCC

10

Seq ID NO: 331 Protein sequence
Protein Accession #: AA52398

15

1 11 21 31 41 51
MIQTVDPDAA HIKEALSUVS EDQSLFECAY GTPELAKTEM TASSSSDYGQ TSKMSPRVPO 60
QDWLSQPPAR VTIKMECNPS QVNGSRNSFD ECSVAKGGKM VGSPTDVGMN YGSYMEEKEM 120
PPFNMTTNER RVIVPADPTL WSTDDEVQWL ENAVKEYGLP DVNILLFQNI DGKELCKMTK 180
DDFQRLTFSY NADILLSLHL YLRETFPLPH TSDDVDKALQ NSPRLMHARN TDLFPYEPFR 240
SAWTGHGHPT PQSKAAQSP STVPKTEDQR PQLDPYQILG PTSSRLANPG SQQIQWLQFL 300
LELLSDSSNS SCITWEGTNG EFMIDPDDEV ARRWGERKSK PNMNYDKLSR ALRYYDKNI 360
MTKVHGKRYA YKFDPHGIAQ ALQPHPESS LYKYPSDLPY MGSYHAHPQK MNFVAPHPPA 420
LPVTSSSFFA APNFPWNSPT GGIYPNTRLP TSHMPSHLGT YY 462

25

Seq ID NO: 332 DNA sequence
Nucleic Acid Accession #: NM_000020
Coding sequence: 283-1794

30

1 11 21 31 41 51
AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60
AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCCGGC CAGCTGCGCC 120
GAGCGAGCCC CTCCCGGCT CCAGCCGGT CCGGGGCGC GCGGACCCC AGCCCGCGT 180
CCAGCGCTGG CGGTCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCGA 240
AGGCTAGGCG CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CCATGACCTT GGGCTCCCC 300
AGGAAAGGCC TTCTGATGCT GCTGATGGCC TTGGTGACCC AGGGAGACCC TGTGAAGCG 360
TCTCGGGGCC CGCTGGTGAC CTGCACTGT GAGAGCCAC ATTGCAAGGG GCCTACCTGC 420
CGGGGGGCT GTGTCACAGT AGTCTGGTG CCGGAGGAGG GGAGGACCC CCAGAACAT 480
CGGGGCTGCG GGAACCTGCA CAGGAGCTC TGCAGGGGCG GCCCACCGA GTTCGTCAAC 540
CACTACTGCT GCGACAGCCA CCTCTGCAAC CACAAGTGT CCTGTGTGCT GGAGGCCACC 600
CAACCTCCTT CGGAGCAGCC GGGAACAGAT GGCCAGCTGG CCTGTATCTT GGGCCCGTG 660
CTGGCCTTGC TGGCCTGCTT GGCCTGGGT GTCTGGGCC TGTGGCATGT CCGACGGAGG 720
CAGGAGAGC AGCGTGGCT GCACAGCGAG CTGGGAGAGT CCACTCTCAT CCGTGAAGCA 780
TCTGAGCAGG GCGACACGAT GTTGGGGGAC CTCTGGACA GTGACTGCAC CACAGGAGT 840
GGCTCAGGGC TCCCTTCTCT GGTGCAGAGG ACAGTGGCAC GGCAGGTTGC TCTGGTGGAG 900
TGTGTGGGAA AAGGCGGCTA TGGOGAAGTG TGGCGGGCT TGTGGCAOAG TGAGAGTGTG 960
GCGCTCAAGA TCTTCTCTC GAGGGATGAA CAGTCTGTGT TCCGGGAGAC TGAGATCTAT 1020
AACACAGATC TGCTCAGACA CGACAAATC CTAGGCTTCA TCGCTCAGA CATGACTCTC 1080
CGCAACTCGA GCACGAGCT GTGGCTCATC ACCTACTACC ACAGGACAGG CTCCCTCTAC 1140
GACTTTCTGC AGAGACAGAC GCTGGAGCCC CATCTGGCTC TGAGGCTAGC TGTGTCCGG 1200
GCATGCGGCC TGGCGACCT GCACTGGAG ATCTTGGTA CACAGGCGAA ACCAGCCATT 1260
GCCACCGGCG ACTTCAAGAG CGCAATGTG CTGGTCAAGA GCAACCTGCA GTGTGTGATC 1320
GCCGACCTGG GCTTGGCTGT GATGACTCA CAGGCGAGCG ATTAAGTGA CATGGCAAC 1380
AACCGAGAG TGGGACCAA GCGGTACATG GCACCGAGG TGCTGGAGCA GCAGATCCGC 1440
ACGGAAGTCT TTGATGCTA CAAGTGGACT GACATCTGGG CCTTTGGCCT GTGTGTGTG 1500
GAGATTGGCC GCGGACCAT CTGGAATGGC ATGCTGGAG ACTATAGACC ACCCTCTAT 1560
GATGTGTGCG CCAATGACC CAGCTTTGAG GACATGAAGA AGGTGTGTGT TGTGGATCAG 1620
CAGACCCCA CCATCCCTAA CCGGCTGGCT GCAGACCGG TCTCTCAGG CTAAGCTCAG 1680
ATGATGGGG AGTGTCTGTA CCCAAACCCC TCTGCCCGAC TCACCGCGCT GCGGATCAG 1740
AAGACACTAC AAAAATTAG CAACAGTCCA GAGAAGCCTA AAGTGATTA ATAGCCACAG 1800
AGCACTCTGC TCTTTCTGC CTGCAGGGGG CTGGGGGGGT GGGGGGCACT GGATGGTGTG 1860
CTATCTGGGT AGAGTAGTGT TGAATGTGTT GTGTGCTGG GATGGGCGC TGGCCTGCC 1920
TGCTGGGCC CCAGCCACCC CAGCCAAAA TACAGCTGGG CTGAAACCTG ATCCCTGTCT 1980
GTCTGGCCTG CTCGAAGGCG CAGGCTCCCT GAGCGCTGGC TCTCTCCCA CCCCTATGGC 2040
CAGCATGTGT CACCCCTAC CACTCCCGGG ACAGGATGCA AAGAGGCTC CAGAGTCAGA 2100
GTGCCAAGCC AGGGAATCCC AGTCCCAGAC TCAGAGCCCG GGCTGCACT TTGCCCTCTG 2160
CCCTTGATCA ACCCACTGC CCAACAGAG CTGCCAGGCT GGCACAGGGC CCTGTCCAGC 2220
CCCTGGCACA CACTTCCCTG CCAGGCTTCA GCCTTAGCA TAAGCTCCAG AGAGCCAGG 2280
CCCATCAGTT TCTCTGTG GATTTGTATC TCAGCTCCAT GATGCTTGG GCTTCTGTG 2340
TCTCAACAA GAGTGAGCT TGCTGAATGT CAGCTGCCGT AGAGAGCTGG GGCCTGACTT 2400
ACTAGGGCAT TAAATCTTAA GAGGTCTTAC TGAGGTGTGG CAGGATCACA GGCCAGTGG 2460
AAAAGGGCAG GTGATGTGG CAAGGCCAG GACTTTCAGA TTAAGTGA GAATATCGAG 2520
GCCAAGCATG GCAGGGGAA GGTCAAGTGG TGTCAAGAGA CCCAGGCTG ACCCCGGATG 2580
TTTGCTCCAT GTGACAAAG CAGGCTGTG TCAGGACCTT TTTTCTCTT TTTTCTCTT 2640
TTTTTTTTT GACACGAGT TCGCTCTGT TTGTCCAGG TAGAGTGCAA TGGCATGATC 2700
CCAGCTCACC GCAAGCTCTA CCTCCAGGT TCAATCAT CTCTGCTC AGACTCCCGA 2760
GTAGCTGGGA TTACAGGAC ATGCCACAT GCCTGGCTAA TTTTGTATAT TTAGTAGAAA 2820
CAGGGTTTCA CCATGCTGGC CATGCTGGTT CTGGAACCTC TGACCTCAGG TGTTCACCT 2880
ACCTCAGCTT CCAAGAGTGC TGGGGTTACA GGTGTGAGCC ATGCGCCCTG GCCAGGACT 2940
TTGTTTCTTA TCTCATATT GGAAGATTGT GCTCTGATGT CCTTTGAGG TCTTTAGCT 3000
CTAGTTCTCT GACATCTAG CCTATATCAC AGCTAACTTC YTCAGTCTCA TCTATTCTT 3060
ATGCTCCAGC CCTGGCAAT TTGCTCAAG ATGGGGGTTT GAAATAACT TTACTTGACT 3120
CAAGGAGTGT CTGAGCACC TCCTAGTCTA AGTCTGCAAG CTCAGTCTC TGCTTAAAC 3180
CATGCCAGTG GCAACCTTG GCTCAGACA GCTCTGGGCC TTTTACCAC AAGCCAGCCC 3240
CTGCCCTCT CTGTGGCATA GTCTTCTCTG CCCCAGGACT GCAGGGCGGC TTCTCCAGG 3300
GCTTCCAGG CTCAAAAGAA ATTGGCTCC ATCCAAAGAG GCTCCAGCTC CCTACTGCT 3360
CCCTGGCTTC AGGCCACAC CCCTGGGCCA GSCCAGAGA GTGTGTCTCA GGGAATTCA 3420
ATGGGCTCTA GAGAGACACA CAGAAAGTTT GGGCATTGG GAAATTTCA AGGRTGTATG 3480

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TATGGTTCAC	GTATGGNGCA	GGTTGTCTCTG	GTCCYKGGGT	GCAGGGAAGT	GGGCTGCAGG	3540
GAAGTGGATT	GGAGGGGAGC	TTGAGGAATA	TAAGGAGCGG	GGGTGGAGAC	TCAGGCTATG	3600
GACAAGGACA	GCCCCAAGGT	TGGGAAGACC	TGGCCTTAGT	CCTCCTCAGC	CTAGGGCAGG	3660
CCAGTGAAGA	AAGCTCTCC	CGCTCCTGCT	GTAATGACCC	AGAGTAGCCT	CCCCAGGCCG	3720
GCATCTTATG	TGTGTCTTCC	ACCATCTCTCA	TGGTGGCACT	TTTCTAGGCC	TGCTCTCCAG	3780
CATTGTGCAA	GGCTCGGAAG	AGAACCAGGA	AGTGAAACTG	GSTGAAAACA	GAAAGCTCAA	3840
TGGATGGGCT	AGGTTCGCCAG	ATCATTAGGG	CAGAGTTTGC	ACGTCTCTCTG	GTTCACTGGG	3900
AATCCACCCA	GCCCCAGAAAT	CATCTCCCTC	TTTGAAGGAT	TTTWTATTCT	ACTGGGTTTT	3960
GGAAACAACT	CCTCTCTGAGA	CCCCACAGCC	AGAAACTGAA	AGCAGCAGCT	CCCCAAAGCC	4020
TGGAAAATCC	CTAAGAGAAG	GCCTGGGGGA	MAGGAATG	AGTGACAGGG	GACAGGTAGA	4080
GAGAAGGGGG	CCCAATGGCC	AGGAGGTGAA	GGAGGTGGCG	TTGCTGAGAG	CAGTCTGCAC	4140
ATGCTTCTGT	CTGAGTGCAG	GAAGGTGTTT	CAGGGTCGAA	ATTACACTTC	TGTTACCTGG	4200
AGACGCTGTT	TGTGGGAGCA	CTGGGCTCAT	GCCTGGCACA	CAATAGGTCT	GCAATAAACC	4260
ATGGTTAAAT	CCTGAAAAAA	AAAAAAA				

Seq ID NO: 333 Protein sequence
 Protein Accession #: NP_000011

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1	11	21	31	41	51	
MTLGSPRKGL	LMMLMALVTQ	GDPVKPSRGP	LVTCTCESPH	CRGPTCRGAW	CTVVLVREBG	60
RHPQHRGCG	NIHRELRCGR	PTFPVNHVCC	DSHLCHNVNS	LVLEATQPPS	EQPGTDGQLA	120
LILGFLVALL	ALVALGVVLG	WHVRRRQEKQ	RGLHSELGES	SLILKASEQG	DTMLGDLDS	180
DCTTGGSGSL	PFLVQRTVAR	QVALVECVGK	GRYGEVVRGL	WHGESVAVKI	FSSRDEQSWF	240
RETEIYNTVL	LRHENVLGP	ASDMTSRNS	TQLMLITHYH	EHGSLYDFLO	RQTLLEPHLAL	300
RLAVSAACGL	AHLEVBPGT	QGKPAIAHRD	FKSRNVLVKS	NLQCCIADLG	LAVMESQSGD	360
YLDIGNPRV	GTRYMAPEV	LDEQIRTDCT	BSYKWDIWA	PGLVLWEIAR	RTIVNGIVED	420
YRPFYDVVP	NDPSFEDMKK	VVCVDQQTPT	IPNRLAADPV	LSGLAQMMRE	CWYPNPSARL	480
TALRIKKTILQ	KISNSPEKPK	VIG				

Seq ID NO: 334 DNA sequence
 Nucleic Acid Accession #: NM_004126.1
 Coding sequence: 108-329

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 40
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1	11	21	31	41	51	
GGCAGGAGCT	CGTCCCGGCC	TTCACTTGT	TCGGGACCGG	CGGAGCTTCG	CGGCTCTTCC	60
AGCGGCTCG	CTGCCAGAGC	TAGCCCGAGC	COGGTTCTGG	GGCGAAAATG	CCTGCGCTTC	120
ACATCGAAGA	TTTGCCAGAG	AAGGAAAAAC	TGAAAATGGA	AGTTGAGCAG	CTTCGCAAG	180
AAGTGAAGTT	CGACAGACAA	CAAGTGTCTA	AATGTTCTGA	AGAAATAAAG	AACTATATTG	240
AAGAAGCTTG	TGCAGAGGAT	CCTCTAGTAA	AGGGAATTCC	AGAAGACAAG	AACCCCTTTA	300
AAGAAAAAGG	CAGCTGTGTT	ATTTCATAAA	TAACCTGGGA	GAAACTGCAT	CCTAAGTGGG	360
AGAACTAGTT	TGTTTATAGT	TTCCAGATA	AAACCAACAT	GCTTTTAAAG	GAAGGAAGAA	420
TGAAATTAAG	AGGAGACTTT	CTTAAGCACC	ATATAGATAG	GTTTATGTAT	AAAAGCATAT	480
GTGCTACTCA	TCTTTGCTCA	CTATGCAGTC	TTTTTTAAGA	GAGCAGAGAG	TATCAGATGT	540
ACAATTATGG	AAATAAGAAC	ATTACTTGAG	CATGACACTT	CTTTCAGTAT	ATTGCTTGAT	600
GCTTCAAAATA	AAGTTTGTG	TT				

50
 Seq ID NO: 335 Protein sequence
 Protein Accession #: NP_004117.1

55

1	11	21	31	41	51	
MPALHIEDLP	EKEKLMEVE	QLRKEVKLQR	QOVSKCEEI	KNYIEERSGE	DPLVKGIPED	60
KIPFKEKGSC	VIS					

60
 Seq ID NO: 336 DNA sequence
 Nucleic Acid Accession #: NM_005795
 Coding sequence: 555-1940

65
 70
 75
 80
 85

1	11	21	31	41	51	
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CAAGCTCTGC	TAACCTGAAT	TCATCCTAAT	TGCAGGATCA	CATTGCAAG	CTTTCACCTCT	120
TTCCCACTTT	GCTTGTGGGT	AAATCTCTTC	TGCGGAATCT	CAGAAAGTAA	AGTTCCATCC	180
TGAGAAATATT	TCACAAAGAA	TTTCTTAAG	AGCTGGACTG	GGTCTTGACC	CCTGGAATTT	240
AAGAAATCT	TAAAGACAA	GTCAAATATG	ATCCAAGAGA	AAATGTGATT	TGAGTCTGGA	300
GACAAATGTG	CATATCGTCT	AATAATAAAA	ACCCATACTA	GCCTATAGAA	AACAAATATT	360
GAATAATAAA	AACCCATACT	AGCCTATAGA	AAACAATATT	TGAAAGATTG	CTACCACTAA	420
AAAGAAAACT	ACTACAACTT	GACAAGACTG	CTGCAAACTT	CAATTGGTCA	CCACAACCTTG	480
ACAAAGTTGC	TATAAAAACA	GATTGCTACA	ACTTCTAGTT	TATGTTATAC	AGCATATTTT	540
ATTGGGCTTT	AATGATGGAG	AAAAGTGTG	CCCTGTATTT	TCTGGTTCTC	TTGCCCTTTT	600
TTATGATTCT	TGTTACAGCA	GAATTAGAAG	AGAGTCTCTG	GGACTCAATT	CAGTTGGGAG	660
TTACTAGAAA	TAAATCATG	ACAGCTCAAT	ATGAATGTGA	CCAAAAGATT	ATGCAAGACC	720
CCATTCAACA	AGCAGAGGCC	GTTTACTGCA	ACAGAACCTG	GGATGGATGG	CTCTGCTGGA	780
ACGATGTGTC	AGCAGGAACCT	GAATCAATGC	AGCTCTGCCC	TGATTACTTT	CAGGACTTTG	840
ATCCATCAGA	AAAAGTTACA	AAGATCTGTG	ACCAAGATGG	AAACTGGTTT	AGACATCCAG	900
CAAGCAACAG	AACATGACGA	AATTATACCC	AGTGAATGT	TAAACCCAC	GAGAAAGTGA	960
AGACTGCACT	AAATTTGTTT	TACCTGACCA	TAATTGGACA	CGGATTGTCT	ATTGCATCAC	1020
TGCTTATCTC	GCTTGGCATA	TTCTTTTATT	TCAAGAGCCT	AAGTTGCCAA	AGGATTACCT	1080
TACACAAAAA	TCTGTTCTTC	TCAITTTGTT	GTAACCTCTG	TGTAACAATC	ATTCACTCA	1140
CTGCAGTGGC	CAACAACAG	GCCTTAGTAG	CCACAATATC	TGTTAGTTGC	AAAGTGTCCC	1200
AGTTCAATCA	TCTTTACCTG	ATGGGCTGTA	ATTACTTTTG	GATGCTCTGT	GAAGGCATTT	1260
ACCTACACAC	ACTCAITGTG	GTGGCGTGT	TTGCAGAGAA	GCAACATTTA	ATGTGGTATT	1320
ATTTTCTTGG	CTGGGGATT	CCACTGATTC	CTGCTTGAT	ACATGCCATT	GCTAGAAGCT	1380

TATATTACAA TGACAAATTGC TGGATCAGTT CTGATACCCA TCTCCTCTAC ATTATCCATG 1440
 GCCCAATTTG TGCTGCTTTA CTGGTGAATC TTTTCTCTT GTTAAATATT GTACCGGTTT 1500
 TCATCACCAA GTTAAAAAGT ACACACCAAG CGGAATCCAA TCTGTACATG AAAGCTGTGA 1560
 GAGCTACTCT TATCTTGGTG CCATTGCTTG GCATTGAATT TGTGCTGATT CCATGGCGAC 1620
 CTGAAGGAAA GATTGACAGG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACTTCC 1680
 AGGGTCTTTT GGTCTCTACC ATTTTCTGCT TCTTTAATGG AGAGGTTCAA GCAATTCCTGA 1740
 GAAGAAACTG GAATCAATAC AAAATCCAAT TTGGAAACAG CTTTCCAAC TCAGAAAGCTC 1800
 TTCTAGTGTG GTCTTACACA GTGTCAACAA TCAGTGTAGG TCCAGGTTAT AGTCATGACT 1860
 GTCTAGTGA ACACCTTAAAT GGAAAAAGCA TCCATGATAT TGAAAAAGTT CTCTTAAAC 1920
 CAGAAAAATT ATATAATTGA AAATAGAAGG ATGGTTGTCT CACTGTTTGG TGCTTCTCCT 1980
 AACTCAAGGA CTGAGGCCCA TGACTCTGTA GCCAGAAGAC TTCAATATTA AATGACTTTG 2040
 GGGAAATGTA TAAAGAAGAG CCTTCACATG AAATTAGTAG TGTGTTGATA AGAGTGTAAAC 2100
 ATCCAGCTCT ATGTGGGAAA AAAGAAATCC TGGTTGTGTA TGTGTTGCTG TAAATACTCC 2160
 CACTATGCCT GATGTGACGC TACTAACCTG ACATCACCAA GTGTGGAATT GGAGAAAAGC 2220
 ACAATCAACT TTTCTGAGCT GGTGTAAGCC AGTTCACGCA CACCATTGAT GAATTCAAAC 2280
 AAATGGCTGT AAAACTAAAC ATACATGTTG GGCATGATTC TACCCCTATT CCCCCCAAGA 2340
 GAOCATGCTA AGGTCTATAA ACATGAAGGG AAAATTAGCT TTTAGTTTAA AAACCTCTTA 2400
 TCCATCTTGG ATGGGGGAG TTGACTTTTT TTTTTCCTCA GAGTGGCGTA GTCCCTTTTG 2460
 TAACCTACCT CTCAATGGA CAATACCAGA AGTGAATTAT CCTGCTGGC TTTCTTTCT 2520
 CTATGAAAAG CAACTGAGTA CAATTGTTAT GATCTACTCA TTTGCTGACA CATCAGTTAT 2580
 ATCTTGTGGC ATATPCCATT TGGAACTGG ATGAACAGGA TGTATAATAT GCAATCTTAC 2640
 TTCTATATCA TTAGGAAAAG ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
 TGTCTTACCA AACAGTGGGA GGGAAATCCT AGCTGTAAAT ATAAATTTTG CCCTTCCATT 2760
 TCTACTGTAT AAACAAATTT GCAATCATTT TATATAAGA AAATCAATGA AGGATTCTCT 2820
 ATTTTCTTGG AATTTGTGTA AAAGAAATG TGAAAAATGA GCTTGTAAAT ACTCCATTAT 2880
 TTTATTTTAT AGTCTCAAAAT CAAATACATA CAACCTATGT AATTTTAAAG GCAATATAT 2940
 AATGCAACAA TGTGTGTATG TTAATATCTG ATACTGTATC TGGGCTGATT TTTTAAATAA 3000
 AATAGAGTCT GGAATGCT

Seq ID NO: 337 protein sequence
 Protein Accession #: NP_005786.1

1 11 21 31 41 51
 MEKKTLYPL VLLPFFMILV TAELEESPED SIQLGVTRNK IMTAQYECYQ KIMQDPIQQA 60
 BGVCNRTWD GMLCNDVAA GTESMQLCPD YQDFDPSEK VTKICDQDN WFRHPASNRT 120
 WNTYTQCNVN THEKVKALAN LPYLTIIHGH LSIALLLISL GIFFYFKSLR QORITLHKNL 180
 PFSFVCHSVV TIIHLTAVAN NQALVATNPV SKVVSQPIHL YLMGCNPFWM LCEGIYLBTL 240
 IVVAVFAEKQ HLMWYIFLWG GPPLIPACIH AIARSLYND NCMISSDTHL LYIIRGPICA 300
 ALLVNLFFLL NIVRVLTIKL KVTHQAESNL YMKAVRATLI LVPLLGIEPV LIPWRPEGKI 360
 AEEVYDIIMH ILMHFQGLLV STIPCFPNGE VQAILRRNWN QYKIQFQNSF SNSEALRSAS 420
 YTVSTISDGP GYSHDCPSEH LMGKSIHDIE NVLLKPENLY N

Seq ID NO: 338 DNA sequence
 Nucleic Acid Accession #: NM_001795
 Coding sequence: 25-2379

1 11 21 31 41 51
 GCAAGATCTG TTCTCTCTGG GAAGATGCAG AGGCTCATGA TGCTCCTCGC CACATCGGGC 60
 GCCTGCTCTG GCCTGCTGGC AGTGGCAGCA GTGGCAGCAG CAGGTGCTAA CCTGCCCAA 120
 CGGGACACCC ACAGCCTGCT GCCACCCAC CGCGCCCAA AGAGAGATTG GATTTGGAA 180
 CAGATGCACA TTGATGAAGA GAAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG 240
 TCAAGCGTGA GTGCAAGAA TGCCAAGTAC CTGCTCAAG GAGATATGT GGGCAAGGTC 300
 TTCCGGGTG ATGCAGAGAG AGGAGACGTG TTCCGCAATT AGAGGCTGGA CCGGAGAGAT 360
 ATCTCAGAGT ACCACCTCAC TGCTGTCAAT GTGGACAAAG ACACCTGGTA AAACCTGGAG 420
 ACTCCTTCCA GCTTCACCAT CAAAGTTCAT GACGTGAACG ACACTGGGCC TGTGTTCA 480
 CATCGGTTGT TCAATGCGTC CGTGCTGAG TCGTGGCTG TGGGACCTC AGTCATCTCT 540
 GTGACAGCAG TGGATGCAGA CGACCCCACT GTGGGAGACC ACGCTCTGT CATGTACCAA 600
 ATCCTGAAGG GGAAGAGATA TTTTGCCATC GATAATTCTG GACGTATTAT CACAATAAG 660
 AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGAAGC GCGAGATGCC 720
 CAGGGCCTCC GGGGGGACTC GGGCACGGCC ACCGTGCTGG TCACTCTGCA AGACATCAAT 780
 GACAACTTCC CTTCTTCAC CCAGACCAAG TACACATTG TGGTGCCTGA AGACACCCGT 840
 GTGGGCACCT CTGTGGGCTC TCTGTTGTT GAGGACCCAG ATGAGCCCCA GAACCGGATG 900
 ACCAAGTACA GCATCTTGGG GGGCGACTAC CAGGACGCTT TCACCATGTA GACAAACCC 960
 GCGACAAACG AGGGCATCAT CAAGCCCATG AAGCCTCTGG ATTATGAATA CATCCAGCAA 1020
 TACAGCTTCA TCGTCGAGGC CACAGACCCC ACCATCGACC TCGATACAT GAGCCCTCCC 1080
 GCGGGAACCA GAGCCAGGT CATTATCAAC ATCACAGATG TGGAGGAGCC CCCCATTTC 1140
 CAGCAGCCTT TCTACCACT CCAGCTGAAG GAAAACCAAG AGAAGCCTCT GATTGGCACA 1200
 GTGCTGGCCA TGGACCTGTA TGGCGTAGG CATAGCATTG GATACTCCAT CCGCAGGACC 1260
 AGTGACAAAG GCCAGTCTCT CCGAGTCACA AAAAAGGGGG ACATTACAA TGAGAAAGAA 1320
 CTGGACAGAG AAGTCTACCC CTGGTATAAC CTGACTGTGG AGGCCAAAGA ACTGGATTCC 1380
 ACTGGAACCC CCACAGGAAA AGAATCCATT GTGCAAGTCC ACATTGAAGT TTTGGATGAG 1440
 AATGACAAAG CCCCGAGTT TGCCAAGCCC TACCAGCCCA AAGTGTGTGA GAACGCTGTC 1500
 CATGGCCAGC TGGTCTGCA GATCTCGCA ATAGACAAGG ACATAACACC ACGAAACGTG 1560
 AAGTTCAAAAT TCACCTTGAA TACTGAGAAC AACTTTACCC TCACGGATAA TCACGATAAC 1620
 ACGGCCAACA TCACAGTCAA GTATGGGCAG TTTGACCGGG AGCATAACCA GGTCCACTTC 1680
 CTACCCGTGG TCATCTCAGA CAATGGGATG CCAAGTCGCA CGGGCACCAG CAGCTGAC 1740
 GTGGCGGTGT GCAAGTGCAG CAGCAGGGGC GAGTTCACTT TCTGCGAGGA TATGGCGGCC 1800
 CAGGTGGGCG TGGACATCCA GGCAGTGGTA GCCATCTTAC TCTGCATCTT CACCATCACA 1860
 GTGATCACCC TGCTCATCTT CTTGCGCGCG CGCTCCCGGA AGCAGGCCCG CGCGCACGGC 1920
 AAGAGCGTGC CCGAGATCCA CGAGCAGCTG GTCACTACG ACGAGGAGGG CCGCGCGGAG 1980
 ATGACACCCA CAGCTACGA TGTGTGGGTG CTCACCTCGG TCGCGCGGGG CGGGGCCAAG 2040
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 AGGCAACGCG CCGGGGACCA CGGAGGGCCC GGGGAGATGG CAGCCATGAT AGAGGTGAAG 2160
 AAGGACGAGG CCGACCAAGA CCGCGACGGC CCGCCCTACG ACACGCTGCA CATCTACGGC 2220
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	TCTGACGTGG	ATTACGACTT	CCTTAAAGAC	TGGGGACCCA	GGTTTAAGAT	GCTGGCTGAG	2340
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	CTGGGGACCC	AAACCCCTCG	CAGCCAGGC	CAGTCAGACT	CCAGSCACCA	CAGCCTCCAA	2460
	AAATGGCAGT	GACTCCCGAG	CCAGCACCC	CTTCTCTGTG	GGTCCAGAG	ACCTCATCAG	2520
5	CCTTGGGATA	GCAAACTCCA	GGTCTCTGAA	ATATCCAGGA	ATATATGTCA	GTGATGACTA	2580
	TTCTCAAATG	CTGGCAAATC	CAGGCTGGTG	TTCTGTCTGG	GCTCAGACAT	CCACATAACC	2640
	CTGTACCCCA	CAGACCGCG	TCTAACTCAA	AGACTTCTCT	TGGCTCCCCA	AGGCTGCAAA	2700
	GCAAAACACA	CTGTGTTTAA	CTGCTGCAGG	GTCTTTTCT	AGGGTCCCTG	AACGCCCTGG	2760
	TAAGGCTGCT	GAGGTCTCTG	TGCCTATCTG	CCTGGAGGCA	AAGGCTGGA	CAGCTTGACT	2820
10	TGTGGGGCAG	GATTCTCTGC	AGCCCATTC	CAAGGAGAG	TGACCATCAT	GCCTCTCTC	2880
	GGGAGCCCTA	GCCTCTCTCC	AACTCCATAC	TCCACTCCAA	GTGCCCCACC	ACTCCCCAAC	2940
	CCCTCTCCAG	GCCTGTCAAG	AGGGAGGAAG	GGGCCCATG	GCAGCTCCTG	ACCTTGGGTC	3000
	CTGAAGTGAC	CTCACTGGCC	TGCCATGCCA	GTAAGTGTGC	TGTAAGTGC	ACTGAACACC	3060
	ATTCAAGGAA	ATGCTTATTA	AACCTTGAAG	CAACTGTGAA	TTCATTCTGG	AGGGGCACTG	3120
15	GAGATCAGGA	GTGACAGATC	ACAGGCTGAG	GGCCACCTCC	ACACCCACCC	CCTCTGAGAG	3180
	AGGCCTGGAA	GAGCTGAGAG	CTTGCTTTGA	GACTCTCTAG	CACCCCTCCA	GTCTTGGCTG	3240
	AGAAGGGGCA	GATGTTCCCG	GAGATCAGAA	GAOGTCTCCC	CTTCTCTGCG	TCACCTGGTC	3300
	GCCAATCCAT	GCTCTCTTTC	TTTCTCTGT	CTACTCTCTA	TCCCTTGGTT	TAGAGGAACC	3360
	CAAGATGTGG	CCCTTAGCAA	AACTGACAAT	GTCCAAACCC	ACTCATGACT	GCATGACGGA	3420
20	GCGAGCATG	TGCTTTTACA	CCTGCTGTT	GTACATCTCT	AGGGAACTGA	CCCTCAGGCA	3480
	CACCTTGACG	AAGGAAGGCC	CTGCCCTGCC	CAACCTCTGT	GGTCAACCAT	GCATCATTCC	3540
	ACTGGAACGT	TTCACTGCAA	ACACACCTTG	GAGAAGTGGC	ATCAGTCAAC	AGAGAGGGGC	3600
	AGGGAAGGAG	ACACCAAGCT	CACCTTCTGT	CATGGACCGA	GGTCCCACT	CTGGCAAAGC	3660
	CCCTCACACT	GCAAGGGATT	GTAGATAACA	CTGACTTGTT	TGTTTTAACC	AATAACTAGC	3720
25	TTCTTATAAT	GATTTTITTA	CTAATGATAC	TTACAAGTTT	CTAGCTCTCA	CAGACATATA	3780
	GAATAAGGTT	TTTTGATATA	TAAGCAGGTT	GTATTTTAGG	TTAACAATAT	TAATTCAGGT	3840
	TTTTTAGTTG	GAAAAACAAT	TCCTGTAAAC	TTCTATTTTC	TATAATTGTA	GTAATTGCTC	3900
	TACAGATAAT	GTCTATATAT	TGGCCAAACT	GGTGCATGAC	AAGTACTGTA	TTTTTTTATA	3960
30	CCTAAATAAA	GAAAAATCTT	TAGCCTGGGC	AACAAAAAAA			

Seq ID NO: 339 Protein sequence
Protein Accession #: NP_001786

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	NTSLPHEVKG	IKSSVSRKNA	KYLLKGEYVG	KVFRVDAETG	DVPAIERLDR	ENISEYHLTA	120
	VIVDKDTGEN	LETSPSSFTIK	VHDVNDNWPV	FTHRLFNASV	PESSAVGTSV	ISVTAVDADD	180
	PTVGDHASVM	YQILKGEYFP	AIDNSGRIIT	ITKSLDREKQ	ARYEIVVEAR	DAQGLRGDSG	240
40	TATVLVLTQD	INDNFPFFTG	TKYTFVVPED	TRVGTSVGSL	PVEDFDEPQN	RMTRYSLRG	300
	INQDAPFTEI	NPAENEGIIK	PMKPLDYEYI	QQYSFIVEAT	DPTIDLRYMS	PPAGNRAQVI	360
	INTIDVDEPP	IFQPPFYHFP	LKENQKKPLI	GTVLAMDFA	ARHSIGYSIR	RTSDKGQFFR	420
	VTKKGDIIYE	KELDREVYPV	YNLTVEAKEL	DSTGTPPTKE	SIVQVHIEVL	DENDNAPEFA	480
	KPYQPKVCEN	AVHQQLVLQI	SAIDRDIPTP	NVFKFPLTNT	ENNPFLTDNH	DNTANITVKY	540
45	QPDFREHTIV	HFLPVVISDN	GMPSTRGTST	LTVAVCCKNE	QGEPTFCEDM	AAQGVVSIQA	600
	VVAILLCLIT	ITVTTLILFL	RRRLRKQARA	HGKSVPEIHE	QLVTYDEEGG	GEMDITTSYDV	660
	SVLNSVRRGG	AKPRPRPALDA	RPSLYAQVOK	PFRHAPGAEG	GRGEMAAMIE	VKKDEADHDG	720
	DGPPYDTLHI	YGYEGSESIA	ESLSLGLTDS	SDSDVDYDFL	MDWGRPFKML	AELYGSDPRE	780
50	ELLY						

Seq ID NO: 340 DNA sequence
Nucleic Acid Accession #: NM_003088
Coding sequence: 112-1593

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60	AAOCCGACAG	CCGAGGCGGT	GCAGATCCAG	TTCCGCTCTA	TCAACTGCCG	CAACAAGTAC	180
	CTGACGGCCG	AGGGCTTCGG	GTTCAAGGTG	AACGCGTCCG	CCAGCAGCCT	GAAGAAGAAG	240
	CAGATCTGGA	CGCTGGAGCA	GCCCCCTGAC	GAGGCGGGCA	GCGCGGCCGT	GTGCTGCGC	300
	AGCCCACTGG	GGCCCTACCT	GGCGGCGGAC	AAGGACGGCA	AOGTGAACCT	CGAGGCGGAG	360
	GTGCGCGGTC	CGGACTCGCG	TTTCTCATC	GTGGCGCAGG	ACGACGGTCG	CTGGTCGCTG	420
65	CAGTCCGAGG	CGCACCGGCG	CTACTTCGCG	GGCACCGAGG	ACCGCTGTCT	CTGCTTCGCG	480
	CAGACGGTGT	CCCCCGCCGA	GAAGTGGAGC	GTGCACATCG	CCATGCACCC	TCAGGTCAAC	540
	ATCTACAGTG	TACCCCGTAA	GCGCTAGCGG	CACCTGAGCG	CGGGCGGGCC	CGACAGATC	600
	GCGGTGGACC	GCGACGTGCC	CTGGGGCGTC	GACTCGCTCA	TCAACCTCGC	CTTCCAGGAC	660
	CAGCGCTACA	GCGTGCAGAC	CGCCGACCC	CGCTTCTGCG	GCCAGCAGCG	GCGCTCGGTC	720
70	GCGGCGCCCG	AGCGCGCCAC	TGGCTACACG	CTGGAGTTCC	GCTCCGGCAA	GGTGGCCTTC	780
	CGCGACTGCG	AGGGCCGTTA	CCTGGCGCCG	TGGGGGCCCA	GCGGCAGGCT	CAAGGCGGGC	840
	AAGGCCACCA	AGGTGGGCAA	GGACGAGCTC	TTTGCTCTGG	AGCAGAGCTG	CGCCAGGTC	900
	GTGCTGCAGG	CGGCCAACGA	GAGGAACGTG	TCCACGGGCC	AGGGTATGGA	CCTGTCTGCC	960
	AATCAGGACG	AGGAGACCGA	CCAGGAGACC	TTCCAGCTGG	AGATCGACCG	CGACACCAAA	1020
75	AAGTGTGCTT	TCCGTACCCA	CACGGGCAAG	TACTGGACGC	TGACGGCCAC	CGGGGGCGTG	1080
	CAGTCCACCG	CCTCCAGCAA	GAATGCCAGC	TGCTACTTTG	ACATCGAGTG	GCGTGACCGG	1140
	CGCATCACAC	TGAGGGCGTC	CAATGGCAAG	TTTGTGACCT	CCAAGAAGAA	TGGGCGAGTG	1200
	GCGCCCTCGG	TGGAGACAGC	AGGGGACTCA	GAGCTCTTCC	TCATGAAGCT	CATCAACCGC	1260
	CCCATCATCG	TGTTCCGCGG	GGAGCATGCG	TTTCTCGGCT	GCGGCAAGGT	CACGGGCAAC	1320
80	CTGGAGCCCA	CGCGCTCCAG	CTATGACGTC	TTCCAGCTGG	AGTTCAACGA	TGGCGCTTAC	1380
	AACATCAAAG	ACTCCACAGG	CAAATACTGG	ACGGTGGGCA	GTGACTCCGC	GGTCAACCAGC	1440
	AGCGGGGACA	CTCTGTGGGA	CTTCTTCTTC	GAGTTCTGGG	ACTATAACAA	GGTGCCCATC	1500
	AAGGTGGGCG	GGCGCTACCT	GAAGGGGAC	CACGCGAGCG	TCTGGAAGGC	CTCGCGGAA	1560
	ACGCTGGACC	CGCGCTCGCT	CTGGGAGTAC	TAGGGCGGCG	CGTCTCTTCC	CGCGCCCTGC	1620
85	CCACATGGCG	GCTCTGACCA	ACCTTCCCTG	CTAACCCCTT	CTCCGCGAGG	TGGGCTCCAG	1680
	GGCGGGAGGC	AAGCCCCCTT	GCCTTTTCAA	CTGGAAACCC	CAGAGAAAC	GGTGCCCCCA	1740
	CCTGTGCCCC	CTATGGAGTC	CCACTCTCTC	CCTCGCGCGG	GGTCCCTTAC	TCCCTCTGGG	1800

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 5 CTGTCACTGG CCTCCCTGG TGCATGTCC CGAACCCTC TGCTTGGGAA GGGAAAGCTGT 2100
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 ACAGGGTCTG CCCGCTGCAC GTTCTGCCAA GGTGGTGGTG GCGGGCGGGT AGGGGTGTGG 2280
 GGGCGCTCTT CCTCTGTCT CTTTCTTTT ACCCTAGCCT GACTGGAAGC AGAAAATGAC 2340
 10 CAAATCAGTA TTTTATTTAA TGAATATTA TTGCTGAGG CGTCCAGGC AACCTGGCT 2400
 GTAGTAGCGA GTGATCTGGC GGGGGCGGTC TCAGCACCTT CCCAGGGGG TGCACTCTAG 2460
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 15 TCCCCAACAT GCATCTCACT CTGGGTGTCT TGGTCTTTTA TTTTGTGTA GTGTCAITTG 2700
 TATAACTCTA AACGCCATG ATAGTAGCTT CAAACTGGAA ATAGCGAAAT AAAATAACTC 2760
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Seq ID NO: 341 Protein sequence
 Protein Accession #: NP_003079

1 11 21 31 41 51
 25 MTANGTAZAV QIQPLINLNG NKYLTAEAFG PKVNASASSL KKKQIWTLEQ PPDEAGSAAV 60
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 CFAQTVSPAE KWSVHIAHP QVNIYSVTRK RYAHLSARPA DEIAVD RDVP WGVDSLITLA 180
 PQDQRYSVQT ADHRLRHEDG RLVARPEPAT GYTLEFRSGK VAFRDCEGRY LAPSGPSGTL 240
 KAGKATKVGK DELFALBQSC AQVVLQANB RNVSTRQGM DLSANQDETD QBTFLQLEIDR 300
 30 DTKKCAPRTH TGKYWTLTAT GGVQSTASSK NASCYFDIEW RDRRITLRAS NGKPVTSKKN 360
 GQLAASVETA GSELFLMKL INRPIIVFRG EHGFIGCRKV TGTLDANRSS YDVFLQLEFND 420
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Seq ID NO: 342 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 660..1705

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 45 CTGAGCGGGG ACAGATCCAA GTTGGGAGCA GCTCTGCGTG CGGGGCTCA GAGAATGAGG 240
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 50 CCGGAGGGGG GCTCCAAAGA CCGTCTGTTC TGGGTGCGAC TGGAGCGCAG GCGTTCACAC 540
 TGCACTCTGG AGAACGAGCG TTTGCGGGGT TTCTCTCTGC TGCTCTCGCA CCGCGCGGT 600
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 55 TGGACTTCAG TCCACTGGG ACCGAGGTGA GTGCGCTCTG CCGGGGACAG CTCGCGATCT 900
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Seq ID NO: 343 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 75 MKKDFMTKTP KAFATKARID KMDLIKLSKF CTAKETIIRV NSQPTDWQKT FAIYPSDKGV 60
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 GLGKPAVEGG DRAPDTALRP RAGQIQVSS SACGASENEA GVRPVPPLAG ALARAGRRRT 180
 80 PHCRPCLWLG LGGLLQAPPR YHEAAGGRGG LHPARWGAQH RACGRRAARC ARAPAGRPR 240
 RRGLQRAVL GRTGAQAFPL HPGERAFAGP LLAVLRPRRS RKRHAAVGGG APTLLHRAEM 300
 RGTPEHRWGR ARSWKEMRCH LRANGYLCKY QFEVLCPAPR PGAASNLSYR APPQLHSAAL 360
 DFPSPGTEVS ALCRQLPLIS VTCIADEIGA RWDKLSGDVL CPCPGRYLRA GKCAELPNCL 420
 DDLGFPACEC ATGFELGIDG RSCVTSGBGQ PTLGGTGVPY RRPATATSP VPQRTWPIRV 480
 85 DESKLGTEPLV PQDINSVTSI PEIPIRNGSQS TMSLTQMSLQ AESKATITPS GSVISKFPNT 540
 TSSATPQAPV SSSAVVPIFV STAVVVLVIL TMTVLGLVKL CPHESPSSQP RKESWGPPPL 600
 ESDPEPAALG SSSAHCTNNG VKVGDCDLRD RAEGALLAES FLGSSDA

Seq ID NO: 344 DNA sequence
Nucleic Acid Accession #: NM_012072
Coding sequence: 149-2107

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60 TGAACGGGAG ATGATGCACT GTGTTTGAA AGTTGTCAAT TTAAGCAAT TTAGCAGAT 3180
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65 TTGCAATAT TTCTCCCTAT GATAATGCAG TCGATAGTGT GCACTCTTC TCTCTCTCTC 3480
TCTCTCTCAC ACACACACAC ACACACACAC ACACACACAC AGAGACACGG CACCATCTG 3540
CCTGGGGCAC TGAACACAT TCCTGGGGGT CACCGATGTT CAGAGTCACT AGAAGTTACC 3600
TGAGTATCTC TGGGAGGCTT CATGTCTCT GTGGGCTTTT TACCACCACT GTGCAGGAGA 3660
ACAGACAGAG GAAATGTGTC TCCTCCAAG GCGCCAAAGC CTCAGAGAAA GGGTGTCTCT 3720
70 GGTTTTGCTT TAGCAATGCA TCGGTCTCTG AGGTGACACT CTGGAGTGGT TGAAGGGCCA 3780
CAGGTGTCAG GGTAAATAT CTGCGCAGTT TTGAAATATA GATGCTATGG TTCAGATTGT 3840
TTTTAATAGA AAATAAAGG GGCAGGGGAA GTGAAAGGAA AGATGGAGGT TTTGTGCGGC 3900
TOGATGGGGC ATTTGGAAT TCTTTTAAAG GTCATCTCAT GGTCTCCAGT TTTCAAGTTG 3960
75 AACTCTGGTG TTTAACACTT AAGGGAGACA AAGGCTGTGT CCATTGGCA AAATCTCCTT 4020
GGCCACGAGA CTCTAGTGA TGTGTGAAGC TGGSCAGTCT GTGGTGTGGA GAGCAGCCAT 4080
CTGTCTGGCC ATTCAGAGGA TTCTAAAGAC ATGGCTGGAT GCGCTGCTGA CCAACATCAG 4140
CACTTAAATA AATGCAAAAT CAACATTTCT CCCTCTGGGC CTTGAAATCT CTTGCCCTTA 4200
TCATTTGGGG TGAAGGAGAC ATTTCTGTCC TTGGCTTCCC ACAGCCCCAA CGCAGTCTGT 4260
80 GTATGATCCC TGGGATCCAA CGAGCCCTCC TATTTTCACA GTGTTCTGAT TGCTCTCACA 4320
GCCAGGCCCC ATGCTCTGTT CTCTGAATGC AGCCCTGTTT TCAACAACAG GGAGGTCTAT 4380
GAACCCCTCT GTGGAACCCA CAAGGGGAGA AATGGGTGAT AAAGAATCCA GTTCTCTCAA 4440
ACCTTCCCTG GCAAGCTGGG TCCTCTCTCT GCTGGGTGTT GCTTTCTCTT GCACACCACT 4500
CCACCAAGG GGGGAGAGCC AGCAACCCAA CCAGACAGCT CAGGTGTGTC ATCTGATGGA 4560
AACCAGTGG CTCAACACG TGCTTTATTC TCCTGTTTAT TTTTGTGTTT ACTTTGAAGC 4620
85 ATGGAATTTT TGTGTTGGGG GATCTTGGGG CTACAGTAGT GGGTAAACAA ATGCCACCG 4680
GCCAAGAGCC CATTAAACAA TGTCTCTTGT CCTGAGGGGC CCCAGCTTGC TCGGCGGTGG 4740
CACAGTGGGG AATCCAAGGG TCACAGTATG GGGAGAGGTG CACCTGCCA CCTGCTAACT 4800

TCTCGCTAGA CACAGTGTIT CTGCCAGGT GACCTGTTC GCAGCAGAAC AAGCCAGGGC 4860
 CATGGGGAGC GGGGAAGTTT TCACTTGGAG ATGGACACCA AGACAATGAA GATTGTGTGT 4920
 CCAATATAGT CAAATATTTCT GGGAGACTCT TGGAAAAAAC TGAATATATT CAGGACCAAC 4980
 TCTCTCCCTC CCTCATCCOC ACATCTCAAA GCAGACAATG TAAAGAGAGA ACATCTCACA 5040
 5 CACCCAGCTC GCCATGCCCTA CTCATTCCCTG AATTTCAGGT GCCATCACTG CTCCTTTCTTT 5100
 CTCTTTTGTG ATTTGAGAAA GGATGCGAGA GGACAATTCC CACAGATAAT CTGAGGAATG 5160
 CAGAAAAACC AGGGCAGGAC AGTTATCGAC AATGCAITAG AACCTGGTGA GCATCCTCTG 5220
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 CTCTGCCCTT GGTGGCCAC ACACCTAAGC GTCATCGTCA TTGCCATAGC ATCATGATGC 5340
 10 AACACATCTA CSTGTAGCAC TACGACGTTA TGTITGGGTA ATGTGGGGAT GAACTGCATG 5400
 AGGCTCTGAT TAAGGATGTG GGAAGTGGG CTGCGGTCCAC TGTCCGCCCT GCAAGGCCAC 5460
 CTGGAGGCTT GTCTGTAGC CAGTGGTGGG AGAGCAAGGC TTCAGGAAGG GCCAGCCACA 5520
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 15 TGTCTTTGTC TTTTCCATTC TCATCACAAG CCTTGTITG AGTGTCTTAT CCTGAGCAA 5700
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 ATTTCTGTGA AAATAGGAGT AACAGAGATG AGATTGACA AAAAAAATT GAATTAATAA 5820
 TAAACACAGT TTTTAAAC TAACATAGGA AAGCCTTTCC TATTATTCTT CTCTTAGCT 5880
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 20 TTAATGCCCC ATCATATTT CCATCACCTT GAACAATAGC TTTAGCTTGG GAATCTGAGA 6000
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 TGGTTTGTGC ATTTTCTCAA CTAAAAATAG AGATGATAAT CCGAATTCTC CATATATCA 6120
 CTAATCAAAAG ACATAITTTT CATACTAGAT TCCTGAGACA AATACTCACT GAAGGGCTTG 6180
 TTTAAAAATA AATTGTGTTT TGGTCTGTTT TTGTAGATAA TGCCCTTCTA TTTTAGGTAG 6240
 25 AAGCTCTGGA ATCCCTTTAT TGTGCTGTTG CTCTTATCTG CAAGGTGGCA AGCAGTTCTT 6300
 TCTCAGCAGT TTTGCCCATC ATTCTCTGTA GCTGAAGTTC TTTGATAGA TTTGGCTTAA 6360
 GCTTGAATTA GATCCCTGCA AAGGCTTGCT CTGTGATGTC AGATGTAATT GTAAATGTCA 6420
 GTAATCACTT CATGAATGCT AAATGAGAAT GTAAGTATT TTAATGTGT GTATTTCAAA 6480
 TTTGTTTGA TAATTCTGGA ATTACAAGAT TTCTATGCAG GATTACCTT CATCCTGTGC 6540
 30 ATGTTTCCCA AACTGTGAGG AGGGAAGGCT CAGAGATCGA GCTTCTCTC TGAGTTCTAA 6600
 CAAAATGGTG CTTTGAGGGT CAGCCTTAG GAAGGTGCGC CTTTGTGTG CTTTGAAGCT 6660
 TCTGTTATGT GCCTATCCTA ATAACTCTT AAACACATT

Seq ID NO: 345 Protein sequence
 Protein Accession #: NP_036204

1 11 21 31 41 51
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 40 MATSMGLLLL LLLLLTOPGA GTGADTEAVV CVGTACYTAH SGKLSAAEAQ NHCNQNGGNL 60
 ATVKSKEBAQ HVQRVLAQLL RREAALTARM SKFWIGLQRE KGKCLDPSLP LKGFPSWVGGG 120
 EDTPYSNWHK ELRNSCISKR CVSLLLDLQ PLLPNRLPKW SEQPCGSPGS PGSNIEGFVC 180
 KPSFKGMCRP LALGGPGQVT YTTPTQTTSS SLEAVPFASA ANVACGEGDK DETQSHYFLC 240
 KEKAPDVFDW GSSGPLCVSP KYGCNFNNGG CHQDCFEGGD GSFLOGCRPG FRLLDDLVTC 300
 45 ASRNPSCSSP CRGGATCVLG PHGKNYTCRC PQGYQLDSSQ LDCVDVDECO DSPCAQECVN 360
 TPGGFRCBWC VGYEPGPGGE GACQDVDECA LGRSPCAQGC TMTDGSFPCS CEEGYVLAGE 420
 DGTQCQVDE CVGPGGLCD SLCFNTQGSF HCGCLPGMVL APNGVSTMG FVSLGPPSGP 480
 PDEEDKGEK GSTVPRAATA SPTRGPEGTP KATPTTSRPS LSSDAPITSA PLMLAPSGS 540
 SGVWRPSIH HATAASGPQE PAGGDSSVAT QNNDGTDGQK LLLFYILGTV VAILLLLLALA 600
 50 LGLLVYRKR ARREEKKEK PQNAADSYW VPERAESRAM ENQYSPTPGT DC

Seq ID NO: 346 DNA sequence
 Nucleic Acid Accession #: Z31560
 Coding sequence: <1-966

55 1 11 21 31 41 51
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 60 CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCGCGG CCGCGAGCAA 60
 ACTTCGGGGG GCGGCGGCGG CAACTCCACC GCGGCGGCGG CCGGCGGCAA CCGAAAAAAC 120
 AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCACTG TGTGTTCCCG CCGGCGAGCG 180
 65 CGCAGATGG CCGCAGAGAA CCGCAAGATG CACAACCTCG AGATCAGCAA GCGCCTGGGC 240
 GCGAGTGGGA AACTTTTGTG GGAGACGGAG AAGCGGCGGT TCATCGACGA GGCTAAGCGG 300
 CTGCGAGCGC TGCACATGAA GGAGCACCCG GATTATAAAT ACCGCGCCCG GCGGAAAACC 360
 AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCGCGGCG GGCTGCTGGC CCGCGGCGGC 420
 AATAGCATGG CGAGCGGGGT CCGGGTGGGC GCGCGGCTGG GCGCGGCGGT GAACACAGCGC 480
 70 ATGGACAGTT ACGCGCACAT GAAACGCTGG AGCAACGGCA GCTACAGCAT GATGAGGAC 540
 CAGCTGGGCT ACCCGCAGCA CCGGGGCTCT AATGCGCAG GCGCAGCGCA GATGAGCGCC 600
 ATGACCGGCT ACGACGTGAG CGCCCTGCAG TACAACCTCA TGACAGCTC GCAGACCTAC 660
 ATGAACGGCT CGCCACCTA CAGCATGTCC TACTGCGAGC AGGCGACCCC TGGCATGGCT 720
 CTGTGCTCCA TGGGTTGCGT GGTCAAGTCC GAGGCGAGCT CCAGCCCCC TGTGTTTACC 780
 75 TCTTCTCTCC ACTCCAGGCG GCCCTGCCAG GCGGGGACC TCGGGGACAT GATCAGCATG 840
 TATCTCCCGG GCGCGGAGGT GCGGAAACCC GCGGCCCCCA GCAGACTTCA CATGTCCAG 900
 CACTACAGGA GCGGCGCGGT GCCCGGCACG GCGATTAAAG GCACACTGCC CCTCTCACAC 960
 ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAGAAAAA ACGAGGGA 1020
 TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAAACCCGG TACGCTCAAA 1080
 AAAAA

Seq ID NO: 347 Protein sequence
 Protein Accession #: CAA83435

80 1 11 21 31 41 51
 | | | | |
 HSARMYNMME TELKPPGPQO TSGGGGNGST AAAAGGNQXN SPDRVKRPMN AFMVWSRGQR 60
 RMAQENPKM HNSISIKRLG AEWKLLSETE KRPFIDRAKR LRALHMKRHP DYKYRPRRET 120
 85 KTLMKDKYT LPSGLLAPGG NSMASGVGVG AGLGAGVNRQ MDSYAHMNGW SNGSYSMQD 180
 QLGYFPQHPGL NABGAQMQLP MERYDVSLAQ YNSMTSSQTY MNGSPYSMS YSQQGTGMA 240
 LGSMSVVKSE EASSPPPVVT SSSHSRAPCQ AGDLRDMISM YLPGAEPVPE AAPSRLEMSQ 300
 HYQSGFVPGT AINGTLPLSH M

Seq ID NO: 348 DNA sequence
Nucleotide Accession #: NM_002638
Coding sequence: 120-473

5
1 11 21 31 41 51
CAATACAGCT AAGGAATTAT CCCTTGTAAG TACCACAGAC CGCCCTGGA GCCAGGCCAA 60
GTGGAGCTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
10 TGAGGGCTCAG CAGCTTCTTG ATCGTGGTGG TGTCTCTCAT CGCTGGGAGC CTGGTTCATG 180
AGGAGCTGT CAOCGGAGTT CCTGTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
TCCGGTGGCC CATGTGGAAT CCCCTAACC GCTGCTTGA AGATACTGAC TGCCAGGAA 420
15 TCAAGAAAGT CTGTGAAGGC TCTTGGGGA TGGCTCTGTT CGTTCCCCAG TGAAGGGAGC 480
CGGTCTCTGC TGCACTCTGT CCGTCCCCAG AGCTACAGGC CCATCTGGT CTAAGTCCC 540
TGCTGCCCTT CCCTTCCCA CACTGTCCAT TCTTCTCCC ATTCAGGATG CCCAGGCTG 600
GAGCTGCCCT TCTCATCCAC TTCCAATAA A

20 Seq ID NO: 349 Protein sequence:
Protein Accession #: NP_002629

25 1 11 21 31 41 51
MRASSFLIVV VFLIAGTLVL EAAVTGVFVK QQDTVKGRVP FNGQDPVKQ VSVKGQDKVK 60
AQEPVKGPIVS TKPSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCEBSCG MACFPVPQ

30 Seq ID NO: 350 DNA sequence
Nucleic Acid Accession #: NM_007183
Coding sequence: 75-2468

35 1 11 21 31 41 51
GAATTCGGA CAGGACGTGA AGATAGTTGG GTTTGGAGGC GGCCGCCAGG CCCAGGCCCG 60
GTGGAGCTGC CGCAGTGCAG GACGGTAACT TCCTGCTGTC GGCCCTGCAG CCTGAGGCCG 120
GCGTGTCTC CTGGGGCTG CCGCTCTGACC TGCAGCTGGA CGCCCGGGGC GCGAGGGGCG 180
CGGAGGCCGA GCGGCTGCGG GCAGCCCGCG TCCAGGAGCA GGTCCGCGCC CGCCTCTTGC 240
40 AGCTGGGACA GCAGCCCGCG CACAACGGGG CCGCTGAGCC CGAGCCTGAG GCGGAGACTG 300
CCAGAGGCAC ATCCAGGGGG CAGTACCACA CCCTGCAGGC TGGCTTCAGC TCTGCTCTC 360
AGGGCTGAG TGGGGAACAG ACCTCGGGCT TCCGCCCAT CGCCAAGCGG GCCTACAGCC 420
CAGCCTCTG GTCTCCCGC TCCGCCGTG ATCTGAGCTG CAGTCCGAGG CTGAGTTTCA 480
CCCAATATGG GGGCAGGCGC TTTGGGGCCG CTGGGTACGG GGGTGGCCAG CCCACCCCTC 540
CCATGCCAC CAGCCCGCTG TCCTTCCATG AGCGCGGTGG GGTGGGAGC CGGGCCGACT 600
45 ATGACACACT CTCCCTGCGC TCGCTGCGGC TGGGGCCCGG GGGCCTGGAC GACCGCTACA 660
GCTGTGTGT TGAGCAGCTG GAGCCCGCG CCACCTCCAC CTACAGGGCC TTTGCGTACG 720
AGCGCCAGCC CAGCTCCAGC TCCAGCCGGG CAGGGGGGCT GACTGTGCC GAGGCCACTG 780
AGGTTTCCC GAGCCGGACC ATCCGTGCCC CTGCGGTGCG GACCTGCAG CGATTCCAGA 840
GCAGCCACCG GAGCCCGCG GTAGCGGGG CAGTCCCGGG GGCCGTCTG GAGCCAGTGG 900
50 CTGAGCGCC ATCTGTGCGC AGCCTCAGCC TCAGCCTGGC TGACTCGGGC CACTGCGCG 960
ACGTGCATGG GTTCAACAGC TACGGTAGCC ACCGAACCTT GCAGAGACTC AGCAGCGTT 1020
TTGATGACAT TGACCTGCCC TCAGCAGTCA AGTACCTCAT GGCTTCAGAC CCCAACCTGC 1080
AGGTGCTGGG AGCGGGCTAC ATCCAGCACA AGTGTACAG CGATGCAGCC GCCAAGAGC 1140
AGGCCCGCAG CCTTCAGGCC GTGCTTAGGC TGGTGAAGCT CTTCAACAC GCCAACCCAG 1200
55 AAGTGCAGC CCAATGCCCA GGTGCCATGC GCAACCTCAT CTAAGACAAC GCTGACACA 1260
AGCTGCGCT GGTGAGGAG AAAGGGATCT TCGAGCTGCT GCGGACACTG CGGAGCAGG 1320
ATGATGAGCT TCGCAAAAT GTCCAGGGA TCCTGTGAA CCTTTCATCC AGCGACCCAC 1380
TGAAGGACCG CCTGGCCAGA GACAOGCTGG AGCAGCTCAC GGACCTGGTG TTGAGCCCCC 1440
TGTGCGGGGC TGGGGGTCCC CCGCTCATCC AGCAGAACCG CTGGAGGGG GAGATCTTCT 1500
60 ACAAAGCCAC CGGCTTCTCT AGGAACCTCA GCTCAGCCTC TCAGGCCACT CGCCAGAAGA 1560
TGCAGGAGTG CCACGGGCTG GTGAGCGCCC TGGTCACTTC TATCAACAC GCCCTGGAAG 1620
CGGGCAATG CGAGGACAAG AGCGTGGAGA ACGCGGTGTG GTCTCTGCGG AACCTGTCTC 1680
ACCGCTCTA CGACGAGATG CCGCGCTCG CGCTGCAGCG GCTGGAGGGT CGCGGCGCA 1740
GGGACCTGGC GGGGGCGCG CCGGGAGAGG TCGTGGGCTG CTTCAAGCGG CAGAGCCCGC 1800
65 GGCTGCGGA GCTGCCCTC GCGCGCATG CGCTCACCTT CGCGGAGGTG TCCAAGGACC 1860
CCAGGGCCT CAGTGGCTG TGGAGCCCC AGATCGTGGG GCTGTACAAC CGGTGCTGC 1920
AGCGCTGCGA GCTCAACCGG CACACGAGG AGCGGGCCCG CGGGCGCTG CAGAACATCA 1980
CGCGAGGGA CCGCAGGTGG GCGGGGGTGC TGAGCCGCTT GGCCCTGGAG CAGGAGGTA 2040
TTCTGAACCC CCGTGTAGAC GGTGTAGGA CCGCGACCA CCACAGCTG CGCTCACTGA 2100
70 CTGGCTCAT CCGAAACCTG TCTGGAAAG CTAGGAACAA GGAAGAGATG TCCAGGAAG 2160
TGGTGAAGCA CCTGATCGAG AAGCTGCCAG GCAGCGTGGG TGAGAAGTGG CCCCAGCCG 2220
AGGTGCTGCT CAACATCATA GCTGTGCTCA ACAACCTGGT GGTGGCCAGC CCTATGCTG 2280
CCGAGAGCT GCTGTATTTT GACGAGTCC GAAAGCTCAT CTTATCAAG AAGAGCGGG 2340
75 ACAGCCCGA CAGTGAAGG TCCTCCCGGG CAGCATCCAG CCTCTGGCC AACCTGTGGC 2400
AGTACAACA GCTCCACCGT GACTTTCGGG CGAAGGGCTA TGGGAAGGAG GACTTCTGG 2460
GCCCATAGT GAAGCCTTCT GGAGGAGAAG GTGACGTGGC CCAGCGTCCA AGGGACAGAC 2520
TCAGCTCCAG GCTGCTTGGC AGCCAGCGCT GGAGGAGAAG GCTAATGAGC GAGGGGCCCC 2580
TGGCTGGGG CCGTGTGTCG ATCTTGGAG GTCTTGGGC ACCAGGAGGG GCAGGGTCTT 2640
80 ATAGCTGGGG ACTTGTGCTC GCAGGGCAG GGGGTGGGG AGGGCTCAAG GCTGCTCTG 2700
TGATGGGGT GGTGAGCCAG TCACATTGGC AGAGGTGGGG GTTGGCTGTG GCTGCGCAGT 2760
ATCTGGGAT AGCCAGCACT GGAATAAAG ATGGCCATGA ACAGTCAAA AAAAAAAAAA 2820
AAAAGGAATT C

85 Seq ID NO: 351 Protein sequence
Protein Accession #: NP_009114.1

1 11 21 31 41 51

	1	11	21	31	41	51	
	MQDGNFLLSA	LQPEAGVCSL	ALPSDLQLDR	RGAEQPEAER	LRAARVQEQV	RARLLQLGQQ	60
	PRHNGAAEPE	PEAETARGTS	RQGYHTLQAG	FSSRSQGLSG	DRTSGFRPIA	KPAYSPASNS	120
5	SRSAVDLSCS	RRLSSAHNGG	SAPGAAGYGG	AQPTPFMPTR	PVSFHERGGV	GSRADYDTLS	180
	LRSLRLGPGG	LDDRYSLVSE	QLEPAATSTY	RAFAYERQAS	SSSSRAGGLD	WPEATEVSFS	240
	RTIRAPAVRT	LQRFQSSERS	RGVGGAVPGA	VLEPVARAPS	VRSLSLSLAD	SGHLPDVHGF	300
	NSYGSHERTLQ	RLSSGPDID	LPSAVKYLMA	SDPNLQVLGA	AYIQHKCYSD	AAAKQQRSL	360
	QAVPRLVRLF	NMANEQVQRH	ATGAMRNLIY	DNADNKLALV	EENGIFELLR	TLREQDDSLR	420
10	KNVTGILMNL	SSSDHLKDRL	ARDTLEQLTD	LVLSPLSGAG	GPFLIQONAS	EAEIPYNATG	480
	FLRNLSASQ	ATRQKRECH	GLVDALVTSI	NHALDAGKCE	DKSVENAVCV	LRNLSYRLYD	540
	EMPPSALQRL	EGGRRDLAG	APGEVVGCF	TPQSRRLREL	PLAADALTFA	EVSKDPKGLF	600
	WLNSPQIVGL	YNRLQLRCEL	NRHTTEAAG	ALQNTAGDR	RWAGVLSRLA	LEQERILNPL	660
	LDRVRTADHH	QLRSLTGLIR	NLSRNARNKD	EMSTKVVSHL	IEKLPGSVGE	KSPPAEVLVN	720
15	IIAVLNLNVV	ASPIAADLL	YFDGLRLIF	IKKKRDSPTS	EKSSRAASSL	LANLWQYNKL	780
	HRDFRAKGYR	KEDFLGP					

Seq ID NO: 352 DNA sequence
Nucleic Acid Accession #: M31469
Coding sequence: 1-651

	1	11	21	31	41	51	
	ATGGCTGCGC	AGGGAGAGCC	CCAGGTCCAG	TTCAAACTTG	TATTTGGTGG	TGATGGTGGT	60
25	ACTGGAAAAA	CGACCTTGGT	GAAACGTCAT	TTGACTGGTG	AAATTTGAGAA	GAAGTATGTA	120
	GCCACCTTGG	GTGTTGAGGT	TCATCCCTTA	GTGTTCCACA	CCAACAGAGG	ACCTATTAAAG	180
	TTCAATGTAT	GGGACACAGC	CGGCCAGGAG	AAATTCGGTG	GACTGAGAGA	TGGCTATTAT	240
	ATCCAAGCCC	AGTGTGCCAT	CATAATGTTT	GATGTAACAT	CGAGAGTTAC	TTACAGAAAT	300
	GTGCCCTAAT	GGCATAGAGA	TCTGGTACGA	GTGTGTGAAA	ACATCCCAT	TGTGTTGTGT	360
30	GGCAACAAA	TGGATATTAA	GGACAGGAAA	GTGAAGGCGA	AATCCATTGT	CTTCCACCGA	420
	AAGAAGAATC	TTCACTACTA	CGACATTTCT	GCCAAAAGTA	ACTACAACCT	TGAAAAGCCC	480
	TTCTCTCGCC	TTGCTAGGAA	GCTCATTGGA	GACCCTAAT	TGGAATTGT	TGCCATGCCT	540
	GCTCTCGCCC	CACCAGAAAT	TGTCATGGAC	CCAGCTTTGG	CAGCACAGTA	TGAGCACGAC	600
35	TTAGAGGTTG	CTCAGACAC	TGCTCTCCCG	GATGAGGATG	ATGACCTGTG	A	

Seq ID NO: 353 Protein sequence
Protein Accession #: AAA36546

	1	11	21	31	41	51	
	MAAQGEPOVQ	FKLVLVGDGG	TGKTTFKVRH	LTGEFEKKYV	ATLGVEVHPL	VFHTNRGPIK	60
40	FNVDITAGQE	KFGGLRDGY	IQACALIMF	DVTSRVTYKN	VPMHRDLVR	VCEINIPVL	120
	GNKVDIKDRK	VKAKSIVFHR	KKNLQYYDIS	AKSNYNFBKP	FLMLARKLIG	DPNLEFVAMP	180
45	ALAPPEVVM	PALAAQYED	LEVAQTALP	DEDDDL			

Seq ID NO: 354 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304-831

	1	11	21	31	41	51	
	CCGGTTCCGA	AAGAAGCTGA	CTTCAGAGGG	GGAAACTTTC	TTCTTTTAGG	AGGCGGTTAG	60
55	CCCTGTTCCA	CGAACCCAGG	AGAACTGCTG	GCCAGATTAA	TTAGACATTG	CTATGGGAGA	120
	CGTGTAACA	CACACTTAT	CATTGATGCA	TATATAAAAC	CATTTTATTT	TGCTATTAT	180
	TTCAAGAGAA	GGGCTCTGA	TTTGTTCTTT	TTTTCCCTTT	TTGCTCTTTC	TGGCTGTGTG	240
	GTGTTGAGAA	AGCACAGTTG	GAGTAGCCGG	TTGCTAAATA	AGTCCGAGC	GCGAGCGGAG	300
	ACGATGCAGC	GGAGACTGGT	TCAGCAGTGG	AGCGTGGCGG	TGTTCTCTGT	GAGCTACGCG	360
60	GTGCGCTCCT	GGGCGGCTC	GGTGAGGGGT	CTCAGCCGCC	GCCTCAAAAG	AGCTGTGTCT	420
	GAAACATCAGC	TCCCTCATGA	CAAGGGGAAG	TCCATCCAAG	ATTACGGCGG	ACGATTCTTC	480
	CTTCACCATC	TGATGCAGAA	AATCCACACA	GCTGAAATCA	GAGCTACCTC	GGAGGTGTCC	540
	CCTAACTCCA	AGCCCTCTCC	CAACACAAAG	AACACCCCG	TCCGATTTGG	GTCTGATGAT	600
	GAGGGCAGAT	ACCTAACTCA	GGAACTAAC	AAGGTGGAGA	CGTACAAAGA	GCAGCCGCTC	660
65	AAGACACCTG	GGAAGAAAA	GAAAGGCAAG	CCCGGGAAG	GCAAGGAGCA	GGAAAGAGAA	720
	AAACGGGGA	CTCGCTCTGC	CTGGTTAGAC	TCTGGAGTGA	CTGGGAGTGG	GCTAGAAGGG	780
	GACCACTCTG	CTGACACCTC	CACAACGTCG	CTGGAGCTCG	ATTACAGGTA	ACAGGCTTCT	840
	CTGGCCCGTA	GCCTCAGCGG	GGTGCTCTCA	GCTGGGTTTT	GGAGCCTCCC	TTCTGCCTTG	900
	GCTTGGACAA	ACCTAGAATT	TTCTCCCTTT	ATGTATCTCT	ATOGATTGTG	TAGCAATTGA	960
70	CAGAGAATAA	CTCAGAAAT	TGCTGCTCT	AAAGCAGTAC	CCCCCTACCA	CACACACCCC	1020
	TGTCTCCAG	CACCATAGAG	AGGCGCTAGA	GCCCATTCCT	CTTCTCCAC	CGTACCCCAA	1080
	CATCAATCCT	TACCACTCT	ACCAATAAAT	TTCATATTCA	AGCTTCAGAA	GCTAGTGACC	1140
	ATCTTCATA	TTTGCTGGAG	AAGTGATATT	CTTCCCTTCA	CTCTCACACC	TGGGCAAACT	1200
	TTCTTCAGTG	TTTTCATT	CTTACGTTCT	TTCACTTCAA	GGGAGAAAT	AGAAGCATT	1260
75	GATATTATCT	ACAAACACTG	CAGAACAGCA	TCATGTCTCA	AAAGATTCTG	AGCCATTCTC	1320
	ACTTTTATT	TAATTAATG	TATTTAATTA	AATCTCAAA	TTATTTTAA	GTAAAGAACT	1380
	TAAATTATGT	TTTAAACACA	TGCCTTAAAT	TTGTTTAAAT	AAATTAACT	CTGGTTTCTA	1440
	CCAGCTCATA	CAAAATAAAT	GGTTTCTGAA	AATGTTTAA	TATTAACCTA	CAAGGATATA	1500
80	GGTTTCTCT	ATGTATCTTT	TTGTTCTATT	GCAAGATGAA	ATAATTTTTC	TAGGGTAATG	1560
	CCGTAGGAAA	AATAAACTT	CACATTAAAA	AAAAA			

Seq ID NO: 355 Protein sequence
Protein Accession #: NM_002820

	1	11	21	31	41	51	
85	MQRRLVQQMS	VAVFLSYAV	PSCGRSVEGL	SRRLKRAVSE	HQLLHDKGKS	IQDLRRRPFL	60
	HELLAEIHTA	EIRATSEVSP	NSKPSPTNKN	HPVRFSGSDE	GRYLQTETNK	VETYEQPLK	120

TPGKKKKGPK GKKRBEQKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSR

Seq ID NO: 356 DNA sequence

Nucleic Acid Accession #: NM_017522

Coding sequence: 1-2100

5

1	11	21	31	41	51	
ATGGGCTCC	CCGAGCCGGG	CCCTCTCCGG	CTTCTGGGCG	TGCTGCTGCT	GCTGCTGCTG	60
CTGCTGCTGC	TGCGGCTCCA	GCATCTTGCG	GCGGCAGCGG	CTGATCCGCT	GCTCGGCGGC	120
CAAGGGCCGG	CCAAGGAGTG	CGAAAAGGAC	CAATTCCAGT	GCCGGAAACGA	GCGCTGCATC	180
CCCTCTGTGT	GGAGATGCGA	CGAGGACGAT	GACTGCTTAG	ACCACAGCGA	CGAGGACGAC	240
TGCCCCAAGA	AGACCTGTGC	AGACAGTGAC	TTCACCTGTG	ACAAAGGCCA	CTGCATCCAC	300
GAACGGTGGG	AGTGTGACGG	CGAGGAGGAG	TGTCTGTATG	GCTCCGATGA	GTCCGAGGCC	360
ACTTGCACCA	AGCAGGTGTG	TCCGTGCAGG	AAGCTGAGCT	GTGGAGCCAC	CAGCCACAAG	420
TGTGTACCTG	CCTCGTGGCG	CTGCGACGGG	GAGAAGGACT	GCGAGGGTGG	AGCGGATGAG	480
GCGGCTGTGT	CTACCTCACT	GGGCACTGCG	CGTGGGAGCG	AGTTCCAGTG	TGGGGATGGG	540
ACATGTGTCC	TTCGAATCAA	GCATCTCAAC	CAGGAGCAGG	ACTGTCCAGA	TGGGAGTGAT	600
GAAGCTGGCT	GCCTACAGGG	GCTGAACGAG	TGTCTGCACA	ACAATGGCGG	CTGCTCACAC	660
ATCTGCACCTG	ACCTCAAGAT	TGGCTTTGAA	TGCACTGGCC	CAGCAGGCTT	CCAGCTCCTG	720
GACCAAGAAG	CTTGTGGCGA	CATTGATGAG	TGCAAGGACC	CAGATGCCCTG	CAGCCAGATC	780
TGTGTCAATT	ACAAGGCGCA	TTTTAAGTGT	GAGTGTCTACC	CTGGCTGCGA	GATGGACCTA	840
CTGACCAAGA	ACTGCAAGGC	TGCTGCTGGC	AAGAGCCCAT	CCCTAATCTT	CACCAACCGC	900
ACGAGTGGCG	AGGATCGACC	TGTGAAGCGG	AACATTTTAC	GCCTCATCCC	CATGCTCAAG	960
AATGTCGTGG	AGTCAAGATG	GGAAGTTGCC	ACCAATCGCA	TCTACTGGTG	TGACCTCTCC	1020
TACCGTAAGA	TCTATAGCGC	CTACATGGAC	AAGGCCAGTG	ACCCGAAAGA	GCGGGAGGTC	1080
TCATTTGAAG	AGCAGTTTGA	CTCTCCAGAG	GGCCTGGCAG	TGGACTGGGT	CCACAAGCAC	1140
ATCTACTGGA	CTGACTCGGG	CAATAAGACC	ATCTCACTGG	CCACAGTTGA	TGGTGGCCGC	1200
CGACGCACCTC	TCTTCAGCCG	TAACCTCAGT	GAACCCCGGG	CCATCGCTGT	TGACCCCTTG	1260
CGAGGGTTCA	TGTATTGGTG	TGACTGGGGG	GACCAAGCCA	AGATTGAGAA	ATCTGGGCTC	1320
AACGGTGTGG	ACCGGCAAGC	ACTGGTGTCA	GACAATATTG	AATGGCCCAA	CGGAATCACC	1380
CTGATCTGTC	TGAGCCGAGG	CTTGTACTGG	GTAGACTCCA	AGCTACACCA	ACTGTCCAGC	1440
ATTGACTTCA	GTGGAGGCAA	CAGAAAGACG	CTGATCTCCT	CCACTGACTT	CCTGAGCCAC	1500
CCTTTTGGGA	TAGCTGTGTT	TGAGGACAA	GTGTTCTGGA	CAGACCTGGA	GAACGAGGCC	1560
ATTTTCAGTG	CAATCGGCTG	CAATGGCCTG	GAAATCTCCA	TCTGGCTGGA	GAACCTCAAC	1620
AACCCACATG	ACATTGTCTAT	CTTCCATGAG	CTGAAGCAGC	CAAGAGCTCC	AGATGCTCTG	1680
GAGCTGAGTG	TCCAGCCTAA	TGGAGGCTGT	GAATACCTGT	GCTTCTCTGC	TCTCTAGATC	1740
TCCAGCCACT	CTCCCAAGTA	CACATGTGCC	TGTCTTGACA	CAATGTGGCT	GGGTCCAGAC	1800
ATGAAGAGGT	GCTACCGAGA	TGCAAAATGAA	GACAGTAAGA	TGGGCTCAAC	AGTCACTGCC	1860
GCTGTTATCG	GGATCATAGT	GCCCATAGTG	GTGATAGCCC	TCTGTGTCAT	GAGTGGATAC	1920
CTGATCTCGA	GAACATGGA	GCGGAAGAAC	ACCAAAAGCA	TGAATTTTGA	CAACCCAGTC	1980
TACAGAAAA	CAACAGAAGA	AGAAGATGAA	GATGAGCTCC	ATATAGGGAG	AACGTCTCAG	2040
ATTGGCCATG	TCTATCCTCG	ACGAGTGGCA	TTAAGCCTTG	AAGATGATGG	ACTACCCCTGA	2100
GGATGGGATC	ACCCCTCTCG	TGCCTCATGG	AATTCAGTCC	CATGCACTAC	ACTCCGGATG	2160
GTGTATGACT	GGATGAATGG	GTTTCTATAT	ATGGGCTGTG	GTGAGTGTAT	GTGTGTGTGT	2220
GATTTTTTTT	TTTAAATTTA	TGTTGCGGAA	AGGTAACCAC	AAAGTTATGA	TGAATGCAAA	2280
ACATCCAAAG	GATGTGAGAG	TTTTTCTATG	TATAATGTTT	TATACACTTT	TTAACTGGTT	2340
GCACTACCCA	TGAGGAATTC	GTGGAATGGC	TACTGCTGAC	TAACTATGAT	CACATAACCA	2400
AATGGGGGCC	AATGGCAGAC	TACCTTACTC	ATCATTTAAA	AACATATATT	ACAGAAGATG	2460
TTTGTGTGCT	GGGGGCTTTT	TTTAGGTTTT	GGGCATTGTG	TTTTTGTAAA	TAAGATGATT	2520
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Seq ID NO: 357 Protein sequence

Protein Accession #: NP_059992

55

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PSVWRCEDD	DCLDHSEDD	CPKKTCAAD	FTCDNGHCII	ERWKCDEGEE	CPDGSDESEA	120
TCIKQVPAE	KLSGPTSHK	CVPASWRCDG	EKDCGGGADE	AGCATSLGTC	RGDEFQCGDG	180
TCVLAIKHCN	QEQDCPDGSD	EAGCLQGLNE	CLHNNGGCSE	ICTDLKIGFE	CTCPAGFOLL	240
DQRTCGDIDE	CKDPDACSQI	CVNYKGYFKC	ECYPGCEMDL	LTRNCKAAAG	KSPSLIFTNR	300
TSAEPRPKR	NYSRLLPMLK	NVVALDVEVA	TNRIYWCDSL	YRKIYSAYMD	KASDPKEREV	360
LIDEQLHSPF	GLAVDWVHHK	IYWTDSGNKT	ISVATVDGGR	RRTLFSRNLS	EPRAIAVDPL	420
RGFMYNWDWG	DQAKIEKSLG	NGVDRQTLVS	DNIEWPNGIT	LDLLSQRLYW	VDSKLHQLSS	480
IDPSGGNRKT	LISSTDFLSH	PFGIAVFEDK	VFWTDLENEA	IFSANRLNGL	BISILAENLN	540
NPHDIVIFHE	LKQPRAPDAC	ELSVQPNGGC	EYLCLEPAQI	SSHSPKYTCA	CPDTMNLGPD	600
MKRCYRDANE	DSKMGSTVTA	AVIGIIVPIV	VIALLCMSGY	LIWRNWKRRN	TKSMNFDNFV	660
YRKTTEEBDE	DELHIGRTAQ	IGHVYPARVA	LSLEDDGLP			

70

Seq ID NO: 358 DNA sequence

Nucleic Acid Accession #: M27826

Coding sequence: <1-503

75

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CTCTCACAGT	GGAGGGTAAG	TCCATCCCTT	GTTTAAATGA	TACGGGGGCT	ACCCACTCCA	180
CGTTGCCCTTC	TTTTCAAGGG	CCTGTTTCCC	TTGCCCCCAT	AACTGTTGTG	GGTATTGACG	240
GCCAAAGCTTC	AAAACCCCTG	AAAACCTCCC	CACTCTGGTG	CCAACCTTGA	CAACACTCTT	300
TTATGCACCTC	TTTTTTAGTT	ATCCCCACCT	GCCCACTTCC	CTTATTAGGC	GGAAATATTT	360
TAACCAAAAT	ATCTGCTTCC	CTGACTATTG	CTGGAGTACA	GCTACATCTC	ATTGCTGCCC	420
TTCTTCCCAA	TCCAAAGCCT	CCTTTGTGTC	CTCTAACATC	CCCACAATAT	CAGCCCTTAC	480
CACAAGAACT	CCCTCTCAGT	TAACTCTCCC	CACCTAGGTT	TCCCAAGCGG	CCCTAATACC	540
CACCTTGAAGC	AGCCCTGAGA	AACATGCCCC	ATTCTCTCTC	CATACCACCC	CCCAAAAATT	600
TTGCGCGCTC	CAACACTTCA	ACACTATTTT	GTTTATTATT	TCTTATTAA	ATCAGAAGGC	660

85

AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCACGTAT 720
 ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAACTG 780
 ATGACATCC ACCATTGTGA TTGTCTCTG CCCACCCCTA ACTGATCAAT GTACTTTGTA 840
 ATCTCCCCA CCTTAAGAA GGTTCCTTGT AATTCTCCCC ACCCTTGAGA ATGTACTTTG 900
 TGAGATCCAC CCTGTCCAC CAGAGAACA CCCCTTTGA TTGTAATTTT TTATTACCTT 960
 CCCAAATCCT ATAAAACAGC CCCACCCCTA TCTTCTCTCA CTGACTCTCT TTTCGGACTC 1020
 AGCCACCGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC

Seq ID NO: 359 Protein sequence
 Protein Accession #: AAA65999

1 11 21 31 41 51
 PKKHLTNFNS DLPLGLATEDW RCPPIASEVPW TITEAELRVT LTVEGKSIPC LIDTGATHST 60
 LPSFQGFVSL APITVVGIDG QASKPLKTPP LWCQLGQHSF MHSFLVIPTC PLPLILGRNII 120
 TKLSASLTIP GVQLHLIALA LPNFKPPLCP LTSFYQYPLP QDLPSA

Seq ID NO: 360 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 162-5582

1 11 21 31 41 51
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 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 TTCTGGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCTCTTA 180
 GGTGGAAGAA GAAAGCGTGG CTCTGGGATT TCACCGTAAC AACCTTCGCA TTGACCTTCC 240
 TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTACTAAAA GCACATAGATT 300
 TTCACAATTC TCCAGAGGGA ATATCAAAAA CAACGCGATT TTGCACAAAC AGAAAGAATT 360
 CTAAGGCTCT AGATACTGCT TACAGAGTTT CAAGCAAGC ACRACTCAGT GCCCAACAAA 420
 AACAGTATT TCCAGGTGGA ACTTTCCAG AAGACTTTTC AATACTATT ACAGTAAAAAC 480
 CAAAAAAGG AATTCACTCT TTCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA 540
 TTGGTGTGTA GGTGGGAGA TCACCTGTTT TTCTGTTGA AGACCACAT GGAACCTG 600
 CCCAGAAGA CTATCCCTC TTCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CGTGGAGAGG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA 720
 CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTGTATAC CAATGGAATC ACGGTTTTTG 780
 GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGGACAT TCAGCAGTTT TTGATCACAG 840
 GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG 900
 CACCAAGGC TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATAA 960
 TCGAATATGA CTATGATGAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020
 GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
 AAGAATACAA CTATGAGAA ATGGAAGTTT ACCAGACAGA AGCTCCTAGG CATGTTTCTG 1140
 GGACAAATGA GCCAAATCCA GTTGAAGAAA TAITTACTGA AGAATATCTA ACGGAGAGG 1200
 ATTATGATT CCAGAGGAAA AATTCTGAGG ATACACTATA TGAAAAAACA GAAATAGAGG 1260
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 CAGAACTGA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCAATATGA GAGAAAGGAC 1440
 AGAAAGGAGA ACCAGCAGTG GTTGAAGCTG GTATGCTTGT CGAAGGACCA CCAGGACCAG 1500
 CAGGACCTGC AGGTATTATG GGTCTCCAG GTCTACAAGG CCCACTGGA CCCCTGGTG 1560
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 TGAGAGGCCC ACCTGGCCCA ATGGGTCTAA CTGGAAGACC AGGTCTGTG GGGGGGCTG 1800
 GTTCATCTGG GGCCTAAGGT GAGAGTGGTG ATCCAGGTCC TCAGGGCCCT CGAGGGGTCC 1860
 AGGCTCCCCC TGGTCCAACT GGAAGACCTG GAAAAAGGGG TCGTCCAGGT CGAGATGGAG 1920
 GAAGAGGAAT GCCAGGAGAA CCTGGGCAAA AGGGAGATCG AGGGTTTATG GACTTCCGG 1980
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 GTGCTGATGG GCCTCCTGGT CATCCTGGGA AAGAAGGCCA GTCTGGAGAA AAGGGGGCTC 2400
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	CAGTTGGTGG	TGTTGGAGAA	AAGGGTGAAC	CTGGAGAAGC	AGGAACCCCA	GGGCTCCTCG	3960
	GGGAAGCAGG	TGTAGCGGTG	CCCAAAGGAG	AAAGAGGAGA	GAAAGGGGAA	GCTGGTCCAC	4020
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	CTGGCCCATC	TGGTGAAGGT	GGCCCAACAG	GTCTCTCTGG	AAAACGAGGT	CCTCTGGGAG	4260
	CTGCAGGTGC	AGAGGGAAGA	CAAGGTGAAA	AAGGTGCTAA	GGGGGAAGCA	GGTGCGAAGG	4320
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10	AAGGTCTTCG	GGGCATCCCT	GGTCTGTGGG	GAGAACCAAGS	TCTCCCTGGA	GCTGCAGGCC	4440
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15	GTCTCAAGGG	CCCAAAGGGT	AACAAAGGCT	CTACTGGACC	CGCTGGCCAG	AAAGGTGACA	4740
	GTGGTCTTCC	AGGGCTCTCT	GGGCTCCAG	GTCCACCTGG	TGAAGTCATT	CAGCTTTTAC	4800
	CAATCTTGTG	CTCCAAAAAA	ACGAGAAGAC	ATACTGAAGG	CATGCAAGCA	GATGCAGATG	4860
	ATAATATTC	TGATTACTCG	GATGGAATGS	AAGAAATATT	TGGTTCCTCT	AAATCCCTGA	4920
	AACAAGACAT	CGAGCATATG	AAATTTCCAA	TGGGTACTCA	GACCAATCCA	GCCCGAATCT	4980
20	GTAAAGACAT	GCAACTCAGC	CATCTGACT	TCCAGATGGS	TGAATATGGG	ATTGATCCTA	5040
	ACCAAGGTTG	CTCAGGAGAT	TCCTTCAAAG	TTTACTGTAA	TTTCACATCT	GGTGGTGAGA	5100
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	AACCAGGAAG	TGTTGTTAGT	GAATTTAAGA	GGGGAACACT	GCTTTCATAC	TTAGATGTTG	5220
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25	GGCAAAATTT	CACCTACCCAC	TGTATCATGT	CAGCAGCCTG	GTATGATGTG	TCATCAGGAA	5340
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	TGTGTTTAAT	AAATTTGAAT	TATTTGTGTG	ACAGTCTCAT	ACTGTTATCT	GTGTCCATTT	6000
	CCAAAACTTG	CACGTGTCCC	TGAATTCOCG	TGACTCTAAT	TTATGAGGAT	GCGAAGCTCT	6060
	GATGGCAATA	ATATATGTAT	TATGAAAATG	AAGTTATGAT	TTCCGATGAC	CCTAAGTCCC	6120
40	TTCTTTTGGT	TAATGATGAA	ATTCCTTTGT	GTGTGTTT			

Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

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	EHGIQQIGVE	VGRSPVFLFE	DHTGKPAPEP	YPLFRVTNIA	DGKMRVAIS	VEKKTVMIV	180
	DKKKTTKPL	DRSERAIVDT	NGITVPGTRI	LDEEVFEGDI	QQPLITGDPK	AAAYDYCEHS	240
50	PDCDSSAPKA	AQAQEPQIDE	YAPEDIIEYD	VEYGEAEYKE	AESVTEGPTV	TEETIAQTEA	300
	NIVDDFOEYN	YGTMESYQTE	APRHVSGTNE	PNFVEEIFTE	EYLTGEDYDS	QRKNSDITLY	360
	ENKEIDGRDS	DLIVDGLDGE	YDFYKEYEYE	DKPTSPPNEE	PGPGVPAETD	ITETSINGHG	420
	AYGEKQKGB	PAVVEPGMLV	EGPPGPAGPA	GIMGPPGLQG	PTGPPGDPGD	RGPGRPGPLP	480
	GADGLPGPPG	TMLMLPFRYG	GDGSKGPTIS	AQEAQAQAIL	QQAIALRGP	PGPMGLTGRP	540
55	GPVGGPGSSG	AKGESGDPGP	QGPGRVQGGP	GPTGKPKGRG	RPGADGGGRM	PGEPGAAGDR	600
	GFDGLPGLPG	DKHGRGERGP	QGPGGPPCDD	GMRGEDGEIG	PRGLPGEAGP	RGLLGPRTGP	660
	GAPQPGPMAG	VDGPPPGKGN	MGPQGEPPGP	QQQGNPQPQG	LPGPQGPFGP	PGEKGPQSKP	720
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60	GEDGPPGPRG	DMGLKEDRGE	VQIGPRGXG	GPSPGKGRAG	PTGDPGPGSQ	AGEKSGKLGVP	840
	GLPGYGRGPG	PKGSTGFPFG	PGANGKRGAR	GVAKPKGPRG	QRGPTGPRGS	RGARGPTGKP	900
	GPKGTSGGDS	PPGPGERGPP	QGPQGPVGF	GPKGPFGPPG	RMGCPGHPPQ	RGETGPGGKT	960
	GPPGPGGVVG	PQGTGTGTGP	IGERGYPGPP	GPPGEQGLPG	AAGKEGAKGD	PQPQGISGKD	1020
	GPAGLRGPPG	ERGLPGAQGA	PGLKGEGGPQ	GPPGPGVSPG	ERGSAGTAGP	IGLRGRPGPQ	1080
65	GPPGPAGEKG	APGEKGPQGP	AGRDGVQGPV	QLPGPAGPAG	SPGEDGDKGE	IGEPQKGSK	1140
	GGKGENGPPG	PPGLQGFVGA	PGIAGDGEP	GPRGQOGMFG	QKGEDEGARG	PGPPIGLQ	1200
	GLPGPPGEKG	ENGDVGFWGP	PGPPGPRGPQ	GPNGADPQPG	PPGVSVSVG	VGEKGEPEGA	1260
	GNPGPPGEAG	VGGPKGERGE	KGEAGPPGAA	GPPGAKGPPG	DDGPKGNPFP	VGFPGDPGPP	1320
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70	GEAGAGPPPG	KTGVPVGPQG	AGKPGPEGLR	GIPGPVGEQG	LPGAAGQDGP	PGPMGPPGLP	1440
	GLKDPGSGK	EKGHPGLIGL	IGFPGEQGEK	GDRGLPGTQG	SPGAKGDGGI	PGPAGPLGPP	1500
	GPPGLPGPQG	PKGNKSGTGP	AGQKDSGLP	GPPGPPGPPG	EVIQPLPILS	SKKTRRHTEG	1560
	MQADADDNIL	DYSDGMEEIF	GSLSLSLKQDI	EHMKFPMTGT	TNPARTCKDL	QLSHPDFFDG	1620
	EYWLDPNQC	SGDSFRVYCN	FTSGGETCIY	PDKKEGVR	SSWPKKPKGS	WFSEFKRGKL	1680
75	LSYLDVEGNS	INMVQMTFLK	LLTASARQNF	TYHCHQSAAM	YDVSSGSYDK	ALRFLGSNDE	1740
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Seq ID NO: 362 DNA sequence
Nucleic Acid Accession #: NM_003107
Coding sequence: 351-1775

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	GGAACTATAA	CTCCTCTGCG	AGAGGCGGAG	AACCTCTTCC	CCAAATCTTT	TGGGGACTTT	180

	TCTCTCTT	CCCCACCTCG	CCCCTGCGAG	GAGTTGAGGG	GCCAGTTCGG	CCGCCGCGGG	240
	CGTCTTCCCG	TTCCGGGGTGT	GCTTGGCCCG	GGGAACCGGG	AGGGCCCGGC	GATCGCGCGG	300
	CGGCCGCGCG	GAGGGTGTGA	GCGCGCGTGG	GCGCCCGCGG	AGCCGAGGCC	ATGGTGCGAGC	360
5	AAACCAACAA	TGCCGAGAAC	ACGGAAGCGC	TGCTGGCCGG	CGAGAGCTCG	GACTCGGGGG	420
	CCGGCTCGA	GCTGGGAATC	GCCTCCTCCC	CCACGCCCGG	CTCCACCGCC	TCCACGGGGG	480
	GCAAGGCGGA	CGACCGGAGC	TGGTGCAAGA	CCCCGAGTGG	GCACATCAAG	CGACCCATGA	540
	ACGCCCTTCA	GCTGTGGTGC	CAGATCGAGC	GGCGCAAGAT	CATGGAGCAG	TGCGCCGACA	600
	TGCACAACGC	CGAGATCTCC	AAGCGGCTGG	GCAAAACGCTG	GAAGCTGCTC	AAAGACAGCG	660
10	ACAAGATCCC	TTTCATTGGA	GAGCGGAGC	GGCTGCGCCT	CAAGCACATG	GCTGACTACC	720
	CGACTACAA	GTACCGGCCC	AGGAAGAAGG	TGAAGTCGGG	CAACGCCAAC	TCCAGCTCCT	780
	CGCGCGCGCG	CTCCTCCAAG	CCGGGGGAGA	AGGGAGACAA	GGTCGGTGGC	AGTGGCGGGG	840
	GCGGCCATGG	GGCGCGCGCG	GGCGCGGGGA	GCAGCAACGC	GGGGGGAGGA	GGCGCGCGTG	900
	CGAGTGGCGG	CGCGCGCAAC	TCCAAACCGG	CGCAGAAAAA	GAGCTCGGGC	TCCAAAGTGG	960
15	CGGGCGCGCG	GGCGCGTGGG	GTTAGCAAAC	CGCAACGCCA	GCTCATCCTG	GCAGGCGGGG	1020
	GCGCGCGCGG	GAAAGCAGCG	GCTGCGCGCG	CGCGCTCCTT	CGCGCGCGAA	CAGGCGGGGG	1080
	CGCGCGCGCT	GCTGCGCGCG	GGCGCGCGCG	CGGACCACTA	CTCGCTGTAC	AAGGCGCGGA	1140
	CTCCAGCGCG	CTCGCGCTCG	GCCTCCTCGG	CAGCCTCGGC	CTCGCGCGCG	CTCGCGCGCG	1200
	CGGGCAAGCA	CTCGCGGAGG	AAGAAGGTGA	AGCGCGTCTA	CCTGTTGGGC	GGCCTGGGCA	1260
20	CGTCTGCTGC	GCCCGTGGGC	GGCGTGGGCG	CGGGAGCGGA	CCCCAGCGAC	CCCTTGGGCC	1320
	TGTACGAGGA	GGAGGGCGCG	GGCTGCTGCG	CGGACGCGCC	CAGCCTGAGC	GGCGCGAGCA	1380
	GCGCGCGCTC	GTCCCGCGCG	CGCGCGCGCT	CGCGCGCGGA	CCACCGCGGC	TACGCCAGCC	1440
	TGCGCGCGCG	CTCGCGCGCG	CGCTCCAGCG	CGCGCTCGCA	CGCGCTCCTC	TGCGCGCTCG	1500
	CGCACTCCTC	CTCTCCTCCT	TCTCGGGGCT	CCTCGTCTCT	CGAGAGCAGG	TTCGAAGACG	1560
25	ACCTGCTCGA	CCTGAACCCC	AGCTCAAACT	TTGAGAGCAT	GTCCCTGGGC	AGCTTCAGTT	1620
	CGTCTGCGCG	GCTCGAGCGG	GACCTGGATT	TTAACTTGA	GCCCGGCTCC	GGCTCGCACT	1680
	TGAGTTTCCC	GGACTACTCG	ACGCCCGAGG	TGAGCGAGAT	GATCTCGGGA	GACTTGGCTG	1740
	AGTCCAGCAT	CTCAACCTCG	GTTTTCACT	ACTGAAGGGC	CGCGAGGCGG	GAGAGAGGGG	1800
	CGGGGGGGGT	AGGAGAGGAG	AAAAAAGGAG	TGAAAAAAG	AAACGAAAG	GACAGAGGAA	1860
30	GAGTTTAAAG	AGAAAAAGGA	AAAAAGAAAG	AAAAAGTAAG	CAGGGCTCGT	TGCGCGCGCT	1920
	TCTGCTGCTC	GGATCAAGGA	GCGCGCGCGC	GTTTTGGACC	CGCGCTCCCA	TCCCCCACT	1980
	TCCCGGGCGG	GGGACCCACT	CTGCCAGCGC	GGAGGGAGCG	GGAGGAGGAA	GAGGGTAGAC	2040
	AGGGGGGACC	TGTGATTGTT	GTTATTGATG	TTGTTGTTGA	TGGCAAAAAA	AAAAAGCGAC	2100
	TTGAGTTTGG	CTCCCTTTTG	CTTGAAGAGA	CCCCCTCCCC	CTTCAACGGA	GCTTCCGAGC	2160
35	TGTTCTGACG	CCCCAGCAAG	AAGGCGAGTT	AGTTTTCTAG	AGACTTGAAG	GAGTCTCCCC	2220
	CTTCTGTCAT	CACCACTCTG	GTTTTGTTTT	ATTTTGCTTC	TTGTTCAAGA	AAGGAGGGGA	2280
	GAACCCAGCG	CACCCCTCCC	CCCCCTTTTT	TAAACGCGTG	ATGAAGACAG	AAGGCTCCGG	2340
	GTTGAGCAAT	TTGGCGGATG	GCAGATGTTT	TGGGGGAACG	CGGGGACTGA	GAGACTCCAC	2400
	GCAGGCGAAT	TCCCGTTTGG	GGCCTTTTTT	TCTTCCCTCT	TTTCCCTTGG	CCCCCTCTGC	2460
40	AGCCGAGGGA	GGAGATGTTG	AGGGGAGGAG	GCCAGCCAGT	GTGACCGCGG	CTAGGAAATG	2520
	ACCCGAGAAC	CCCGTTGGAA	CGCGAGCAGC	GGGAGCTAGG	GCGCGGGGCG	GAGGAGGACA	2580
	CGAATCGAAA	GGGGGTTTAC	GGTCAAACTG	AAATGGATTG	GCACGTTGGG	GAGCTGGCGG	2640
	CGGGCGCTGC	TGGCGCTCCG	CCTTCTTTTC	TACGTGAAAT	CAGTGAGGTG	AGACTTCCCA	2700
45	GACCCGCGAG	GCGTGGAGGA	GAGGAGACTG	TTTGATGTGG	TACAGGGGCA	GTCAGTGGAG	2760
	GGCGAGTGGT	TTCGGAAAAA	AAAAAAGAAA	AAAAGGGG			

Seq ID NO: 363 Protein sequence
Protein Accession #: NP_003098

50	1	11	21	31	41	51	
	MVQQTNNNA	TEALLAGESS	DSGAGLELGI	ASSPTPGSTA	STGGKADDPG	WCKTPSGHIK	60
	RPNQAFVWVS	QIERRKIMEQ	SPDMENABIS	KRLGKRWKLL	KDSKIPFIR	EAERLRKXHM	120
	ADYPTYKYRP	RKKVKSQGNQ	SSSSAAASSK	PGEKGDVKG	SGGGHGGGGG	GGGSSNAGGG	180
55	GGGAGGGGGA	SKPAQKSCG	SKVAGGAGGG	VSKPHAKLIL	AGGGGGGKAA	AAAAAASPAE	240
	QAGAAALPL	GAAADHSLY	KARTPSASAS	ASSAASASAA	LAAPGKHLAE	KVKRVYLP	300
	GLGTSSSPVG	GVGAGADPSD	PLGLYEEBGA	GCSFDAPSLG	GRSSAASSPA	AGRSPADHRG	360
	YASLRAASPA	PSSAPSHASS	SASSHSSSSS	SSGSSSSDDE	FEDDLLDLNP	SSNFESMSLG	420
	SPSSSSALDR	DLDNFNPEGS	GSHPFPDYC	TPEVSEMISG	DWLESSISNL	VFTY	

Seq ID NO: 364 DNA sequence
Nucleic Acid Accession #: U10860
Coding sequence: 123-2204

65	1	11	21	31	41	51	
	TGCCGCGTGC	TCCTCGACCA	GGCCTCCTTC	TCAACCTCAG	CGCGCGCGCG	CGACCCCTCC	60
	GGCACCCCTCC	CGCCCGGTCT	CGTACTGTGG	CGGTCAACGC	CGCGGCTCOG	GCCCTGGCCC	120
70	CGATGGCTCT	GTGCAACGGA	GACTCCAAGC	TGGAGAATGC	TGGAGGAGAC	CTTAAGGATG	180
	GCCACCAACA	CTATGAAGGA	GCTGTTGTCA	TTCTGGATGC	TGGTGCTCAG	TACGGGAAAG	240
	TCATAGACCG	AAGAGTGAGG	GAACTGTTGG	TGCAGTCTGA	AATTTTCCCC	TTGGAACAC	300
	CAGCATTGCG	TATAAAGGAA	CAAGGATTCC	GTGCTATTAT	CATCTCTGGA	GGACCTAATT	360
	CTGTGTATGC	TGAAGATGCT	CCCTGGTTTG	ATCCAGCAAT	ATTCACATAT	GGCAAGCCTG	420
75	TTCTTGGAAT	TTGCTATGCT	ATGCAGATGA	TGAATAAGGT	ATTGAGAGTT	ACTGTGCACA	480
	AAAAAGTGT	CAGAGAAGAT	GGAGTTTTC	ACATTAAGTT	GGATAATACA	TGTTTATTAT	540
	TCAGGGGCGT	TCAGAAGGAA	GAAGTTGTTT	TGCTTACACA	TGGAGATAGT	GTAGACAAAG	600
	TAGCTGATGG	ATTCAAGGTT	GTGGCACGTT	CTGGAAACAT	AGTAGCAGGC	ATAGCAAAATG	660
	AATCTAAAAA	GTTATATGGA	GCACAGTTCC	ACCTGAAAGT	TGGCCTTACA	GAAAAATGGAA	720
80	AAGTAATACT	GAAGAATTTC	CTTTATGATA	TAGCTGGATG	CAGTGGAAAC	TTCAACCGTGC	780
	AGAACAGAGA	ACTTGATGTT	ATTCGAGAGA	TCAAAGAGAG	AGTAGGCACG	TCAAAAGTTT	840
	TGTTTCTTAC	CAGTGGTGGG	GTAGACTCAA	CAGTTTGTAC	AGCTTTGCTA	AATCGTGCTT	900
	TGAACCAAGA	ACAAGTCATT	GCTGTGCACA	TTGATAATGG	CTTTATGAGA	AAACGAGAAA	960
	GCCAGTCTGT	TGAAGAGGCC	CTCAAAAAGC	TTGGAATTCA	GGTCAAAAGT	ATAAATGCTG	1020
85	CTCATTTCTT	CTACAAATGA	ACAACAACCC	TACCAATATC	AGATGAAGAT	AGAACCCAC	1080
	GGAAAGAAAT	TTAAATATGA	CCCAAGTCC	TGAAGAGAAA	AGAAAAATCA		1140
	TTGGGGATAC	TTTTTGTAA	ATTGCCAATG	AAGTAATTGG	AGAAATGAAC	TTGAAACCA	1200
	AGGAGTGT	CCTTGCCCAA	GGTACTTTAC	GGCTGATCT	AATTGAAAGT	GATCCTCTG	1260

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TTGCAAGTGG CAAAGCTGAA CTCATCAAAA CCCATCACAA TGACACAGAG CTCATCAGAA 1320
AGTTGAGAGA GGAGGGAAAA GTAATAGAAC CTCTGAAAGA TTTTCATAAA GATGAAGTGA 1380
GAATTTTGGG CAGAGAACTT GGACTTCCAG AAGAGTTAGT TTCCAGGCAT CCATTTCCAG 1440
GTCTCTGGCT GGCAATCAGA GTAATATGTG CTGAAGAACC TTATATTGTG AAGGACTTTC 1500
CTGAACCAAA CAATATTTTG AAAATAGTAG CTGATTTTTC TGCAAGTGTT AAAAGCCAC 1560
ATACCCATT ACAGAGAGTC AAAGCCTGCA CAACAGAAGA GGATCAGGAG AAGCTGATGC 1620
AAATTACCAG TCTGCATTCA CTGAATGCCT TCTTGTCTGC AATTAAGTGT GTAGGTGTGC 1680
AGGGTGACTG TGTTCTCTAC AGTTACGTGT GTGGAATCTC CAGTAAAGAT GAACCTGACT 1740
GGGAATCACT TATTTTCTG GCTAGGCTTA TACCTGCGAT GTGTCAACAC GTTAACAGAG 1800
TTGTTTATAT ATTGGCCCA CCAGTTAAAG AACCTCCTAC AGATGTTACT CCCACTTCT 1860
TGACACAGG GGTGCTCAGT ACTTTACGCC AAGCTGATT TGAGGCCCAT AACATTCTCA 1920
GGGAGTCTGG GTATGCTGGG AAAATCAGCC AGATGCCGGT GATTTTGACA CCATTACATT 1980
TTGATCGGGA CCCACTTCAA AAGCAGCCTT CATGCCAGAG ATCTGTGGTT ATTGGAACCT 2040
TTATTACTAG TGACTTCATG ACTGGTATAC CTGCAACACC TGGCAATGAG ATCCCTGTAG 2100
AGGTGGTATT AAGATGGTCT ACTGAGATTA AGAAGATTCC TGGTATTCTT GGAATTATGT 2160
ATGACTTAAC ATCAAAGCCC CCAGGAACCTA CTGAGTGGGA GTAATAAACT TC
  
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Seq ID NO: 365 Protein sequence
 Protein Accession #: AAA60331

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 25
 30
 35

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1 11 21 31 41 51
MALCNGDSLK ENAGGDLKDG HHYSGAVVI LDAGAQYGRV IDRRVREL PV QSEIFPLETP 60
APAIKEQGRF AIIISGGPNS VYAEADAPWF PAIFTIGKPV LGICYGMQMM NKVPGGTVHK 120
KSVREDEGVN ISVDNTECSLF RGLQKEEVLV LTHGDSVDKV ADGFKVVARV GNIVAGIANE 180
SKLKYGAQHF PEVGLTENGL VILKNFLYDI AGCSGTFVQ NRELECIRES KERVGTSKVL 240
VLLSGGVDSV VCTALNRLR NQEQVIAVHI DNGFMKRRES QSVVEALKKL GIQVKVINAA 300
HSFYNGTTTL PISDEDRTPR KRISKTLNMT TSPEEKRKII GDTFVKIANE VIGEMNLKPE 360
EVFLAQGTLR PDIESASLV ASGKAEIKT HHNDTELIRK LREEGKVIEP LKDFHKDEVR 420
ILGRELGLEP ELVSRHPFPG PGLAIRVICA EEPYICKDPF ETNNILKIVA DPSASVKKPH 480
TLQLQRKACT TEDEQKELMQ ITSLSHLNAP LLPIKTVGVQ GDCSRYSYVC GISSKDEPDW 540
BSLIFLARLI PRMCHNNVRV VYIPGPVKE PPTDVTPTPL TTGVLSTLRQ ADPEAHNLR 600
ESGYAGKISQ MPVILTPLHF DRDPLQKQPS QRSVVIRTP ITSDFMGTIP ATPGNBIPVE 660
VVLKMWTEIK KIPGISRIMY DLTSKPPGTT EWE
  
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Seq ID NO: 366 DNA sequence
 Nucleic Acid Accession #: NM_004219
 Coding sequence: 46-654

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1 11 21 31 41 51
GOGGCTCAG ATGAATGCGG CTGTTAAGAC CTGCAATAAT CCAGAATGGC TACTCTGATC 60
TATGTTGATA AGGAAAAATGG AGAACCAAGG ACCCGTGTGG TTGCTAAGGA TGGGCTGAAG 120
CTGGGGTCTG GACCTTCAAT CAAAGCCCTTA GATGGGAGAT CTCAGTTTC AACACCAAGT 180
TTTGGCAAAA CGTTCAGTGC CCCACCAGCC TTACTTAAG CTACTAGAAA GGCTTTGGGA 240
ACTGTCAACA GAGCTACAGA AAAGTCTGTA AAGACCAAGG GACCCCTCAA ACAAAAACAG 300
CCAAGCTTTT CTGCCAAAAA GATGACTGAG AAGACTGTTA AAGCAAAAAG CTCTGTTCT 360
GCCTCAGATG ATGCCATATC AGAAATAGAA AAATCTTTTC CCTTCAATCC TCTAGACTTT 420
GAGAGTTTGG ACCTGCTGGA AGAGCACCAG ATTGCGCAC CCCCCTTGAG TGGAGTGCT 480
CTCATGATCC TTGACGAGGA GAGAGAGCTT GAAAGCTGT TTCAGCTGGG CCCCCTTCA 540
CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCAGTCTCC TTCAAGCATT 600
CTGTGCGACT TGGATGTTGA ATTGCCACCT GTTTGCTGTG ACATAGATAT TTAAATTCT 660
TAGTGCTTCA GAGTTTGTGT GTATTGTAT TAATAAGCA TTCTTCAACA GAAAAAATA 720
AAAAAAA
  
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Seq ID NO: 367 Protein sequence
 Protein Accession #: NP_004210

60
 65

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1 11 21 31 41 51
MATLIYVDKE NGEPTGRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT 60
RKALGTVNRA TERSVTKTGP LKQKQPSFSA KQMTKTVKA KSSVPASDDA YPEIEKFFPF 120
NPILDFFSFDL PEEHQIAHLF LSGVPLMILD ERELEKLFQ LGPPSPVKMP SPPWESNLLQ 180
SPSSILSTLD VELPPVCCDI DI
  
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Seq ID NO: 368 DNA sequence
 Nucleic Acid Accession #: NM_000597
 Coding sequence: 118-1104

70
 75
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1 11 21 31 41 51
ATTGCGGGCG AGGAGGAGG AAGAAGCGGA GGAGGCGGCT CCGCTCGCA GGGCCGTGCA 60
CCTGCCCGCC GSCCGCTGCG CTGCTGCGCC GCGCGCGCG GCTGCGGAC GCGCAGCATG 120
CTGCCGAGAG TGGCTGCCCC GCGCTGCGCG CTGCGCGCG GCGCGCTGCT GCGCGTGTG 180
CGGCTGCTGC TGCTGTACT GGGCGCGAGT GGGCGCGCG GCGGGGCGCG GCGCGAGGTG 240
CTGTTCGGCT GCGCGCGCTG CACACCGAG GCGCTGCGCG CCGCGGGCC CCGCGCGGTT 300
GCGCGCGCG GCGCGGTGCG GCGAGTGGCC GGAGGCGCCC GCATGCCATG GCGCGAGCTC 360
GTCCGCGAGC GCGCTGCGCG CTGCTGCTCG GTGTGCGGCC GGTGCGAGGG CGAGGCGTGC 420
GGGCTCTACA CCGCGCGCTG GCGCGAGGGG CTGCGCTGCT ATCCCCACCC GGGCTCGAG 480
CTGCCCTGCG AGGCGCTGCT CATGGCGAG GGCACCTGTG AGAAGCGCG GGCAGCGAG 540
TATGCGCGCA GCGCGGAGCA GGTTCAGAC AATGGCGATG ACCACTCAGA AGGAGGCGTG 600
GTGGAGAAC ACGTGACAG CACCATGAAC ATGTGGCGCG GGGAGGCGAG TGCTGGCGCG 660
AAGCCCTTCA AGTGGGTAT GAAGGAGCTG GCGGTGTTC GGGAGAGGT CACTGAGCAG 720
CACCGCAGCA TGGCGAAGG TGGCAAGCAT CACCTTGGCC TGGAGGAGCC CAAGAAGCTG 780
OSACCACCCC CTGCGAGGAC TCCCTGCCAA CAGGAACCTG ACCAGGTCTT GAGCGGATC 840
  
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TCCACCATGC GCCTTCGGGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
 CCCAACTGTG ACACGATGGC CCTGTACAAC CTCAAACAGT GCAAGATGTC TCTGAACGGG 960
 CAGCGTGGGG AGTGTGGGTG TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
 ACCATCCGGG GGGACCCCGA GTGTCACTCT TCTACAAATG AGCAGCAGGA GGCTTGGGGG 1080
 GTGCACACCC AGCGGATGCA GTAGACCGCA GCCAGCGGGT GCCTGGGGCC CCTGCCCCCC 1140
 GCGCTCTCC AACACCGGC AGAAACCGGA GAGTGCTTGG GTGGTGGGTG CTGGAGGATT 1200
 TTCCAGTCTT GACACACGTA TTTATATTTG GAAAGAGACC AGCACCGAGC TCGGCACCTC 1260
 CCGGCTCTCT CTCTTCCAGC CTGCAGATGC CACACCTGCT CCTTCTTGCT TTCCCGGGG 1320
 GAGGAAGGGG GTTGTGGTGG GGGAGCTGGG GTACAGGTTT GGGGAGGGGG AAGAGAAATT 1380
 TTTATTTTGG AACCCCTGTG TCCCTTTTGC ATAAGATTAA AGGAAGGAAA AGT

Seq ID NO: 369 Protein sequence
 Protein Accession #: NP_000588

1 11 21 31 41 51
 MLPRVGCPL PLPPPLPLPL LPLLLLLLGA SGGGGGARAE VLFRCPPCTP ERLAACGPPP 60
 VAPPAVAAV AGGARMPCAE LVREPGCGCC SVCARLEGEA CGVYTPRCQG GLRCYPHPGS 120
 ELPLQALVMG EGTCKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGGSAG 180
 RKPLSGMKKE LAVPREKYTE QHRQMGKGGK HHLGLEBEPK LRPPPAPTPC QQELDQVLER 240
 ISTMLRPDER GPLEHLYSLH IPNCDKHGLY NLKQCKMSLN GQRGECWCVN PNTGKLIQGA 300
 PTIRGDPECH LFNNEQGEAC GVHTQRMQ

Seq ID NO: 370 DNA sequence
 Nucleic Acid Accession #: NM_004264
 Coding sequence: 6-440

1 11 21 31 41 51
 GGAACATGGC GGATCGGCTC ACGCAGCTTC AGGACGCTGT GAATTCGCTT GCAGATCAGT 60
 TTTGTAATGC CATTGGAGTA TTGCAGCAAT GTGGTCTCTC TGCTCTCTTC AATAATATTC 120
 AGACAGCAAT TAACAAGAAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTTC 180
 CAGCACTGAT TGACGAACA GCAAAAGACA TTGATGTTTT GATAGATTCC TTACCCAGTG 240
 AAGAATCTAC AGCTGCTTTA CAGGCTGCTA GCTTGATATA GCTAGAGAA GAAACACCAT 300
 AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
 AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
 AGTCTCTTCC AGACTCATAG CATCAGTGGG TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
 GTGCCATTAA GAATCTGCA TCAGACTTAG ATACAAGCCT TACCAACAA TACAGAAACA 540
 TTAACACTA TGACACATTA CCTTTTAGC TATTTTAAAT AGTCTTCTAT TTCACTCTT 600
 GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTTAACT 660
 GAGTGAAATT ATTAAGGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
 AATTCTGTTA TGACATAATT TATGTCCTCA TTTGTTGTA TTGGCCAGTA CTTTACAAT 780
 C

Seq ID NO: 371 Protein sequence
 Protein Accession #: NP_004255

1 11 21 31 41 51
 MADRLTQLQD AVNSLADQFC NAIGVLQCG PPASFMNIQT AINKDQNPANP TEEYAQLFAA 60
 LIARTAKDID VLIDSLPSEE STAAALQAASL YKLEENHEA ATCVEDVVYR GDMLEKIQS 120
 ALADIAQSQL KTRSGTHSQS LPDS

Seq ID NO: 372 DNA sequence
 Nucleic Acid Accession #: AJ271091
 Coding sequence: 1-1113

1 11 21 31 41 51
 ATGGAGAATC AGGTGTTGAC GCGCATGTC TACTGGGCTC AGGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCGAAGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAACCC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGTGGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAATAAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
 TTCTCCGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCCTT 540
 TATGACATCA TCCATCTGT GGTGACATG ATGTATTCTT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTGT GTTTTATTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
 TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAAGTGC TCACATGGCT TCGTTACACT 840
 CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGGACGATT AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAGTATAGT TTCTCTTTT TCTTCAGATT TATCTTATAA TGATATTTT AGGTTTATAC 1020
 ATAAATTTTC GTACACTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
 CATGCCTGTG ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 373 Protein sequence
 Protein Accession #: CAB69070

1 11 21 31 41 51
 MENQVLTPHV YNAQRHRLY LRVLSDVQN PAISITENVL HFKAQGHGAK GDNVYEPHLE 60
 PLDLVKPEPV YKLTRQVNI TVQKKVSQWM ERLTKQEKRP LPLAPDFDRW LDESDAEMEL 120
 RAKEERLINK LRLSEBSPE TLNLRKGYL FMYNLVQPLG FSWIFNLTV RPCILGKESP 180

YDTPHTVADM MYFCQMLAVV ETINAAIGVT TSPVLP SLIQ LLGRNFILPI IPGTMEMQN 240
KAVVFFVFPYL WSAIIFRYS FYMLTCIDMD WKVLTLWRYT LWIPLYPLGC LAEAVSVIQS 300
IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA 360
HACDPSALGG

Seq ID NO: 374 DNA sequence
Nucleic Acid Accession #: NM_016395
Coding sequence: 1-1113

1 11 21 31 41 51
| | | | |
ATGAGAGAATC AGGTGTGTGAC GCGCATGTC TACTGGGCTC AGGACACCG CGAGCTATAT 60
CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
CATTTCAAAG CTCAAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAAACATT 240
ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCTGAA 420
ACTCTTACAA ACTTAAGGAA AGGATACTCG TTTATGTATA ATCTGTGCA ATTCTTGGGA 480
TTCTCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCTTT 540
TATGACACAT TCCATACGTG GCGTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG 600
GAAACTATCA ATGCAGCAAT TGGAGTCACT ACCTCACCGG TGCTGCTTC TCTGATCCAG 660
CTTCTTGAAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
AAAGCTGGG TTTTCTTTGT GTTTTATTG TGGAGTGCAA TTGAAATTT CAGTACTCT 780
TTCTACATGC TGACGTGATG TGACATGGAT TGAAGGTGTC TCACATGGCT TGGTACACT 840
CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAATATC 960
AAAGTTAGAT TTTCTTTTCT TCTTCGATT TATCTTATAA TGATATTTT AGGTTTATAC 1020
ATAAATTTTC GTCACTTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
CATGCTGTG ATCCAGCGC TTTGGGAGGC TGA

Seq ID NO: 375 Protein sequence
Protein Accession #: NP_057479

1 11 21 31 41 51
| | | | |
MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
FLDLVKPEPV YKLTQRQVNI TVQKVSQWM ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
RAKEERENLNK LRLESRGSPR TLNLRKGYL FMYNLVQFLG FSNIFVNLTV RFCILGKESF 180
YDTPHTVADM MYFCQMLAVV ETINAAIGVT TSPVLP SLIQ LLGRNFILPI IPGTMEMQN 240
KAVVFFVFPYL WSAIIFRYS FYMLTCIDMD WKVLTLWRYT LWIPLYPLGC LVEAVSVIQS 300
IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RRRYKGRKR 360
STKKDLDFG LPV

Seq ID NO: 376 DNA sequence
Nucleic Acid Accession #: NM_005987
Coding sequence: 1-270

1 11 21 31 41 51
| | | | |
ATGAATTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG 60
GTGAACAAC CTTCGCCGCC TCCACCCCGAG GAACCATGCA TCCCAAAAC CAAGGAGCCC 120
TGCCAAACCA AGGTGCTTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG 180
ATTCCAGAGC CTTGCCAGCC CAAGGTGCGT GAGCCCTGCC CTTCAACGGT CACTCCAGCA 240
CCAGCCACGC AGAAGACCAA GCAGAAGTAA

Seq ID NO: 377 Protein sequence
Protein Accession #: NP_005978

1 11 21 31 41 51
| | | | |
MNSQQQKQPC TPPPQPOQQQ VRQPCQPPPO EPCIPKTKEP CQPKVPEPCR PKVPEPCQPK 60
IPEPCQPKVP EPCPSTVTPA PAQQKTKQK

Seq ID NO: 378 DNA sequence
Nucleic Acid Accession #: NM_002105
Coding sequence: 74-505

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GTGCGGCTCG TCGCGGCGCG GCGTCCAGTT CCCAGTGGCG CGTGACACC GCGTCTGCG 180
GAAGGCGCAC TAGCGCGAGC GCGTGGCGCG GCGCGCGCCA GTGTACCTGG CGGCACTGCT 240
GGAGTACCTC ACCGCTGAGA TCTTGAGCT GCGGCGCAAT GCGGCGCGCG ACAACAAGAA 300
GAGCGAATC ATCCCGCGCC ACCTGCAGCT GGCCATCCCG AACGACGAGG AGCTCAACAA 360
GCTGCTGGCG GGCGTGACGA TCGCCAGGG AGGCTGCTG CCAACATCC AGGCGGTGCT 420
GCTGCCCAAG AAGACAGCG CCACCGTGGG GCGGAAGCG CCCTCGGGCG GCAAGAAGGC 480
CACCCAGGCC TCCAGGAGT ACTAAGAGGG CCGCGCGCG GCGCGCGCG CCGAGCTCCC 540
CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACGCGCC TCATGGAAG AGCTGAGCG 600
CTTCAGACTG CGGGCAAGC GGGCGCGCG TCCCTTCCCC TCCCTCCCC TCGCGCGCT 660
TGGCGCGCG GCGTGGAGT CCGCGCGCG CCGCTGCGG GCGTTCGGG CTTTCGGATG 720
CGGCTGCGG CCGCGCTGT CCGCGCTGCG CCGCTGCGG GCGTTCGGG CTTTCGGATG 780
CGGCTGCGG GCTCTTGGG GACCTCGTG GCGCGGAAGA CCGAGGCTG CCGGGGGAG 840

GCCGCGCGCG CGCACCTGCG CGCCTCGCG GTTCGTGACT CAGCGCGCCC ATCCCAGATC 900
 GCTAAGGGGGC TCGGGGAGG CGCAGCACC TTCTGGAAGA CTGTGCTTC CGCTCTGACG 960
 CAGGCGCGAG GTGGGCGAGT CAGGCGGAGA GCCGCGCGCC CTGAAGGTGA GTGAGGCGCT 1020
 CGGCAGCTGC AGCGGGGGT TCTGGTACCC CCGCGCGGTG GTGCTTAGCC CAGGACTTTC 1080
 5 AGACGCGCGC TGGCGCGGAG GCTTTGGTGG GAGAGACGGG ATGCGCGATT TCGGTCTGGC 1140
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 AGGTCTGCGC TGGGCGCGG AGAAGCACT TGGTAACAGG CACATCTTCC TCCGAGTGA 1260
 CTGCTCTCTA GGAGGACATT TAGGGGAGGG CAGAGGCGTG CAGTTTGGCT TCACGCGCTG 1320
 10 CTATGTGGAC AGCAAGAGT GTTTTGGCGA ACGGACTGG CAGCGAGGCC TGTGCGGCCC 1380
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 CTGCAGCTAA CCTTCCACG ACTAGAACCT TAGGCATTGG GGAGTTTATG ATGGACTAAT 1560
 TTTATTAAAG GATTGTTTTT TTTT

Seq ID NO: 379 Protein sequence
 Protein Accession #: NP_002096

1 11 21 31 41 51
 20 MSGRGKTGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGHY AERVGAGAPV YLAADVLEYLT 60
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 TSATVGPAPK SGGKATQAS QEY

Seq ID NO: 380 DNA sequence
 Nucleic Acid Accession #: AL136942
 Coding sequence: 184-864

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 CAGGCGAGGC GGTGCGAGCT CCGGAAACT TCGCGCGCGC CTGCGCGCAC TCGCGCGGGA 180
 35 GCGATGAGGA TGGTGGCGCC CTGACGCGGG TTCTACTCCA ACAGCTGCTG CTGTGCTGCTG 240
 CATGTCCGCA CGGCGACCAT CCGTCTCGGC GTCTGGTATC TGATCATCAA TGCTGTGGTA 300
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 CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT GCATTGCCAT TCGGATTTCT 420
 CTTCTCATGA TCCTGATATG TGCTATGGCT ACTTACGAG CGTACAAGCA ACGCGCAGCC 480
 40 TGGATCATCC CATTCTCTG TTACAGATC TTGACTTTG CCTGAACAT GTTGGTTGCA 540
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 45 ACTACGGTGC TGCTACCGCC GTATGATGAT GCCACTGTGA ATGGTGTGCG CAAGGAGCCA 840
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 50 TGGGATATA ACGGCTTCA CTAACCTTCC CTAGGCATTG AAACCTTCCC CAATCTGAT 1140
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 TCCCTCTCTT TTGAAATGT AAAATAAAG CAAAATAGA CAACTTTTTC TTCAGCCATT 1260
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 ATTAGGTAAA TAGAAGTCTT TATGTATGTG TTACAAGAA TTCCCCACA ACATCCTTTA 1380
 55 TGACTGAAGT TCAATGACAG TTGTGTTTGT GTGGTAAAGG ATTTTCTCCA TGGCCTGAAT 1440
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 60 TATCAAGTGG AATTGGGATA TATTGTATAT ACTTCTGCTT AACCAATGCG AAAAGGGTTT 1740
 TCTTTTCCCT GCAAGCTACA TCCTACTGCT TTGAACCTCC AAGTATGTCT AGTCACCTTT 1800
 TAAATGTAA ACATTTTCAG AAAATGAGG ATTGCCTTCC TTGTATGCGC TTTTACCTT 1860
 GACTACCTGA ATTGCAAGG ATTTTATAT ATTATATGT TACAAAGTCA GCACTCTCC 1920
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Seq ID NO: 381 Protein sequence
 Protein Accession #: CAB66876

1 11 21 31 41 51
 70 MDMVAPWTRF YNSNCLCCH VRTGTLILGV WYLIINAVVL LILLSALADP DOYNFSSSEL 60
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 TVLIYPNSIQ EYIRQLPFPN PYRDDVMSVN PTCLVLIILL PISILITFKG YLISCVWNCY 180
 RYINGRNSSD VLVVVISNDT TVLLPFYDDA TVNGAAKEPP PPVSA

Seq ID NO: 382 DNA sequence
 Nucleic Acid Accession #: NM_002510
 Coding sequence: 92-1774

1 11 21 31 41 51
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 85 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCGCAA CGATTTTCATG ATGTGCTGGG 180
 CAATGAAAGA CCTCTGCTT ACATGAGGGA GCACAAATCAA TTAATGGCT GGTCTTCTGA 240
 TGAATATGAC TGAATGAAA AACTCTACCC AGTGTGGAAG CCGGGAGACA TGAGGTGGAA 300
 AAACCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTGTACC AGTGACTCAC CAGCCCTCGT 360

	GGGCTCAAA	ATAACATTG	CGGTGAACCT	GATATTCCT	AGATGCCAAA	AGGAAGATGC	420
	CAATGGCAAC	ATAGTCTAT	AGAAGAACTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
	ATATGTTTAC	AACTGGACAG	CATGGTCAGA	GGACAGTGAC	GGGGAATAATG	GCACCGGCCA	540
5	AAGCCATCAT	AAGTCTTCC	CTGATGGGAA	ACCTTTTCT	CACCAACCCG	GATGGAGAAG	600
	ATGGAATTC	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCCAGAAAT	TGGGACGATG	660
	TTCAGTGAGA	GTITCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCTCTAAC	TCATGGAAGT	720
	GACTGTCTAC	AGAAGACATG	GACGGGCATA	TGTTCCCATC	GCACAAGTGA	AAGATGTGTA	780
	CGTGTAACA	GATCAGATTC	CTGTGTTTGT	GACTATGTTC	CAGAAGAACG	ATCGAAATTC	840
	ATCCGAGGAA	ACCTTCCTCA	AAGATCTCC	CATTATGTTT	GATGTCTGA	TTCATGATCC	900
10	TAGCCACTTC	CTCAATTATT	CTACCAATTA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960
	CCTGTGTTGT	TCCACCAATC	ATACTGTGAA	TCACACGTAT	GTGCTCAATG	GAACCTTCAG	1020
	CCTTAACCTC	ACTGTGAAAG	CTGCAGCACC	AGGACCTTGT	CGGCCACCGC	CACCAACACC	1080
	CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAAACCCC	TGGAGCTGAG	1140
15	TAGGATTCCT	GATGAAAACT	GCCAGATTAA	CAGATATGGC	CACTTTCAAG	CAACATCAC	1200
	AATTGTAGAG	GGAATCTTAG	AGGTTAATCAT	CATCCAGATG	ACAGACGTCC	TGATGCCGGT	1260
	GCCATGGCCT	GAAGCTCCCT	TAATAGACTT	TGTCTGAGCC	TGCCAAGGGA	GCATTCCTCC	1320
	GGAGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGAGATC	ACCCAGAAC	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGATGAGA	TGTGTCTGCT	GACTGTGAGA	OGAACCTTCA	ATGGGTCTGG	1440
20	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGCTCTCA	OGAGCACCTC	1500
	GATTTCTGTT	CTTGACAGAG	ACCCAGCCCT	GCCTTTAAGG	ATGGCAAAAC	GTGCCCTGAT	1560
	CTCCGTGGGC	TGCTTGCCCA	TATTTGTGAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAAC	1620
	CAAGGAATAC	AAACCAATAG	AAAATAGTCC	TGGGAATGTG	GTCAAGAAC	GAAGCCTGAG	1680
	TGTCTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCAAGAAA	AGGATCCGCT	1740
25	ACTCAAAAC	CAAGAATTTA	AAGGAGTTTC	TTAAATTTTC	ACCTTGTTC	TGAAGCTCAC	1800
	TTTTCAGTG	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTT	TTCTTAAAGA	1860
	TTATTTGTA	ATAGATATTG	TGGTTTGGG	AAGTTGAATT	TTTTATAGT	TAAATGTCAT	1920
	TTTAGAGAT	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACT	AGCAAGCTT	CTTTTCATTA	TTTTTTATGT	TTCACTTATA	AAGTCTTAGG	2040
30	TAACTAGTAG	GATAGAACAC	CTGTGTCGCG	AGAGTAAGGA	GAGAAGCTAC	TATTTAGTAG	2100
	AGCCTAACCC	AGGTTAATCT	CAAGAAGAGG	CGGATACTT	TCAGCTTTCC	ATGTAAGTGT	2160
	ATGCATAAAG	CCAATAGTAG	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCAC	2220
	TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTAGACTCA	GAATAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
35	TGACAACTTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCAT	2400
	GGACATTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460
	ATTTCACAA	TTTGTATAG	TGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGGTC	CTGTGTTT	CATGGCAACT	TGATCAGTAA	GGATTTCAAC	TCTGTTGTA	2580
40	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTCCTTT	TCTCTCCTTC	CTGAAAAATA	2640
	AAGTGTGGGA	AGAGACAAAA	AAAAAATA				

Seq ID NO: 383 Protein sequence
Protein Accession #: NP_002501

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45	MECLYYFLGP	LLLAARLPLD	AAKRFHDVIG	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
	VWKRGMWRWK	NSWKGGRVQA	VLTSDSPALV	GSNITFAVNL	IFPRCQKEDA	NGNIVYEKNC	120
	RNEAGLSADP	VYINWTAWSE	DSGNGTGGQ	SHENVFPDGG	PPPHHPGWR	WNFIYVFTL	180
50	QGYFQKLGRG	SVRVSVNTAN	VTGFLQIMEV	TVYRRHGRAY	VPIAQVKDQV	VVTDQIPVTV	240
	TMFQKNDKNS	SDETFLKDLF	IMFDVLHDP	SHFLNYSTIN	YKSPGDNQNT	LFVSTMTN	300
	HTYVLNGTFS	LNLTVKAAAP	GPCPPPPPPP	RPSKPTPSLG	PAGDNFLFELS	RIPDENQIN	360
	RYGHFQATIT	IVEGILEVNI	IQMTDVLMPV	PWPESSLIDF	VVTCCQSIP	EVCTIISDPT	420
	CEITQNTVCS	PVDVDEMCLL	TVRRTPNGSG	TYCVNLTLGD	DTSLALSTL	ISVPDRDPAS	480
55	PLRMANALI	SVGCLAIPTV	VISLLVYKX	KEYNPIENSP	GNVRSKGLS	VFLNRAKAVF	540
	FPNQEKDPL	LBNQEFKGV					

Seq ID NO: 384 DNA sequence
Nucleic Acid Accession #: NM_001134
Coding sequence: 48-1877

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65	AATATGGAAT	AGCTTCCATA	TTGGATTCTT	ACCAATGTAC	TGCAGAGATA	AGTTTAGCTG	180
	ACCTGGCTAC	CATATTTT	GGCCAGTTTG	TTCAAGAAGC	CACCTACAG	GAAGTAAGCA	240
	AAATGGTGAA	AGATGCATTG	ACTGCAATTG	AGAAACCCAC	TGGAGATGAA	CAGTCTTCAG	300
	GGTGTTTAGA	AAACCCAGCTA	CCTGCCTTTC	TGGAAGAACT	TTGCCATGAG	AAAGAAATTT	360
70	TGGAGAAAGTA	CGGACATTCA	GACTGCTGCA	GCCAAAGTGA	AGAGGGAAGA	CATAACTGTT	420
	TTCTTGCACA	CAAAAAGGCC	ACTCCAGCAT	CGATCCCACT	TTTCCAAGTT	CCAGAACCTG	480
	TCACAAGCTG	TGAAGCATAT	GAAGAAGACA	GGGAGACATT	CATGAACAAA	TTCATTTATG	540
	AGATAGCAAG	AAGGCATCCC	TTCTGTATG	CACCTACAAT	TCTTCTTTGG	GCTGCTCGCT	600
	ATGACAAAAT	AATTCATCT	TGCTGCAAG	CTGAAAATGC	AGTTGAATGC	TTCCAAACAA	660
75	AGGCAGCAAC	AGTTACAAA	GAATTAAGAG	AAAGCAGCTT	GTTAAATCAA	CATGCATGTG	720
	CAGTAATGAA	AAATTTTGGG	ACCCGAACCT	TCCAAGCCAT	AACTGTTACT	AAACTGAGTC	780
	AGAAGTTTAC	CAAGTTAAT	TTTACTGAAA	TCCAGAACT	AGTCTCTGAT	GTGGCCCATG	840
	TACATGAGCA	CTGTTGCGA	GGAGATGTGC	TGGATTGTCT	GCAGGATGGG	GAATAATCA	900
	TGTCTTCAAT	ATGTTCTCAA	CAAGACACTC	TGTCAAACAA	AATAACAGAA	TGCTGCACAC	960
80	TGACCAAGCT	GGACGTTGGT	CAATGTATAA	TTTATGACGA	AAATGATGAA	AAACCTGAAG	1020
	GTTCTATCTC	AAATCTAAAC	AGGTTTITAG	GAGATAGAGA	TTTTAACCAA	TTTTCTTCTG	1080
	GGGAAAAAAA	TATCTTCTTG	GCAAGTTTTC	TTTATGAATA	TTCAAGAAGA	CATCCTCAGC	1140
	TTGCTGTCTC	AGTAATTTCTA	AGAGTTGTCTA	AAGGATACCA	GGAGTTATTTG	GAGAAGTGT	1200
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85	TCAGAGGAG	CCAAGCATTTG	GCAAAAGGAA	GCTGCGGCTC	CTTCCAGAAA	CTAGGAGAA	1320
	ATTACTTACA	AAATGCGTTT	CTCGTTGCTT	ACACAAAGAA	AGCCCCCAG	CTGACCTGCT	1380
	CGGAGCTGAT	GGCCATCACC	AGAAAAATGG	CAGCCACAGC	AGCCACTTGT	TGCCAATCA	1440
	GTGAGGACAA	ACTATTGGCC	TGTGGCGAGG	GAGCGGCTGA	CATTATTATC	GGACACTTAT	1500

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 ATGCCAACAG GAGGCCATCG TTCAGCAGCT TGGTGGTGA TGAAACATAT GTCCCTCCTG 1620
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 TGCACACGAT GAAGCAAGAG TTTCTCATT ACCTTGTGAA GCAAAAGCCA CAAATAACAG 1740
 AGGAACAAC TGAAGGCTGTC ATTGCAGATT TCTCAGGCT GTTGAGAGAA TGCTGCCAAG 1800
 GCCAGGAACA GGAAGTCTGC TTTGCTGAAG AGGACACAAA ACTGATTTC AAAAACTGCTG 1860
 CTGCTTTGGG AGTTTAAAT ACTTCAGGGG AAGAGAAGAC AAAACGAGTC TTTTATTCGG 1920
 TGTGAACCTT TCTCTTTAAT TTTAACTGAT TTAACACTTT TGTGAATTA ATGAAATGAT 1980
 AAAGACTTTT ATGTGAGATT TCCTTATCAC AGAAATAAAA TATCTCCAAA TG

Seq ID NO: 385 Protein sequence
 Protein Accession #: NP_001125

1 11 21 31 41 51
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 RHNCFIAHKK TPASIPLPQ VPEVTSCEA YEEDRETFM KPIYIARRH PFLVAPTILL 180
 NAARYDKIIP SCCKAENAVE CFQTKAATVT KELRESSLLW QHACAVMKNV GTRTFQAITV 240
 TKLSQKPTKV NPTEIKLVL DVAHVHEHCC RGDVLDCLQD GEKIMSYICS QODFLSNKIT 300
 ECCCKLTTLER GQCIHAEND EKPEGLSPNL NRFLGDRDFN QFSSGKRNIF LASFVHEYSR 360
 RHPQLAVSVI LRVAQYQEL LEKCPQENP LECQDKGEE LQKYIQESQA LAKRSOGLFQ 420
 KLGEYILQNA FLVAYTKKAP QLTSSSELMAI TRKMAATAAT CCQLSEDKLL ACGEGAADII 480
 IGHLCIRHEM TPNPVGVCQ CTSSYANRRP CFSLLVDEIT YVPFAPSDDK FIFHKDLQQA 540
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 SKTRALGV

Seq ID NO: 386 DNA sequence
 Nucleic Acid Accession #: NM_002205.1
 Coding sequence: 1..3149

1 11 21 31 41 51
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 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGGTGA 840
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 CTCAGCCCTC CAGCCACCTC TGATGCTGTA

Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MGSRTPESSL HAVQLRWGFR RRPPLLPPLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120
LESSLSSESE EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DFIGTCYLST 180
10 DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
IAESYYPEYL INLVQQLQT RQASSIYDDS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300
GYVTILNGSD IRLYNFSGE QMASYFGYAV AATDVNGDGL DDLVGVAPLL MDRTPDGRPO 360
EVRGVVYVLQ HPAGIEPTPT LTLTGHDFFG RFGSSLTPLG DLDQDGYNDV AIGAPFPGGT 420
QQGVVVFVPG GPGLGSKXPS QVLQPLMAAS HTPDFGQSAL RGGRLDNGG YPDLIVGSPG 480
15 VDKAVVYRGR FIVSASASLT IFPAMFNPEE RSCSLBGNFV ACINLSFCLN ASGKHVADSI 540
GPTVRELQDM QKQKGGVRRR LFLASRQATL TQTLILQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALNLF SLDPQAPVDS HGLRPAHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GBQNHVYLGD KNALNLTFAH QNVGEGGAYE ASLRVTAPPE AEYSGLVRRP GNFSSLSQDY 720
FAVNSRLLV CDLGNFMKAG ASLWGGRLPT VPHLRDTKKT IQPDFQILSK NLANSQSDVV 780
20 SFRLSVEAQA QVTLNGVSKP EAVLFFVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHFINPKGL ELDPGSLHSH QQKREAPSR 900
SASSGPOLLK CPEAECFRLR CELGPLHQOE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960
YKALMKPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILPLGL LLLGLLIYIL 1020
YKLGFFKRLS PYGTAMEKAQ LKPPATSDA

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Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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30      1      11      21      31      41      51
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AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAATC CTGTGTCTGT TGTGTCTGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCAGCAGAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAC AGTTTAGAAG 180
35 AAAGGACAGT AATCTCATTG TTAATAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCTCGAAGTT GGTCACTTCA GCTCCTTTCC TGGCATGCGG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAGTCTT GGAAGAGGTT GACTCCACTC ACATTCCTCA GGCTGTATGA 480
40 AGGAGAGGCT CATATAATGA TCTCTTTCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCATTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA AACTGAAGC 720
TTTGATGTAC CCACTCTACA ACTCATTAC AGAGCTCGCC CAGTTCGCC TTTCGCAAGA 780
45 TGATGTGAAT GGCATTCTCT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCA CAATCTGTTT CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCTCTGCTT 900
GTCCCTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTAAAG ACAGATATT 960
TTGGGGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCT TGATTCTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTGAG ATGCTGCATA TGAAGTTAAG AGCAGGGACA CCGTTTAT 1080
50 TTTTAAAGTA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTGC AGCGACAAA TACTGGAGAT TTGATGAAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
55 ACAGTTTGAG TTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAGA GTAACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAT AAATCTAATA 1500
ATTATTATC TAATGTATTA TGAGCCAAAA TGGTTAATT TTCTGCTGAT TTCTGTGACT 1560
GAAGAAGATG AGCCTTGCGAG ATATCTGCAT GTGTCTGATA GAATGTTTCT GGAATTCTTC 1620
ACTTGCTTTT GAATTGCACT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
60 ATGTATTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
CTT

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Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

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65      1      11      21      31      41      51
      |      |      |      |      |      |
MHLAFLVLLC LFVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQF RRDNSNLIVK 60
KIQQNQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGRFSS FPGMPKWRKT HLYRIVNYT 120
70 PDLPRDAVDS AIEKALKVME EVTPLTFSRL YEGEADIMIS FAVKEHGDYF SFDGPGHSLA 180
HAYPPGPGLY GDHFDDEK WTEDASGTNL PLVAHELGH SLGLFHSANT EALMYPLVNS 240
FTBLAQFRLS QDDVNGIQSL YGPPFPASTE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
RGEYLFPPEDR YFWRSHWNP EPEFHLSAP WPSLPSYLD AYEVSNDTV FIPKGNPMA 360
75 IRGNEVQAGY PRGIHTLGF PTIRKIDAAV SDKEKKKTYF PAADKYWRFD ENSQSMQGF 420
PRLIADDPFG VEPKDAVLQ AFGFPFYPFG SSQFEFDPA RMVTHILKSN SWLHC

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Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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80      1      11      21      31      41      51
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ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTG ACACAGCTTC 60
CCAGCGACTC TAGAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
85 TACTACAACC TGAAGAAATG TGGGAGGCAA GTTGAAGAAC GGAGAAATAG TGGCCAGTGG 180
GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGAAGTG GAAACAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300

```

5
10
15
20

GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
TACAGGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAAGC CTTCCAATCT 420
TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
CTTGCTCATG CTTTTCACCC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAAATC 660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCTAGCTAC 720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
GGAAGTTCCC AAAATCCTGT CCAGCCATC GGGCCACAAA CCCCAAAAGC ATGTGACAGT 840
AAGCTAACTT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCA TTCTGTTTTT 960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
CTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTT 1260
GGAATTGGCC ACAAGATTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTTCT 1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 391 Protein sequence

Protein Accession #: NP_002412.1

25
30
35

1 11 21 31 41 51
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTGEGNPRWE QTHLTYRIEN 120
YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSSEGQADIM ISPVRGDHRD NSPFDGPGGN 180
LAHAFQPGPG IGGDAHFDED ERWTTNFRFY NLHRVAHAEL GHSLGLSHST DIGALMYPST 240
TFSGDVQLAQ DDIDGIIQAIY GRSQNFVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
FYMRNPFYYP EVELNPIISVF WPQLPNGLEA AYEFAADRDEV RFPKGNKYWA VQGNVNLHG 360
PKDIYSSSPG PRTVXHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDFG YPKMIAHDFP 420
GIGHKVDVAV MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 392 DNA sequence

Nucleic Acid Accession #: NM_002421.2

Coding sequence: 1..1409

40
45
50
55
60
65

1 11 21 31 41 51
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CCAGCGACTC TAGAACAACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAGAAA 120
TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180
GTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
TACAGGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAAGC CTTCCAATCT 420
TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
CTTGCTCATG CTTTTCACCC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
GGCCATTCTC TTGGAATCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCTAGCTAC 720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
GGAGCTTCCC AAAATCCTGT CCAGCCATC GGGCCACAAA CCCCAAAAGC ATGTGACAGT 840
AAGCTAACTT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCA TTCTGTTTTT 960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
CTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTT 1260
GGAATTGGCC ACAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTTCT 1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 393 Protein sequence

Protein Accession #: NP_002412.1

70
75
80

1 11 21 31 41 51
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTGEGNPRWE QTHLTYRIEN 120
YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSSEGQADIM ISPVRGDHRD NSPFDGPGGN 180
LAHAFQPGPG IGGDAHFDED ERWTTNFRFY NLHRVAHAEL GHSLGLSHST DIGALMYPST 240
TFSGDVQLAQ DDIDGIIQAIY GRSQNFVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
FYMRNPFYYP EVELNPIISVF WPQLPNGLEA AYEFAADRDEV RFPKGNKYWA VQGNVNLHG 360
PKDIYSSSPG PRTVXHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDFG YPKMIAHDFP 420
GIGHKVDVAV MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 394 DNA sequence

Nucleic Acid Accession #: NM_014331.2

Coding sequence: 1..1506

85

1 11 21 31 41 51
| | | | |

	ATGGTCAGAA	AGCCTGTTGT	GTCCACCATC	TCCAAAGGAG	GTTACCTGCA	GGGAAATGTT	60
	AACGGGAGGC	TGCTTCCCT	GGGCAACAAG	GAGCCACCTG	GGCAGGAGAA	AGTGCAGCTG	120
	AAGAGGAAAG	TCACCTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATTGGAGCA	180
5	GGAAATCTCA	TCCTCTCTAA	GGGCGTGCTC	CAGAACACGG	GCAGCGTGGG	CATGTCTCTG	240
	ACCATCTGGA	CGGTGTGTGG	GGTCTGTGCA	CTATTTGGAG	CTTTGTCTTA	TGCTGAATTG	300
	GGAAACAATA	TAAAGAAATC	TGGAGGTGAT	TACACATATA	TTTTGGAAGT	CTTTGGTCCA	360
	TTACCAAGCT	TTGTACGAGT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTGGG	ACGCTACATT	CTGGAAACCAT	TTTTTATTCA	ATGTGAAATC	480
10	CCTGAACTTG	CGATCAAGCT	CAITACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTAAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACCTTTTG	CAAGCTCACA	600
	GCAATTCGTA	TAATTTATAGT	CCCTGGAGTT	ATGCAGCTAA	TTAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTTCAGG	AAGAGATTCA	AGTATTACGC	GGTTGCCACT	GGCTTTTAT	720
	TATGGAATGT	ATGCATATGC	TGGCTGGTTT	TACCTCAACT	TTGTACTGTA	AGAAGTAGAA	780
15	AACCTGAAA	AAACATTCC	CCTTGCAATA	TGTATATCCA	TGGCCATTGT	CACCATGGC	840
	TATGTGCTGA	CAATGTGGC	CTACTTTACG	ACCATTAAATG	CTAGGAGCT	GCTGCTTCA	900
	AATGCAGTGG	CAGTGACCTT	TTCTGAGCGG	CTACTGGGAA	ATTTCTCAT	AGCAGTTCCG	960
	ATCTTTGTTC	CCCTCTCCCT	CTTTGGCTCC	ATGAAACGGT	GTGTGTTTGC	TGCTCCAGG	1020
	TTATTCATATG	TTGGCTCTCG	AGAGGGTCAC	CTTCCAGAAA	TCCTCTCCAT	GATTCTATGT	1080
20	CGCAAGCACA	CTCCTCTACC	AGCTGTTTAT	GTTTTGCAAC	CTTTGACAAT	GATAATGCTC	1140
	TTCTCTGAGG	ACCTCGACAG	TCCTTTGAAT	TTCTCTAGTT	TGCGCAGGTG	GCTTTTATT	1200
	GGGCTGGCAG	TTGCTGGGCT	GATTATCTCT	CGATACAAAT	GCCCAGATAT	GCATCGTCC	1260
	TTCAAGGTGC	CACCTTCTCAT	CCCAGCTTTG	TTTTCTCTCA	CATGCTCTT	CATGGTTGCC	1320
	CTTTCCTCT	ATTGGACACC	ATTAGTACA	GGGATTGGCT	TGCTCATCAC	TCTGACTGGA	1380
25	GTCCCTCGCT	ATTATCTCTT	TATTATATGG	GACAAGAAAC	CCAGGTGGTT	TAGAATAATG	1440
	TCAGAGAAAG	TAACGAGAAC	ATTACAAATA	ATACTGGAAG	TGTACCAGA	AGAAGATAAG	1500
	TTATGAACATA	ATGGACTTGA	GATCTTGCCA	ATCTGCCCAA	GGGGAGACAC	AAATAGGGA	1560
	TTTTTACTTG	ATTTTCTGAA	AGTCTAGAGA	ATTACRACTT	TGGTGATAAA	CAAAAGGAGT	1620
	CAGTTATTTT	TATTCATATA	TTTTAGCATA	TTGGAACATA	TTTCTAAGAA	ATTTAGTTAT	1680
30	AACCTCTATG	AGTTATAGAA	AGTGAATATG	CAGTTATTTCT	ATGAGTCCGA	CAATCTCTGA	1740
	GTCTCTGATA	CCTACCTATT	GGGTTAGGA	GAAAGAGCTA	GACAAATTACT	ATGTGGTCAT	1800
	TCTCTACAC	ATATGTTAGC	ACGGCAAGA	ACCTTCAAA	TGAAGACTGA	GATTTTCTG	1860
	TATATATGGG	TTTTGTAAAG	ATGGTTTAC	ACACTACAGA	TGCTTACTAT	GTGAAAAGTG	1920
	TTTTCAATTC	TGAAAAAAG	CATACATCAT	GATTATGGCA	AAGAGGAGAG	AAAGAAATT	1980
35	ATTTTACATT	GACATGTCAT	TGCTTCCCT	TAGATACCAA	TTTAGATAAC	AAACACTCAT	2040
	GCTTTAATGG	ATTATACCCA	GAGCACTTTG	AACAAAGGTC	AGTGGGGATT	GTGGAATACA	2100
	TTAAAGAGAA	GTCTTAGGG	GCTACTGTTT	ATGAGACACA	TCCAGGAGTT	ATGTTTAAAT	2160
	AAAAATCCCT	GAGAATTTAT	TATGTCAGAT	GTTTTTCTAT	TCATTATCAG	GAAAGTTTAG	2220
	TTATCTGTCA	TTTTTTTTTT	TCACATCAGT	TTGATCAGGA	AAGTGATATA	CACATCTTAG	2280
40	AGCAGAGATT	AGTTTGGTAT	TAAATCTCTA	TTAGAACAC	CACCTGTTTC	ACTAATAACT	2340
	TACCCCTGAT	GAGTCTATCT	AAACATATGC	ATTTTAAAGC	TTCAAATTAC	ATTATCAACA	2400
	TGAGAGAAAT	AAACCAACAA	GAAGATGTTT	AAAAATATAG	TCCCATATCT	GTAATCATAT	2460
	CTACATGCAA	TGTTAGTAA	TCTGAAGTTT	TTTAAATTTA	TGGCTATTTT	TACACGATGA	2520
	TGAAATTTGA	CAGTTTGTGC	ATTTTCTTTA	TACATTTTAT	ATTCCTCTGT	TAAATATCT	2580
45	CTTCAGATGA	AACCTGCCAG	ATTAATTAGG	AAAAGGCATA	TATTAACATA	AAAATTGCAA	2640
	AAGAAATGTC	GCTGTAAATA	AGATTTACAA	CTGATGTTTC	TAGAAAATTT	CCACTTCTAT	2700
	ATCTAGGCTT	TGTCAGTAA	TTCCACACCT	TAATATATCAT	TCAACTTGCA	AAAGAGACAA	2760
	CTGATAAGAA	GAAAAATGAA	ATGAGAATCT	GTGGATAAGT	GTTTGTGTTT	AGAAGATGTT	2820
	GTTTGGCCAG	TATTAGAAAA	TACTGTGAGC	CGGGCATGGT	GGCTTACATC	TGTAATCCCA	2880
50	GCACCTTGGG	AGGCTGAGGG	GGTGGATCAC	CTGAGGTGGG	GAGTTCTAGA	CCAGCCTGAC	2940
	CAACATGGAG	AAACCCCATC	TCTACTAAAA	ATACAAAAAT	AGCTGGGCAT	GGTGGCCAT	3000
	GCTGTGAATC	TCAGCTATTG	AGGAGGCTGA	GGCAGGAGAA	TTGCTTGAA	CCGGGAGGCG	3060
	GAGGTTGCA	TGAGCCAAAG	TTGCACCAC	GTACTCCAGC	CTGGGTGACA	AAGTCAGACT	3120
	CCATCTCCAA	AAAAAAA	AAAA				

Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

	1	11	21	31	41	51	
60	MVRKPVVSTI	SKGGYLGQNV	NGRLPSLGNK	EPFGQEKVQL	KRKVTLRQV	SIIIGTIIGA	60
	GIFISPKVL	QNTGVSQMSL	TIWTVQVLS	LFGALSYAEL	GTTIRKSGGH	YTYILEVFGP	120
	LPAPVRVWVE	LLIIRPAATA	VISLAFGRYI	LEPFFIQCEI	PELAIKLITA	VGITVVMVLN	180
	SMVSWSARI	QIFLTFCKLT	AIIIIIVPGV	MQLIKGQTON	FKDAPSGRDS	SITRLPLAFY	240
65	YGMAYAGWPF	YLNFTVEEVE	NPEKTIPLAI	CISMAITIGV	VVLNVAYFT	TINAEELLS	300
	NAVAVTFSE	LLGNFSLAVP	IFVALSCFGS	MNGGVPAVSR	LFYVASREGH	LPEILSMIEV	360
	RKHTPLPAVI	VLHPLTMINL	PSGDLDSLIN	PLSFARWLP	GLAVAGLIVL	RYKCPDMERP	420
	FKVPLFIPAL	PSPTCLFMVA	LSLYSDPFST	GIGFVITLTG	VPAYYLFIIW	DKKPRWFRIM	480
	SEKTRTLQI	ILEVVEEDK	L				

Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

	1	11	21	31	41	51	
75	GCCGCCAGCG	GCTTTCTCGG	ACGCCCTGGC	CAGCGGGCCG	CCCGACCCCC	TGCACCATGG	60
	ACCCCGCTCG	CCCCCTGGGG	CTGTGATTC	TGCTGCTTTT	CCTGACGGAG	GCTGCACCTG	120
	CGGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
80	ACGGACCCCTG	CCGGGCCCTA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCTCT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	CGGACGATGC	TGCTGGAGGG	ATAGAAAAAG	TTCCCAAAGT	TTGCGGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCTT	TAATCTAAGT	TCCATGACAT	420
	GTGAAAAATT	CTTTTCCGGT	GGGTGTCAAC	GGAAACCGAT	TGAGAACAGG	TTTCCAGATG	480
85	AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAAITCC	ATCATTTTGC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCATGTGTA	CTCGCTATTA	TTTTAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACTTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660

AGGATTGCGA ACGTGCAATG GCAAAAGCTT TGA AAAAGAA AAAGAAGATG CCAAAGCTTC 720
 GCTTTGCCAG TAGAATCCGG AAAATTCCGA AGAAGCAATT TTAACATTC TTAATATGTC 780
 ATCTTGTGTTG TCTTTATGGC TTATTTCCTT TTATGGTTGT ATCTGAAGAA TAATATGACA 840
 GCATGAGGAA ACAATCAAT GGTGATTAT TCACCACTTT TTATTAATAC AAGTCACCTT 900
 TTTCAAAAT TGGATTTTT TATATATAAC TAGCTGCTAT TCAATGTGA GTCTACCAAT 960
 TTTAATTTAT GGTTCACCTG TTTGTGAGAC GAATTCCTGC AATGCAATAG ATATAAAGC 1020
 AAATATGACT CACTCATTTT TTGGGGTCGT ATTCCTGATT TCAGAAGAGG ATCATAACTG 1080
 AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG 1140
 CC

Seq ID NO: 397 Protein sequence
 Protein Accession #: NP_006519

1 11 21 31 41 51
 MDPARPLGLS ILLFLFLTEA LGDAAQEPTG NNAEICLLPL DYGPCRALLL RYYVDRYTQS 60
 CRQFLYGGCE GNANFYTW E ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
 TCEKFPSSGCG HRNIENRFP DEATCMGFCA PKKIPSPCYS PKDEGLCSAN VTRYFYNPRY 180
 RTCDAPFTYG CGGDDNNFVS REDCKRACAK ALKKKKKMPK LRFASIRIKI RKKQF

Seq ID NO: 398 DNA sequence
 Nucleic Acid Accession #: NM_001508.1
 Coding sequence: 1..1361

1 11 21 31 41 51
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC 60
 CCGAGATTGG AGGTGGCCAC CTGGATCAAA ATCACCCCTTA TTCTGGTGA CCTGATCATC 120
 TTCTGATAGG GCTTCTCTGG GAACAGCGTC ACCATTGGG TCACCCAGGT GCTGCAGAAG 180
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGGACATC 240
 TTGTGTTTCC TCATCGGCAT GCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTTGACC 300
 ACGTCCAGCT ACACCCCTGT CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGACGCTGCT GACGCTCAGC TTGAGCGCT ACATGCGCAT CTGTCAACCC 420
 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
 GTCACCTCCG CCTGTGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTCG 540
 GTGAAGCTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCAG CCACCAACAG 600
 CAGCCGAGGA TCCTCAATAT GTCCATCTGT ACCAACCTCT CCAGCGCTG GACCGTGTTC 660
 CAGTCCAGCA TCTTCGCGCG CTTCGTGCTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGCTCGCT GGCCGGGGGC 780
 ACGCGGCTTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
 ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACAGC 900
 ATTCGGAGGA TCATGCTGTC GGCCAAACCC AAGCAAGACT GGAAGAGTGC CTACTTCGGG 960
 GGGTACATGA TCCTCTCCC CTTCCTGGAG ACGTTTTCCT ACCTCAGCTC GGTTCATCAAC 1020
 CCGCTCCTGT ACACGGTGTG CTGCGCAGAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC 1080
 TGCCGCTCTG CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
 ACCACCGACA GCGCCGCTTT TGTGCGCGC CCGTTGCTCT TCGCGTCCCG GCGCCACTCC 1200
 TCTGCAAGGA GAAGTGAAGG GATTTCCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCGAG 1260
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAACC 1320
 AATTCTGCTG CAGAGAAATG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 399 Protein sequence
 Protein Accession #: NP_001499.1

1 11 21 31 41 51
 MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNV TIRVTQVLQK 60
 KGYLQKEVTD HNVSLACSDI LVFLIGMME FYSIIWNPLT TSSYTLCKL HTFLFEACSY 120
 ATLLHVLITLS FERYIAICHP PRYKAVSGPC QVKLLIGFVM VTSALVALPL LFAMGTEYPL 180
 VNVPSERGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTFV QSSIFGAPVV YLVVLLSVAP 240
 MCWNMMQVLM KSGKSLAGG TRPPQLRKSE SEESRTARRQ TIIIFLRLIV TLAVCMFNPQ 300
 IRRIMAAAKP KHDWTRSYFR AYMIILLPFE TPFYLSVVIN PLYTVSSQQ FRFVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTKIFL STFQSEAEPEQ 420
 SKSQSLSLBS LEPNSGAKPA NSAAENGPOE HEV

Seq ID NO: 400 DNA sequence
 Nucleic Acid Accession #: NM_006475.1
 Coding sequence: 28..2538

1 11 21 31 41 51
 AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTTCTACTA 60
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 AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCTTCAACA GATTTTGGGC 180
 ACCAAAAGA AATACCTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
 AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
 TGCCCGCAGC TTTTGCCCAT TGACCATGTT TATGGCAGTC TGGGCATCGT GGGAGCCACC 360
 ACAACGCGAG GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
 TTCACCTACT TTGCACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCGGTAGA 480
 GGTTTTGAGA GCAAGGTGAA TGTGGAATTA CTGAATGCTT TACATAGTCA CATGATTAA 540
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 TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTTGTCA CTGTTAATTG TGCTCGAATC 660
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 CAAATTTGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
 GCAGCTGCCA TCACATCGGA CATATTGGAG GCCTTTGGAA GAGACGGTCA CTTCACACTC 840
 TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCACGAGG GTGTCTAGA AAGGTTTCA 900
 GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
 TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

	GGATGTGACG	GTGACAGTAT	AACAGTAAAT	GGAATCAAAA	TGGTGAACAA	AAAGGATATT	1080
	GTGACAAATA	ATGGTGTGAT	CCATTTGATT	GATCAGGTCC	TAATTCTCTGA	TTCTGCCAAA	1140
	CAAGTTATTG	AGCTGGCTGG	AAAACAGCAA	ACCACCTTCA	CGGATCTTGT	GGCCCAATTA	1200
5	GGCTTGGCAT	CTGCTCTGAG	GCCAGATGGA	GAATACACTT	TGCTGGCACC	TGTGAATAAT	1260
	GCATTTTCTG	ATGATACTCT	CAGCATGGTT	CAGCGCCTCC	TTAAATTAAT	TCTGCAGAAAT	1320
	CACATATTGA	AAGTAAAAAT	TGGCCTTAAT	GAGCTTTTACA	ACGGGCAAAAT	ACTGGAAGCC	1380
	ATCGGAGGCA	AACAGCTCAG	AGTCTTCGTA	TATCGTACAG	CTGCTGCGAT	TGAAAAATTC	1440
	TGCATGGAGA	AAGGGAGTAA	GCAAGGGAGA	AACGGTGCGA	TTACATATT	CCGGAGATC	1500
10	ATCAAGCCAG	CAGAGAAATC	CTCCATGAA	AAGTTAAAAA	AAGATAAGCG	CTTTAGCACC	1560
	TTCTTCAGCC	TACTTGAAGC	TGCAGACTTG	AAAGAGCTCC	TGACACAACC	TGGAGACTGG	1620
	ACATTATTGG	TGCCAACCAA	TGATGCTTTT	AAGGGAATGA	CTAGTGAAGA	AAAAGAAATT	1680
	CTGATACGGG	ACAAAAATGC	TCTTCAAAAC	ATCATTCTTT	ATCACCTGAC	ACCAGGAGTT	1740
	TTCAITGGAA	AAGGATTGGA	ACCTGGTGIT	ACTAACATT	TAAAGACCAC	ACRAGGAAGC	1800
15	AAAATCTTTC	TGAAGAAGT	AAATGATACA	CTTCTGGTGA	ATGAATTGAA	ATCAAAAGAA	1860
	TCGACATCA	TGACAAACAA	TGGTGAATTT	CATGTTGTAG	ATAAACTCCT	CTATCCAGCA	1920
	GACACACCTG	TTGGAAATGA	TCAACTGCTG	GAAATACTTA	ATAAAATTAAT	CAAATACATC	1980
	CAAAITTAAGT	TTGTTCTGAG	TAGCACCTTC	AAAGAAATCC	COGTGACTGT	CTATACAACT	2040
	AAAATTATTA	CCAAAGTTGT	GGAAACCAAA	ATTAAAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100
20	ATTATCAAAA	CTGAAGGACC	CACACTAACA	AAAGTCAAAA	TTGAAGGTGA	ACCTGAATTTC	2160
	AGACTGATGA	GGAAGGTGGA	AACAATAACT	GAAGTGATCC	ATTGAGAGCC	AATTATTAAA	2220
	AAATACACCA	AAATCATTTG	TGGAGTGCCT	GTGGAATAAA	CTGAAAAAGA	GACACGAGAA	2280
	GAACGAATCA	TTACAGGTCC	TGAAATAAAA	TACACTAGGA	TTTCTACTGG	AGGTGGAGAA	2340
	ACAGAAGAAA	CTCTGAAGAA	ATTGTTACAA	GAAGAGGTCA	CCAAGGTCAC	CAAATTCATT	2400
25	GAAGGTGGTG	ATGGTCATTT	ATTTGAAGAT	GAAGAAATTA	AAAGACTGCT	TGAGGAGAC	2460
	ACACCGGTGA	GGAAGTTTGA	AGCCAAACAA	AAAGTTCAAG	GTTCAGAGAG	ACGATTAAAG	2520
	GAAGGTGGTG	CTCAGTGAAA	ATCCAAAAAC	CAGAAAAAAA	TGTTTATACA	ACCTTAAGTC	2580
	AATAACCTGA	CCTTAGAATA	TTGTGAGAGC	CAAGTTGACT	TCAGGAACCTG	AAACATCAGC	2640
	ACAAAGAAGC	AATCATCAAA	TAATTCGTAA	CACAAATTTA	ATATTTTTTT	TTCTGAATGA	2700
30	GAAACATGAG	GGAAATTTGT	GAGTTAGCCT	CCGTGGTAA	AGGAATTGAA	GAATAATATA	2760
	CACCTTACAC	CTTGACATTA	AAAGTCTCTG	CTAACTTTGG	AATCCATTAG	AAATCCATTAG	2820
	AGAAAAATCC	TTGTACACAG	ATTCTATACA	ATTCAAAATG	AAGAGTTGTG	AACCTGTTATC	2880
	CCATTGAAAA	GACCGAGCCT	TGTATGTATG	TTATGGATAC	ATAAAATGCA	CGCAAGCCAT	2940
	TATCTCTCCA	TGGGAAGCTA	AGTTATAAAA	ATAGGTGCTT	GGGTATACAA	ACTTTTATTA	3000
35	TCAAAAGGCT	TTGCACATTT	CTATATGAGT	GGGTTTACTG	GTAATTTATG	TTATTTTATA	3060
	CAACTAATTT	TGTACTCTCA	GAATGTTTGT	CATATGCTTC	TTGCAATGCA	TATTTTATAA	3120
	TCTCAACGCT	TTCAATAAAA	CCATTTTTC	GATATAAAGA	GAATTACTTC	AAATTGAGTA	3180
	ATTCAGAAAA	ACTCAAGATT	TAAGTTAAAA	AGTGGTTTGG	ACTTGGGAA		

Seq ID NO: 401 Protein sequence

Protein Accession #: NP_006466.1

	1	11	21	31	41	51	
45	MIPFLPMFSL	LLLLIVNPIN	ANNHYDKILA	HSRIRGRDQG	PNVCAQLQIL	GTKKKYFSTC	60
	KWYKKSICG	QKTTVLYECC	PGYMRMEGKM	GCPAVLPIDH	VYGTGLIVGA	TTTQRYSDAS	120
	KLREBIEGKG	SFTYFAPSNP	AWDNLDSDIR	RGLESNVNVE	LLNALHSEMI	NKRMLTKDLK	180
	NGMIIPSMYN	NLGLFINHYP	NGVVTVNCAR	IIHGNQIATN	GVVHVIDRVL	TQIGTSIQDF	240
	IEAEDDLSSP	RAAAITSDIL	EALGRDGHFT	LPAPTNEAPE	KLPRGVLERP	MGDKVASEAL	300
50	MKYHLNLTQ	CSBSIMGGAV	FETLEGNTIE	IGCDGDSITV	NGIKMVNKKO	IVTNNGVIEL	360
	IDQVLIPDSA	KQVIELAGKQ	QTTFTDLVAQ	LGLASALRPD	GEYTLAPVNV	NAFSDDTLSM	420
	VQRLKLLKIL	NHILKVKVLG	NELYNQOILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKSGSKG	480
	RNGAIHIFRE	IIKPAEKSLH	EKLKQDKRPS	TFLSLLEAAD	LKELLTPQPD	WTLFVPTNDA	540
	FKGMTSEEKE	ILIRDKNALQ	NIILYHLTPG	VFVGKGFEPG	VTNLLKTTQG	SKIFLKEVND	600
	TLNLVNLKSK	ESDINTNGV	IHVVDKLLYP	ADTPVGNQDL	LEILNKLIKY	IQIKFVRGST	660
55	FKEIPVTYVT	TKIITKVVEP	KIKVIEGSLQ	PIIKTEGPTL	TKVKIBGEPE	FRLLKEGETI	720
	TEVIHGEPII	KKYTKIIDGV	PVEITEKETR	EERIITGPEI	KYTRISTGGG	ETETELKQLL	780
	QEEVTKVTKF	IEGGDGLHFE	DEBIKRLLLQ	DTPVRKIQAN	KKVQGSRRRL	REGRSQ	

Seq ID NO: 402 DNA sequence

Nucleic Acid Accession #: NM_002416

Coding sequence: 40..417

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65	ATCCAATACA	GGAGTGACTT	GGAACCTCCAT	TCTATCACTA	TGAAGAAAAG	TGGTGTCTCT	60
	TTCTCTCTGG	GCATCATCTT	GCTGGTCTCTG	ATTGGAGTGC	AAGGAACCCC	AGTAGTGAGA	120
	AAGGGTCTCG	GTTCCTGCAT	CAGCACCAAC	CAAGGGACTA	TCCACCTACA	ATCCTTGAAA	180
	GACCTTAAAC	AATTTGCCCC	AAGCCCTTCC	TGCGAGAAAA	TTGAAATCAT	TGCTACACTG	240
70	AAGAAATGGAG	TTCAAAATCG	TCTAAACCCA	GATTCAGCAG	ATGTGAAGGA	ACTGATTAAA	300
	AAGTGGGAGA	AACAGGTCAG	CCAAAAGAAA	AAGCAAAAGA	ATGGGAAAAA	ACATCAAAAA	360
	AAGAAAGTTC	TGAAGTTCG	AAAATCTCAA	CGTCTCTGCT	AAAAGAAGAC	TACATAAGAG	420
	ACCACCTCAC	CAATAAGTAT	TCTGTGTTAA	AAATGTTCTA	TTTAAATTAT	ACCGCTATCA	480
	TTCCAAAGGA	GGATGGCATA	TAATACAAAG	GCTTATTAAAT	TTGACTAGAA	AATTTAAAC	540
75	ATTACTCTGA	AATTGTAACT	AAAGTTAGAA	AGTTGATTTT	AAGAAATCCA	ACGTTAAGAA	600
	TGTTTAAAGG	CTATGATTGT	CTTTGTTCTT	CTACCAACCA	CCAGTTGAAT	TTCAATCATG	660
	TTAAGGCCAT	GATTTTAGCA	ATACCCATGT	CTACACAGAT	GTTCAACCAA	CCACATCCCA	720
	CTCACACAGC	CTGCTGGGAA	GAGCAGCCCT	AGGCTTCCAC	GTAAGTCAGC	CTCCAGAGAG	780
	TATCTGAGCG	ACATGTGACG	AAGTCTTAAG	CTGTTTAGCA	TGCTGGTGGG	CCAAGCAGTT	840
80	TGAAATTTAG	CTGGACCTCA	CCAAGCTGCT	GTGGCCATCA	ACCTCTGTAT	TTGAATCAGC	900
	CTACAGGCCCT	CACACCAAT	GTGCTGAGA	GATTCATGCT	GATTGTTATT	GGGTATCACC	960
	ACTGGAGATC	ACCAGTGTGT	GGCTTTTCTG	GCTCTCTTTC	TGGCTTTGGA	AGCCATGTGA	1020
	TTCCATCTTG	CCGCTCAGGG	CTGACCACTT	TATTTCTTTT	TGTTCCCTCT	TGCTTCATTC	1080
	AAGTCAGCTC	TTCTGCATCC	TACCACAATG	CAGTGCCTTT	CTTCTCTCCA	GTGCACCTGT	1140
	CATATGCTCT	GATTTATCTG	AGTCAACTCC	TTTCTCATCT	TGTCCCAAC	ACCCACAGAG	1200
85	AGTGCCTTCT	TCTCCCAATT	CATCCTCACT	CAGTCCAGCT	TAGTTCAAGT	CCTGCTCTCT	1260
	AAATAAACCT	TTTTGGACAC	ACAAATTATC	TTAAACTCC	TGTTTCACTT	GGTTCAGTAC	1320
	CACATGGGTG	AACATCAAT	GGTTAACTAA	TTCTTGGGTG	TTTATCTCAT	CTCTCCAAAC	1380

5 AGATTGTCAG CTCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
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 TGGCAACCCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACCTCTT ACTTATATC TTCAGGACAC TCCTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTTGCTTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAGATAG CCACCGAGAT CCTTATOGAA ACTCATTTTA GGCAATATG 1920
 10 AGTTTTATTG TCGGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTGGT 2040
 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAACC TCCTTCCAGG 2100
 GGAGGTTTCA TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATT AGAGTGTCTG CCGTGGGAGA 2220
 15 TCCCACCCGA AGCTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
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 GTAGACAGTA TATAACTAAC AACCAGAGAC TACATATTGT CACTGACACA CACGTTATAA 2400
 TCAATTATCA TATATATACA TACATGCATA CACTCTCAA GCAATAAAT TTTCACTTCA 2460
 20 AAACAGTATT GACTTGTATA CCTTGTAAAT TGAATATTT TCTTTGTATA AATAGAATGG 2520
 TATCAATAAA TAGACCATTA ATCAG

Seq ID NO: 403 Protein sequence
Protein Accession #: NP_002407

25 1 11 21 31 41 51
 MKKSGVLFLL GIILLVLIGV OGTFVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IEIIATLKNQ VQTCLNPDSA DVKELIKKWE KQVSQKKQK NGKKHQKKV LKVRKSQRSR 120
 QKKTT

Seq ID NO: 404 DNA sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

35 1 11 21 31 41 51
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 40 GAGCGGGTCT TGGGGCTGGC GGGACTAGCG CTGCTACTCC TGGGCTGGGT CTCTCGTCT 180
 TCTCCCACTT CCTCGGCATC CTCTTCTCC TCCTCGGCGC GGTTCCTGGC TTCCGCGCTG 240
 TCCGCGCAGC CCGCGCTGCC GGACCACTGC CCGCGCTGCT GCGAGTGTCT CGAGGCAGCG 300
 CGCACAGTCA AGTGGTTAA CGCAATCTG ACCGAGGTGC CCAAGGACCT GCCCGCTAC 360
 GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCCGTGC TCCCTGCGCG CGCCTTCCG 420
 CGCGCGCGCG CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCGC CCTGGAAGAG 480
 45 GTGCGCGCGG GCGCCTTCGA GCATCTGCC AGCCTGCGCC AGCTGACCT CAGCCACAAC 540
 CCACTGGCGC ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTGGGCCCC 600
 AGTCCCTCTG TGGAACTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGGAGCTTGG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
 CGCGCTTGG AGTGGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
 50 CTGCGCCAGC TCAGGCACTG GCACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTC 840
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 CTTCAACAAT GCACCTGGCC TGAGTTGCAA GGTCTACCCC ACATTAGGTT TTTCTGGAC 960
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 55 GAGGTAGTCA TGGGAGGCTA CCGGCTCACC TGTGCAATAT CGGAAAAAAT GAGGAATCGG 1080
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 GTTTTGTATT TGAACGCGAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCCTG 1260
 AGGGATCAGA TGGGAGGCTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAAAC 1320
 60 AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACCTCTG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCAATA 1440
 TAGATACAA GGACTTTGAC TAAAGCAGT GAAGGGGATT TGCTTCTCTG TTATGTAAAG 1500
 TTTCTCGGTG TGTCTGTGTA ATGTAAGAG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
 TTTCTTTTCT TGGAACTCCT CAACAGTAT GGAGGGATT TTCAGGTTTC AGCATGAACA 1620
 65 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAAA GCTGCCCTCA CTTTTCGAG AAAAAATACT TATTCAATAA 1740
 TATCAGTTT ATTCTCATGT ACCTAAGTTG TGGAGRAAAT AATTGCATCC TATAAATGTC 1800
 CTGCAGAGT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGTCAT ATTACAAAA ATAACCTGCA ACTTCATAAC 1920
 70 TTTCTTGACA AAGTAAATTA CTTTTTGTAT TGCAGTTTAT ATGAAAAATG ACTGATTTT 1980
 TTTTAATAAA CTGATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
 ATTCTTAAAA GAA

Seq ID NO: 405 Protein sequence
Protein Accession #: NP_006661

75 1 11 21 31 41 51
 MPGGCSRGA AGDGLRLAR LALVLLGWVS SSSPTSSASS FSSAPPLAS AVSAQPLPFD 60
 80 QCPALCBCEB AARTVRCVNR MLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGSLR DEVRAGAFPH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL 180
 NHIVPPEDER QNRSPFGMVV AALLAGRALQ GLRRLLEASN HFLVLPEDVL AQLPSLRHLD 240
 LSNNSLVSLT YVSRNLTHL ESLHLEDNAL KVLENGTLAE LQGLPHIRVF LDNNPNWDCD 300
 HMDHMTWLK ETEVVQKDR LTCAYPERMR NRVLLELSA DLDCLPILPP SLQTSYVFLG 360
 85 IVLALIGALF LLVLYLNRKG IKKWMENIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

Seq ID NO: 406 DNA sequence
Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

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Seq ID NO: 407 Protein sequence
Protein Accession #: Bos sequence

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Seq ID NO: 408 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

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80 |      |      |      |      |      |
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Seq ID NO: 409 Protein sequence
Protein Accession #: NP_000086.1

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 ADCVLERDGS RSCVCRVGWA GNGILOGRDT DLDGFPDEKL RCEPQCRKD NCVTVPNSGQ 300
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 FGVDSSSFY VVMWQMEQT YWQANPFRV AEPGIQLKAV KSSTGPGEL RNALWHTGDT 660
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Seq ID NO: 410 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67..363

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 CCTGTTAATC CAAGGTCTTT AGAAAAACTT GAAATTAATC CTGCAAGCCA ATTTTGTCCA 240
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 TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
 TAAAACCGA GGGGAGCAAA ATCGATGCG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
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Seq ID NO: 411 Protein sequence
 Protein Accession #: NP_001556.1

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 Coding sequence: 143..874

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 Protein Accession #: XP_057014

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 GKIAECTFTK MRNSALRYL FSGSLRLKCR NACQRMWYF PNGAECSGFL PIEAIYLDQ 180
 GSPENNSTIN IHTSSVEGL CBGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
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WO 02/086443

Seq ID NO: 414 DNA sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 138..2405

PCT/US02/12476

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Protein Accession #: XP_084007

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FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHDSHS DHEHSDHER HSDHEHSDH 120
EHSDDHDSHS HNHAAAGKIN KRKALCPDED SDSSGKDPNN SQKGARPE HASGRNRVKD 180
75 SVSASEVTST VYNTVSEGTN FLETIETPRP GKLPFKDVSS STPPSVTSKS RVSLAGRKT 240
NESVSEPRKG PMYSRNTNEN PQECFNASKL LTRSGMGIQV PLANATEPNYL CPAIINQIDA 300
RSLIHTSEK KAEIIPKTYL LQIAWVGFI AISIISFLSL LGVILVPLMN RVFFKFLSLP 360
LVALAVGTLG GDAPLHLLEPH SHASHHSHS HEEFAMEMKR GPLFSLSSQ NIESAYFDS 420
TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KKKNQKKPEN DDDVEIKKQL SKYESQLSTN 480
EEKVDTDDRT EGYLRADSQE PSHFDSQQPA VLEEEVMIA HAHPQEVYNE YVPRGCKNK 540
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MMDGLEHNSD GLAIGAAFTG GLSSGLSTSV AVFCHPELPE LGDFAVLLKA GMTVKQAVLY 660
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Seq ID NO: 416 DNA sequence
Nucleic Acid Accession #: NM_015419.1
Coding sequence: 1..8487

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10	GACCTCAGCT	CTCTTCAGGT	TTTCAAGTTC	AGCTACAACA	AGCTGAGAGT	GATCACAGGA	360
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	GAGTCCCTTC	TGAGACAGAA	CAGGAGCAGG	AGTATTGAGG	AGGAGCAAGA	ACAGGAAGAG	900
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	AAATATGACG	ACGAGCACGG	GAAACATGGT	AACCTGGTCT	GTGACATCAA	GAAACCAATG	1020
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	CAGTGGACCA	ACAAACCGGA	AATAACTACA	TATCCTTCTG	GGGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACAA	CTCCAAGATT	ATCAAGTACA	ACAATTCTCT	TCCCATTGCA	CATGTCCAAA	5040

	CCCAGCATTC	CTAGTAAAGTT	TACTGACCGA	AGAACTGACC	AATTCATAGS	TTACTCCAAA	5100
	GTGTTTGGAA	ATAACAACAT	CCCTGAGGCA	AGAAACCCAG	TTGGAAAGCC	TCCAGTCCA	5160
	AGAATTCTCT	ATTATTCCAA	TGGAAGACTC	CCTTCTTTTA	CCAAACAAGAC	TCTTCTTTT	5220
5	CCACAGTGGG	GAGTCACCGG	GAGACCCAG	ATACCCACTT	CTCCTGCCCC	AGTAATGAGA	5280
	GAGAGAAAAG	TTATTCCAGG	TTCTTACAA	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
	GACTTTGGCC	CTCCGACACC	TCCGTGTGTG	CACACTCCGC	AGACCAAGGG	ATCACCCTCA	5400
	ACTAACTTAC	AGAAATATCC	TATGGTCTCT	TCCACCCAGA	GTTCTATCTC	CTTTATAACA	5460
	TCTTCTGTCC	AGTCTCTCAG	AAGCTTCCAC	CAGAGCAGCT	CAAAAGTTCTT	TGCAGGAGGA	5520
10	CCTCCTGCAT	CCAAATTCTG	GTCTCTTGGG	GAAAAGCCCC	AAATCTCTAC	CAAGTCCCCA	5580
	CAGACTGTGT	COGTACCCGC	TGAGACAGAC	ACTGTGTTC	CCTGTGAGGC	AACAGGAAAA	5640
	CCAAAGCCTT	TOGTTACTTG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAATACC	5700
	AGGATACAA	GGTTTGAAGT	TCTCAAGAAC	GGTACCTTAG	TGATACGGAA	GGTTCAAGTA	5760
	CAAGATCGAG	GCCAGTATAT	GTGCAACGCC	AGCAACCTGC	ACGGCCTGGA	CAGGATGSGT	5820
15	GTCTTGCTTT	CGGTACCCGT	GCAGCAACCT	CAAACTCTAG	CCTCCCACTA	CCAGGACGTC	5880
	ACTGTCTACC	TGGGAGACAC	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCCAGCCCCC	5940
	CAAAATTTCT	GGATCTTCCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	CGCATCAACC	TGCAACAAAA	CCGGACCCCT	TCCATCAAGG	AGGCGTCCCT	CTCAGACAGA	6060
	GGGTCTATA	AGTGGGTGGC	CAGCAATGCA	GCGGGGGGG	ACAGCCTGGC	CATCCGCTGT	6120
20	CAGTGGGGG	CAGTGGCCCC	CGTTATCCAC	CAGGAGAAGC	TGGAGAACAT	CTCGCTGCCC	6180
	CCGGGGCTCA	TCACTGCACAT	TCACGTGACT	GCCAGGCTG	CGCCCTGGCC	CAGCGTGGCC	6240
	TGGGTCTCTG	GGGACGGTAC	CCAGATCCGC	CCCTCGCAGT	TCTTCCACGG	GAACCTGTGT	6300
	GTTTTCCCAA	ACGGGACGCT	CTACATCCGC	AACCTCGCGC	CCAAGGACAG	CGGGCGCTAT	6360
	GAGTGGGTGG	CGGCCAACCT	GGTAGGCTCC	GCGCGCAGGA	CGGTGCAGCT	GAACGTGCAG	6420
25	CGTGACGACG	CCAAACGCGG	CATCACGGGC	ACCTCCCGCC	GGAGGACGGA	CGTCAGGTAC	6480
	GGAGGAACCC	TCAAGCTGGA	CTGCAGCGCC	TGGGGGGGAG	CCTGGCCGGG	CATCCTCTGG	6540
	AGGCTCGCGT	CCAGAGGAGT	GATCGACGCG	CTCTTCAAGT	TGATAGCAG	AATCAAGGTG	6600
	TTTGCCAAAT	GGACCTTGGT	GGTGAATCA	GTGACGGACA	AAGATGCGGG	AGATTACCTG	6660
	TGCGTAGCTC	GAATTAAGGT	TGGTGATGAC	TACGTGGTGC	TCAAAGTGGA	TGTGGTGATG	6720
30	AAACCGGCCA	AGATTGAACA	CAAGGAGGAG	AACGACCCCA	AAGTCTTCTA	CGGGGGTGAC	6780
	CTGAAGGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCG	AGATCTCCTG	GAGCCTCCCA	6840
	GACGGGAGTC	TGGTGAATCG	CTTCATGCAG	TGCGATGACA	GCGGTGGACG	CACCAAGCGC	6900
	TATGTGCTCT	TCAACAAATG	GACACTCTAC	TTTAAAGGAG	TGGGGATGAG	GAGGAGAGGA	6960
	GACTACACCT	GCTTTGTGTA	AAATCAGGTC	GGGAAGGACG	AGATGAGAGT	CAGAGTCAAG	7020
35	GTGGTGACAG	CGCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGGTTCA	GGTGCCCTAT	7080
	GGAGAGCTGG	CTGACTGAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
	TTGTCCCCAA	CCCAAGAGGT	GATCCCAACC	TCCTCTGAGA	AGTATCAGAT	ATACCAAGAT	7200
	GGCACTCTCC	TTATTGAGAA	AGCCAGCGT	TCTGACAGCG	GCAACTACAC	CTGCGTGGTC	7260
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	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	7620
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	CGGAACTGCA	TTGACTGCAA	AGCTGAAAGG	ATCCCAACCC	CGAGGGTGTG	ATGGGCTTTT	7740
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	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	8220
55	AAGATCAAGC	GTAAACCCAA	CCCCATCACC	ACCGTGGGGG	AGATAGCAGC	CGGGGGCAGT	8280
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	CCGAGGGGTG	TGGTCTTGCC	AGCTCCATAC	TATGAAAACC	GGATCACTGT	CCATGGCAAC	8400
	GGTCTCTCTC	TTATTCAGAA	AGCCAGCGT	TCTGACAGCG	GCAACTACAC	CTGCGTGGTC	8460
	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	8520
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	CGGAACTGCA	TTGACTGCAA	AGCTGAAAGG	ATCCCAACCC	CGAGGGTGTG	ATGGGCTTTT	8640
	CCGAGGGGTG	TGGTCTTGCC	AGCTCCATAC	TATGAAAACC	GGATCACTGT	CCATGGCAAC	8700
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65	AAGATCAAGC	GTAAACCCAA	CCCCATCACC	ACCGTGGGGG	AGATAGCAGC	CGGGGGCAGT	8880
	CGGAACTGCA	TTGACTGCAA	AGCTGAAAGG	ATCCCAACCC	CGAGGGTGTG	ATGGGCTTTT	8940
	CCGAGGGGTG	TGGTCTTGCC	AGCTCCATAC	TATGAAAACC	GGATCACTGT	CCATGGCAAC	9000
	GGTCTCTCTC	TTATTCAGAA	AGCCAGCGT	TCTGACAGCG	GCAACTACAC	CTGCGTGGTC	9060
	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	9120
70	AAGATCAAGC	GTAAACCCAA	CCCCATCACC	ACCGTGGGGG	AGATAGCAGC	CGGGGGCAGT	9180
	CGGAACTGCA	TTGACTGCAA	AGCTGAAAGG	ATCCCAACCC	CGAGGGTGTG	ATGGGCTTTT	9240
	CCGAGGGGTG	TGGTCTTGCC	AGCTCCATAC	TATGAAAACC	GGATCACTGT	CCATGGCAAC	9300
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	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	9420
75	AAGATCAAGC	GTAAACCCAA	CCCCATCACC	ACCGTGGGGG	AGATAGCAGC	CGGGGGCAGT	9480
	CGGAACTGCA	TTGACTGCAA	AGCTGAAAGG	ATCCCAACCC	CGAGGGTGTG	ATGGGCTTTT	9540
	CCGAGGGGTG	TGGTCTTGCC	AGCTCCATAC	TATGAAAACC	GGATCACTGT	CCATGGCAAC	9600
	GGTCTCTCTC	TTATTCAGAA	AGCCAGCGT	TCTGACAGCG	GCAACTACAC	CTGCGTGGTC	9660

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	NLGFNSIQAL	SETSPAGLTK	LELLMIHGN	IPSIIDGALR	DLSSLQVFKF	SYNKLREVTG	120
	QTLQGLSNLM	RLHIDENXIE	PIHPQAFNGL	TSRLRLHLEG	NLLHQLHPST	PSTPTFLDYP	180
	RLSTIRHLYL	AENMVRTLPA	SMLRNMPLE	NLYLQGNPWT	CDCEMRWFLE	WDAKSRGILE	240

	CKRDKAYEGG	QLCAMCFSPK	KLYKHEIHLK	KDMTCLKPSI	ESPLRQNRSR	SIEEEQEQEE	300
	DGGSQILIEK	FQLPQWSISL	NMTDEHGMV	NLVCDIKKPM	DVYKIHLNQT	DPPDIDINAT	360
	VALDFECFMT	RENYEKLMKL	IAYSEVPVK	LHREMLMSKD	PRVSYQVRQD	ADEEALYYTG	420
5	VRAQILAEP	WVMPSPIDIQ	LNRRQSTAKK	VLLSYTYQVS	QTISTKDTRO	ARGRSWWMIE	480
	PSGAVQRDQT	VLEGGPCQLS	CNVKASESPS	IFWVLPDGS	LKAPMDDPDS	KPSILSSGWL	540
	RIKSMFSDS	GLYQCIQVR	DEMDRMVYRV	LVQSPSTQPA	EKDTVTIGKN	PGESVTLPCN	600
	ALAIPEAELS	WILPNRRIIN	DLANTSHVYM	LPNGTLSIPK	VQVSDSGYYR	CVAVNQGGAD	660
	HFTVGTITVK	KSGGLPSKRG	RRPGAKALSR	VREDIVEDEG	GSGMGDEENT	SRRLHHPKQD	720
10	EVFLTKDDA	INGDKKAKRG	RRKLKLWKHS	EKEPETNVAE	GRRVFSRRR	INMANKQINP	780
	ERNADILARV	RGKNLPKGT	VPLIKTTTSP	PSLSLEVTPP	PPAVSPPSAS	PVQTVTSABE	840
	SSADVFLGGE	EEHVLGTISS	ASMGLEHNNH	GVILVEPEVT	STPLEEVVDD	LSEKTEITS	900
	TEGDLKGTA	PTLISEPYEP	SPTLHTLDTV	YEKPTHEETA	TEGWSAADVG	SSSEPTSSEY	960
	EPPLDAVSLA	ESEPMQYFDP	DLETKSQPDE	DKMKEDTFAH	LTPPTTIWVN	DSSTSQLFED	1020
15	STIGEPPVGP	QSHLQGLTDN	IHLVKSSSLT	QDTLLIKXGM	KEMSQTLQGG	NMLEGDPHIS	1080
	RSSSEGGQES	KSTLTPDSTL	GIMSSMSFVK	KPAETTVGTL	LDRDITTVTT	TPRQKVAPSS	1140
	TMSTHPSRRR	PNRRRLRKN	KPRHRHKQTP	PTTFAPSETP	STQPTQAPDI	KISSQVLESS	1200
	VPTANVMDTV	NTPKQLEMEK	NAEPTSKGTP	RRKHGKRPNK	HRYPSTVSS	RASGSKPSPS	1260
	PENKHNIVIT	PSSETILLPR	TVSLKTEGYP	DSLDMYTTTR	KIYSSYPKVQ	ETLFTVTKPT	1320
20	SDGKEIKDDV	ATNVDRKESD	ILVTGESITN	AIPTSRSLVS	TMGEPEKESS	PVGPFGPTPW	1380
	NPSTRAQFDR	LQTDIPVTT	GENLTDPLL	KELEDVDFTS	EPLSSLTVST	PPHQRAGSS	1440
	TTLSLKVVEV	ASSQAETFTL	QDHLLETTVA	ILLSETRPON	HTPTAARMKE	PASSSPSTIL	1500
	MSLGQTITTK	PALPSPRISQ	ASRDSKENVF	LNYYGNPETE	ATPVNNEGTO	HMSGFNLST	1560
	PSSDRDAFNL	STKLELEKQV	PGSRSLPRGP	DSQRQDGRVH	ASHQLTRVPA	KPILPTATVR	1620
25	LPESMTQSAS	RYFVTSSQSP	HWTNKPEITT	YPSGALPENK	QFTTPRLSST	TIPPLPHEMSK	1680
	PSIPSKFDR	RTDQFNGVSK	VPGNNNIPEA	RNPVGKPPSP	RIPHYNGRL	PPFTNKTLSF	1740
	PQLGVTRRPQ	IPTSAPVVMR	ERKVI PGSYN	RIHSHSTFHL	DFGPPAPPLL	HTPQTGSPS	1800
	TNLQNPIMVS	STQSSISPT	SSVQSGSFB	QSSSKFPAGG	PPASKFWSLG	EKPQILTKSP	1860
	QTVSVTAETD	TVPPCEATGK	PKPFVTWTKV	STGALMTFNT	RIQRFEVLKN	GTLVIRKVVQ	1920
30	QDRGQYMTCT	SNLHGLDRMV	VLLSVTVQQP	QILASHYQDV	TVYLGDTIAM	ECLAKGTAPAP	1980
	QISWIFPPDR	VWQTVSPVES	RITLHENRTL	SIKEASFSDR	GVYKCVASNA	AGADSLAIRL	2040
	HVAALPPVHH	QEKLENI SLR	PGLSIHICT	AKAAPLPSVR	WVLGDGTQIR	PSQFLHGNLF	2100
	VFPNGTLYIR	NLAPKDSGRY	BCVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSPRRITDVR	2160
	GGTLKLDCSA	SGDPWPRILW	RLPSKRMIDA	LPSPDSRIKV	PANGTLVVKS	VTDKADGDYL	2220
35	CVARNKVQDD	VYVLKVDDVM	KPAKIEHKEE	NHDKVYFGDG	LKVDCAVATGL	PNPBIWSLSP	2280
	DGSLVMSPMQ	SDDSGGRTRK	YVFNNGTLY	PNEVGMREEG	DYTCFAENQV	GKDEMVRVRK	2340
	VVTAPATIRN	KTYLAVQVPE	GDVVTVACEA	KGEFMPKVTW	LSPTNKVIPT	SSEKYQIYQD	2400
	GTLLIQAQR	SDSGNYTCLV	RNSAGEDRKT	VNIHVNVPQP	KINGNPNPIT	TVREIAAGGS	2460
	RKLIDCKAEG	IPTPRVLMAF	PEGVVLPAFY	YGNRITVHGN	GSLDIRSLRK	SDSVQLVOMA	2520
40	RNEGGEARLI	VQLTVLEPME	KPIFHPDISE	KITAMAGHTI	SLNCASAGPT	TPSLVWVLPN	2580
	GTDLQSGQQL	QRPHYKADGM	LHISGLSSVD	AGAYRCVARN	AAGHTERLVS	LKVLGLKPEAN	2640
	KQYHNLVSI	NGETLKL PCT	PPGAGQGRFS	WTLFNGMHLE	GPQTLGRVSL	LDNGTLTVRE	2700
	ASVDFRGTIV	CRMETSYGFS	VTISIPVIVIA	YPPRITSEPT	PVIYTRPGNT	VKLNCMAMGI	2760
	PKADITWELP	DKSHLKAGVQ	ARLYGNRFLH	PQGSLLTQHA	TQRDAGFYKC	MAKNILGSDS	2820
45	KTYYIHVF						

Seq ID NO: 418 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..5001

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	CAGTCTGTGC	TGTGTCTCTG	GGTGGATCCT	GTTCTGGAAA	AACAGAAGAA	AGTTGTGTGCA	180
55	TCAAGACAGT	ACACCGTGGC	CTATCGAGAG	AAGGGGGAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGTGT	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATTT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAAATGA	GTACGTCACT	CTTCCAAAGA	360
	ACACCAAGAT	CTGCCCTTAC	CACAGCTCCT	GAAAACCTGA	ACGTCTGGCC	AGTCAATGGC	420
60	AAACCTACAG	TGTGTCTCTG	ATCTTGGGAT	CGCTTACCAG	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGTCTGC	TGGACACAGG	ACTGTTTCA	GTTTCTCTCT	TCCCAACATC	TGCCAAATCA	540
	TTTCAGAAAT	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTGGAGACA	AAGTCCCTCA	600
	CCTATCTCTG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCTGGGG	GAACGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
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65	ATCGATATCC	AAACCAACCA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
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	ATGTGCTATG	AAGACCCAMN	TGTTTCTTCT	TTGACAGGCA	ATTCCTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAAAACCGA	AAAACCTGAG	1020
70	CCTTCTCAC	CTTCTCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGCGC	CCGAAAACCC	CCAGCTTCGC	GCCAAGAAGG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCAGTGGGGA	GGAGGAGCTG	GTTTCCCGGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGAACAGAA	ACGGAACCTG	AGGCGGCCAA	GTAGACACGG	CCACTCGGTG	1320
75	GTTGCTCCCG	GCAGGACTGC	AGTGAGGGCC	CGGATGCCAG	CGCTGCCCGG	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CTGGGCCACG	CAGCCCGGCC	CAGGGGCGCC	CCCTCGGCTT	1440
	TOGGCTCTC	CTGCCCAACA	CGGCTCCACC	CAGGGCACCT	CTCATGCTCC	TTCCCTGCTT	1500
	GCCAGCTTGA	ATGACAACTA	CTTGGTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCGCTTT	GCCTCAGCCC	CGGCCAGCCC	TGTCCTCCAG	CCGCGAGTCC	1620
	CGGTCCAGCG	TTCTTCGCGA	CAGAAGCTCT	GTGCACCCCG	GGGCAAGCC	AGSCTCGCGG	1680
80	GCGGAGGAG	CCCCCAATTC	AGGGGCGCGA	GAGGAAGATT	CCAGTGCTCT	AGCCCCACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTGGGCTGC	TGCCACCCCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAGAGG	CGGGAAGGAT	GGTGAGGAGC	CCCCAGCCAC	CAACTCCAAT	1860
	GCGCATCAAC	GGTCCACCAT	GTCTCTCTCC	GTCTCTCTCT	ATCTCTGCTC	CAGGACGCGA	1920
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85	GCGGGAAGGC	AGGCGGAGGC	CAGGCGCCAG	ACGCTGCGGG	CCCGGCTCTG	CTCTGGACAC	2040
	TTCCATTGTC	TCAGACACAA	ACCCCTTGGT	GCCACCGGGA	GGTCTCCACG	CAGGTTACGC	2100
	ATTGGGCGGG	GACCTGGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCCTCCCGA	2160

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	TCCTCCAGGC	AGCCCATCTC	COGGGGCTGG	GAGGACTTAA	GGAGAAAGCC	GCAGAGAGGG	2340
5	GCCAGCCTGC	ATCGGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
	CATCCTCAGG	GCAAGTACTC	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTCA	ACAGAGCACA	2460
	GAGCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CCGCCACGGG	2520
	TCCTCTGCTC	GTCTCTCCGC	AGCAOGGTCA	CAGCAGCATC	CCAGTGTTC	CAGAAGGATG	2580
	ACACCGGCGC	GGGCCCCAGA	ACAGCAGCCC	CCTCCTCCCG	TCGCCACGTC	CCAGCACCAC	2640
	COGGGACCCC	AGAGCAGAGA	CGGGGTGGG	TCACTTCC	AGCCAGGCT	CTACTGACC	2700
10	CAGGCGGGC	GGCCCCGCC	CACTGCGCAG	GCGCGCTCCC	ACTCTCTC	GGACCTTAC	2760
	ACGGCGAGCT	CCAGAGGGAT	GCTCCCAAG	GCCCTCCAGA	ACCAGGACGA	GGATGCCACG	2820
	GGCAGCTACG	ACGACGACAG	CACAGAAATC	GAGGCCAGG	ATGTGGGGG	CCCGGCGCAC	2880
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15	AGGCCACAGC	GACCCGCGG	CCCCCAGTCC	GCGCGCGGG	TCCCCAGCAG	GGCAGCGCG	3060
	GGGAGTCCG	AGCTCTCTTC	CAAGCGGCCC	CTGTCTTCCA	AGTCCACAGA	GTGCGTCTCA	3120
	GCGAGGACG	AGGAGGAGGA	GGACGCGGG	TTTTTTAAAG	GCGGGAAGA	AGACCTTCTG	3180
	TCCTCTCTG	TGCCAAAGTG	GCCCTCTTCC	TCCACTCCCA	GGGGGCGCAA	AGAGCGCGAT	3240
	GGGAGCCTCG	CCAAGGAAGA	GAGGGAGCCT	GCCATCGGCG	TTGCCCTCG	CGGAGGAGC	3300
20	CTGGCTCTCT	TGAAGGAGCC	TCTCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCTCCAC	3360
	GTCCCTTCCC	GACCGCGCC	TGCGAGCGCT	GCCACCGTGA	GCCCGGTCG	GGGCACCCAC	3420
	CCCTGGCGC	GGTACACCA	GCGCGCCCV	CCTGGCCACT	TCTCCACCA	CCCGATGCTG	3480
	TCCTTGCGC	AGAGGATGAT	GCATGCCAGA	TTCGTAAACC	CTCTCTCCG	ACAGCCTGCC	3540
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	GGTAGTAATG	GAAACCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
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30	CCTCTGGCA	ATGCCCAAGA	TAGCCCAAT	TTGAGTCTTG	GAGGAAAGCC	GCTGCTGGC	3900
	TTGGAGTCA	TCAAAACCA	CACCCATCCC	CCTACCACTA	CCATGACGCC	CACCACTACT	3960
	ACGACGCCCC	TGCTTACCAC	TACAACCCCG	AGGCCACCA	CTGCCACCA	CATGACGCC	4020
	ACCACTACTA	CGACGCGCT	GCCTACCACT	ACACCGAGGC	CCACCACTGC	CACCAACCCG	4080
	CGCACGACCA	CCAGGCTGCC	AACAACCA	GTCCGAACCA	CTAGCGGAC	AACCAACACC	4140
35	ACCACCCCA	AACCCACCAC	TCCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAAACGGC	4200
	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260
	GATGAGTCTC	CAGGCTTGA	GACTGACACT	GCAGTACCTA	CGGAAGAGGC	CTAGTTTATA	4320
	TATGATGAG	ATTATGAAT	TGAGAGTCA	AGGCCACCA	CCACCACTGA	GCCTTGGACC	4380
	ACTGCTACCA	CACGAGGGT	GATCCAGAG	GAAGGCGCCA	TCAGTCTCTT	TCCTGAAGAA	4440
40	GAATTTGATC	TGGCTGGAAG	GAAACGATT	GTGCTCTCT	ACGTGAGCTA	CCTAAATAAA	4500
	GACCCATCAG	CCCGTGCTC	TCTGACTGAT	GCAGTGGATC	ACTTCCAGT	GGACAGCCTG	4560
	GATGAAATCA	TCCCAATGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCGC	4620
	AACATCACCG	TGCTGCGCT	GGAGGTTGC	CATCTATTG	TCAITGTGGA	TTGGGACAAA	4680
	GCCACCCAG	GAGATTGGT	CACAGTTAT	TTGTTTACA	GTGCATCTTA	TGAAGATTTT	4740
45	ATCAGGAACA	AGTTTTCAC	TCAAGCTTCA	TCAGTAACCT	ACTTGGCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCAT	TGTCAACGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCC	4920
	CCAGCGGCTG	AGCTATCGG	ATCCCATTCG	CTTTCAAA	TGATCCACG	TACACGGACT	4980
	GCCATGGAGC	GCAATATGTG	AAGCGCACGT	GGTATCGAAA	GTTCGTGGGA	GTGTTCTTT	5040
50	GTAAATCTACT	GAGGTATAAA	ATCTACTCTA	GTGACAACT	GAAAGATACA	TTCTACAGCA	5100
	TTGGAGACAG	CTGGGGAAGC	GGTGAAGACC	ATTGCCAAT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAAGGC	TACTATCGCC	5220
	AGTATGCTCA	GGAGCGTGTG	AGGTTGGGA	ACATCGGCTT	GGGAACCC	TACTACTATG	5280
	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAAGTG	GTAATCACAG	GACCGTCATG	5340
55	CTGCAAGCTT	GCCTGCCCA	GCCTCACCA	CTAAGTGGCA	CTAGGGGCTG	TGAGCAAGAA	5400
	CAGCCAGCAT	GCTGAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCACAGAT	GGACACTGGC	5460
	CATTCTGTGC	ATCTCAGTCT	GGAACCTAGT	CCCCTCTCT	GGCTGGACA	ATGAACAGGA	5520
	TTCAAGTTTG	CTGTAACTT	TGCTTCTCTA	CTTTTCTTGT	TTGTTTGTGA	ATAGCACATC	5580
	CCAGAGACAT	CAGAAACCA	CAACTGATTC	AGTGTGATTT	CCAGAGCTTT	TTAGGCATGA	5640
60	AATTCGGACA	CTTCAGTATT	TCCAGGAATA	GCAATGTCAC	GCTGTTCTTG	CTTCATGGA	5700
	TGCTACATGC	TTTCTGTTTT	TCTCATTTTG	GATTTCTCCA	AAACTAACTG	AATTTAAGCT	5760
	TCAGGTCCCT	TTGTATGCA	TAGAAAGGAA	TTATTAAAA	CACCACAAA	GAAATAAAT	5820
	ATATCTTACT	TGAAATTTAC	TCTATGGACT	TACCACCTGC	TAGAATAAAT	GTATCAAATC	5880
	TTATTGTTAA	ATCTCAATT	TTGATATATA	TATGATATATA	TGATATATA	TATCCACT	5940
65	TGCTGCAAG	AATATTGATT	AAAATTGCTA	AATTTGTACT	TGTTACCAA	AAAAAAAAA	6000
	AAAAAA						

Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

70	1	11	21	31	41	51	
	MPGTLKTRTG	APADYRVILK	TSQEDLDVDP	DDISVRVMSS	QSVLVSVDVP	VLEKQKKVVA	60
	SRQYTVRYRE	KGELARWDYK	QIANRRVLIE	NLIPDTVYEF	AVRISQGERD	GKNSTSVFQR	120
75	TPESAPTAP	ENLNVWVWNG	KPTVVAASWD	ALPETEGVKV	VCLLDLGLPS	VSSFPQSAKS	180
	FQNTFFHTPR	LSNLEBQSPS	PILETLLELPW	WMVCSLGNAI	FSKSGPQTGE	ANDLTPKPSL	240
	SLCQECSTC	QKDFSCSLAYL	IDIQTKQVKN	DPQLBGSVPG	PCFLPYFLTF	MLDIGGFSTI	300
	MCYEDPVSSL	TGNSLKSVA	SKADVQQNTB	DNGKPEKPEP	SSPSRAPAS	SRHPSVPASP	360
	QGRNAKDLLL	DLNKLILANG	GAPRKPOLRA	KKAEELDLQS	TEITGEEELG	SREDSPMSPS	420
80	DTQDQKRLR	PPSRHGHVSV	APGRITAVRR	MPALPRREGV	DKPGFSLATQ	PRPGAPPSAS	480
	ASPAHASTQ	GTSHRPSLPA	SLNDNDLVDS	DEDERAVGSL	HPKGAFAPQR	PALSPSRQSP	540
	SSVLDRSSV	HPQAKPASPA	RRTPHSGAAE	EDSSASAPPS	RLSPFHGGSS	RLLPQPHLS	600
	SPLSKGKDG	EDAPATNSNA	PSRSTMSSSV	SSHLSSRTQV	SEGAEADGGE	SHGDGOREDG	660
	GRQARATQTL	LRARPASLH	ELLRHKFFAA	NGRSPSRPSI	GRGRLQPS	SPQSTVPSRA	720
85	HPKVPSSHDS	HPKLSGLH	DEDEKFLPA	TVVNDHVPSS	SRQPIRSGWE	DLRRSPQGA	780
	SLERKEPIPE	NPKSTGADTH	PQKYSSLAS	KAQDVQOSTD	ADTEGHSKPA	PGSTDRHAS	840
	PARPPAARSQ	QHPSPVRMT	PGRAPEQPP	PPVATSQHP	GPQSRDAGRS	PSQFRLSLTQ	900
	AGRPRPTSQG	RSBSSDPYT	ASSRGLMPTA	LQNQDEDAQG	SYDDSDTEVE	AQDVRAHA	960

ARAKEAAASL PKHQVSEPT GAGAGGDHRS QRGHAAASPAR PSRPGGPQSR ARVPSRAAPG 1020
 KSEPPSKRPL SSKSQSVSA EDEEEDAGF FKGGKEDLLS SSVKPNWSSS TPRGGKDADG 1080
 SLAKEEREPA IALAPRGSL APVKRPLPPP PGSSPRASHV PSRPFPSAA TVSPVAGTHP 1140
 WPRYTTTRAP GHPTTFMLS LRQRMHARF RNPLSRQPAR PSYRQGYNGR PNVEGKVLPG 1200
 5 SNGKPNQRI INGPQGTQWV VDLDRGLVLN AEGRYLQDSH GNPLRIKLG GDRITVDLEG 1260
 TPVVSFDGLP LPQGGRHGT LANAQDKPIL SLGGKPLVLG EVIKKTHHP TTTMQPTTTT 1320
 TPLPTTTTTR PTTATTMQPT TTTTLPPTT PRPTTATTR TTRRPTTTT RTTTRTTTTT 1380
 TPKEPTTPT CPPTGLERHD DDGNLIMSSN GIPECYAED EFSGLEDTA VPTBEAVIY 1440
 10 DEDYEPETSR PPTTTEPSTT ATTPRVPEE GAISFPPEE FDLAGRKRFF APYVTYLNKD 1500
 PSAPCSLTD LDRFQVDSL EIIINDLKKS DLFPQHAPRN ITVVAVEGCH SPVIVDWDKA 1560
 TPGDLVTGYL VYSASYDFI RNKPSQASS VTHLPINLK PNTRYFFKVQ AQNPBGYGI 1620
 SPVSFVTES DNPLLVRRFP GGELSGSHSL SNMIPATRTA MDGNM

Seq ID NO: 420 DNA sequence
 Nucleic Acid Accession #: NM_022743
 Coding sequence: 128..1237

1 11 21 31 41 51
 20 GTGGATTITA GAGATACCTC CCCTCCTTCT GCTCAGCTGC CTTCAGTAA TAAACTCTT 60
 TCTCTGCTGC AACACCCCTA CTGTTCTCGG TGTATTGGCT TTTCTGGGCA GCAGGAAGGA 120
 AAAGCTGATG CGATGCTCTC AGTGCGCGGT CGCCAAATAC TGTAGTGCTA AGTGTGAGAA 180
 AAAAGCTTGG CCAGACCACA AGCGGGAATG CAAATGCCTT AAAAGCTGCA AACCCAGATA 240
 25 TCCCTCCAGAC TCCGTTGAC TTCTTGGCAG AGTTGTCTTC AAACCTATGG ATGGAGCACC 300
 TTCAGAATCA GAGAAGCTTT ACTCATTTTA TGATCTGGAG TCAAAATATTA ACAAAGTAC 360
 TGAAGATAAG AAGAGGGGCC TCAGGCAACT CGTAATGACA TTTCAACATT TCATGAGAGA 420
 AGAAATACAG GATGCTCTC AGCTGCCACC TGCTTTGAC CTTTGTGAAG CCTTTGCAAA 480
 AGTGATCTGC AACTCTTTCA CCATCTGTAA TCGGAGATG CAGGAAGTTG GTGTTGGCCT 540
 ATATCCCATG ATCTCTTTGC TCAATCACAG CTGTGACCCC AACTGTTCGA TTGTTGTCAA 600
 30 TGGGCCCCAC CTCTTACTGC GAGCAGTCCG AGACATCGAG GTGGGAGAGG AGCTCACCAT 660
 CTGCTACTCG GATATGCTGA TGACCACTGA GGAGCGCCGG AAGCAGCTGA GGGACCAGTA 720
 CTGCTTTGAA TGTGACTGTT TCCGTTGCCA AACCAGGAC AAGGATGCTG ATATGCTAAC 780
 TGGTATAGAG CAAGTATGGA AGGAAGTTCA AGAATCCCTG AAAAAATTG AAGAACTGAA 840
 GGCACTCTGG AAGTGGGAGC AGGTTCTGGC CATGTGCCAG GCGATCATAA GCAGCAATTC 900
 35 TGAACGGCTT CCGATATCA ACATCTACCA GCTGAAGGTG CTGACTGCG CCATGGATGC 960
 CTGCATCAAC CTGCGCTGT TGGAGGAAGC CTGTCTTAT GGTACTCGGA CCATGGAGCC 1020
 ATACAGGATT TTTTCCAG GAAGCCATCC CGTCAGAGGG GTTCAAGTGA TGAAGTTGG 1080
 CAAACTGCAG CTACATCAAG GCATGTTTCC CCAAGCAATG AAGAACTGGA GACTGGCTTT 1140
 TGATATTATG AGATGACAC ATGGCAGAGA ACACAGCCTG ATTGAAGATT TGATTCTACT 1200
 40 TTTAGAAGAA TGGGAGGCCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAATA 1260
 CGGCGTGTGT CTTGTGTGAA TGCCTTATTG AGGTACACA CTCTATGCTT TGTAGCTGT 1320
 GTGAACCTCT CTTATTGGAA ATTCTGTTC GTGTTGTGT AGGTAAATA AGGCAGACAT 1380
 GGTTTGCAAA CCACAAGAA CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAAC 1440
 ATTTGGTTGA GGATGCCAAA AAAAAA AAAAAA

Seq ID NO: 421 Protein sequence
 Protein Accession #: NP_073580

1 11 21 31 41 51
 50 MRCSQCRVAK YCSAKQKKA WPDHKRECK LKSKPRYP DSVRLGRV FKLMDGAPSE 60
 SEKLYSPYDL ESNINKLTED KKEGLRQLVM TPQHPMREEI QDASQLPPAP DLFEAPAKVI 120
 CNSPTICNAE GVEVGVGLY SLSLNHSCD PNCSTVFNPG HLLLRVARDI EVGEELTICY 180
 LDMLMTSEER RKLRDQYCF BCDPCFQQT DKDADMLTGD EQVWKEVES LKKIEELKAH 240
 55 WKWQVLAMC QAISSNSER LPDINIYOLK VLDCAMDACI NLGLLEALF YGTRTMEFYR 300
 IPPPGSHFVR GVQVMKVGKL QLEQGMFQA MNRLRLAFDI MRVTGREHS LIEDLILILE 360
 ECDANIRAS

Seq ID NO: 422 DNA sequence
 Nucleic Acid Accession #: NM_003014.2
 Coding sequence: 238..648

1 11 21 31 41 51
 65 GGCGGGTTGG CGCCCCAAG GCTGAGAGCT GCGCTGCTC GTGCCCTGTG TGCCAGACGG 60
 CGGAGCTCG CGGCCGACC CGCGGCCCC GCTTTGCTGC CGACTGGAGT TTGGGGGAAG 120
 AAACCTCTCT CGCGCCGAGA AGATTTCTTC CTGCGGGAAG GGACAGCGAA AGATGAGGGT 180
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240
 70 TTCTCTTCCA TCCTAGTGGC GCTGTGCTG TGGCTGCACC TGGCGCTGGG CGTGCGCGGC 300
 GCGCCCTGCG AGCGGTGCG CATCCCTATG TGCGGCGACA TGCCCTGGAA CATCAOGCGG 360
 ATGCCCAACC ACCTGCACCA CAGCAGCGAG GAGAAGCCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGAAGCTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCCCTGGA GTTCTGACAC GACCCTATCA AGCCGTGCAA GTCCGTGTGC 540
 75 CAACGCGCGT GCGACGACTG CGAGCCCTCT ATGAAGATGT ACAACCAACG CTGGCCCGAA 600
 AGCCTGGCCT GCGAGAGCT GCGTGTCTAT GACCGTGGCG TGTGCATTTC GCGTGAAGCC 660
 ATCGTCAAGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAGGCG CTCTTGATGT TGACTGTAAA CGCTTAAGCC CGATCGGTG CAAGTGTAAA 780
 AAGTGAAGC CAACCTTGGC AACGTATCTC AGCAAAAAC ACAGCTATGT TATTATGCC 840
 80 AAAATAAAG CTGTGACAG GAGTGGCTGC AATGAGGTCA CAACGCTGGT GGATGTAAAA 900
 GAGATCTTCA AGCTCTCAT ACCCATCCCT CGAACTCAAG TCCGCTCAT TACAATTCT 960
 TCTTGCCAGT GTCCACACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140
 AAGAAACAG CCGGCGCAC CAGTGTAGT AATCCCCCA AACCAAGGGG AAAGCCTCCT 1200
 85 GCTCCCAAC CAGCCAGTCC CAAGAAGAAC ATTAAACTA GGAGTGCCCA GAAGAGAAC 1260
 AACCCGAAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGA GACTTCCGAC TTCCTTACAG 1320
 GATGAGGCTG GGCATTGCCT GGGACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAAC 1380

	ACTCACTGCA	GTGCTCTTCA	TAGACACATC	TTGCAGCATT	TTTCTTAAGG	CTATGCTTCA	1440
	GTTTTTCTTT	GTAAAGCCATC	ACAAGCCATA	GTGGTAGGTT	TGCCCTTTGG	TACAGAAGGT	1500
	GAGTTAAAGC	TGGTGGAAAA	GGCTTATTGC	ATTGCATTCA	GAGTAACCTG	TGTGCATACT	1560
	CTAGAAGAGT	AGGGAAAAATA	ATGCTTGTTA	CAATTGACCC	TAATATGTGC	ATTGTAAAAAT	1620
5	AAATGCCATA	TTTCAAAACAA	AACACGTAAT	TTTTTTACAG	TATGTTTTAT	TACCTTTTGA	1680
	TATCTGTTGT	TGCAATGTGA	GTGATGTTTT	AAAAATGTAT	GAAAAATATA	TGTTTTTAAG	1740
	AAGGAACAGT	AGTGGGAATG	ATGTAAAAAG	ATCTTTATGT	GTTTATGGTC	TGCAGAAGGA	1800
	TTTTTGTGAT	GAAAGGGGAT	TTTTTGAAAA	ATTAGAGAAG	TAGCATATGG	AAAAATTATA	1860
	TGTGTTTTTT	TACCAATGAC	TTCAGTTTCT	GTTTTTAGCT	AGAAACTTAA	AAACAAAAAT	1920
10	AATAATAAAG	AAAAATAAAT	AAAAAGGAGA	GGCAGACAA	GTCTGGATTG	CTGTTTTTTG	1980
	GTTACCTGAT	TTCATGATC	ATGATGCTTC	TGTGCAACAC	CCTCTTAAGC	AGCACCAGAA	2040
	ACAGTGAGTT	TGCTGTGACC	ATTAGGAGTT	AGGTACTAAT	TAGTTGGCTA	ATGCTCAAGT	2100
	ATTTTATACC	CACAAGAGAG	GTATGTCACT	CATCTTACTT	CCCAGGACAT	CCACCCTGAG	2160
	AATAATTGGA	CAAGCTTAAA	AATGGCCCTC	ATGTGAGTGC	CAAAATTTGT	TTTTCTTCAT	2220
15	TTAAATATTT	TCITTGCGCTA	AATACATGTG	AGAGGAGTTA	AATATAAATG	TACAGAGAGG	2280
	AAAGTTGAGT	TCCACCTCTG	AAATGAGAAT	TACTTGACAG	TGGGATACCT	TTAATCAGAA	2340
	AAAAAGAACT	TATTTGCAGC	ATTTTATCAA	CAAAATTTCT	AATTGTGGAC	AATTGGAGGC	2400
	ATTTATTTTA	AAAAACAATT	TTATTGGCCT	TTTGCTAACA	CAGTAAGCAT	GTAATTTTATA	2460
	AGGCATTCAA	TAAATGCACA	ACGCCCAAG	GAAATAAAA	CCTATCTAAT	CCTACTCTCC	2520
20	ACTACACAGA	GGAATACACT	ATTAGTATTT	TGGCATATTA	TTCTCCAGGT	GTTTGCTTAT	2580
	GCACCTATAA	AATGATTGGA	ACAAATAAAA	CTAGGAACCT	GTATACATGT	GTTTCATAAC	2640
	CTGCTCTCTT	TGCTGGCCCT	TTTATTGAGA	TAAGTTTTC	TGTCAAGAAA	GCAGAAACCA	2700
	TCTCATTTCT	AACAGCTGTG	TTATATTCCA	TAGTATGCAT	TACTCAACAA	ACTGTGTGTC	2760
25	TATTGGATAC	TTAGGTGGTT	TCTTCACTGA	CAATACTGAA	TAAACATCTC	ACCGGAATTC	

Seq ID NO: 423 Protein sequence
Protein Accession #: NP_003005.1.

	1	11	21	31	41	51	
30	MFLSLVILVC	LWLHLALGVR	GAPCEAVRIP	MCRHMPWNIT	RMPNHLHST	QENAILAIEQ	60
	YEELVDVNC	AVLRVFFPCAN	YAPICTLEPL	HDPKPKCKSV	QQRARDDECP	LMKMYNHSWP	120
	ESLACDELTV	YDRGVCSISPE	AIITDLPELV	KWIDITPDM	VQERPLDVDC	KRLSPDRCKC	180
	KKVKPTLATY	LSKNYSYVH	AKIKAVQRSG	CNEVTVVDV	KEIFKSSSPI	PRTVQPLITN	240
35	SSQCPHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRVTQD	300
	KKKTAGRTSR	SNPPKPKGKP	PAPKPAKPKK	NIKTRSAQKR	TNPKRV		

Seq ID NO: 424 DNA sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

	1	11	21	31	41	51	
45	CACAGGCTGG	GAAGCAGCTC	TGGGGGAGCT	CGGAGCTCCC	GATCAAGGCT	TCTTGGGGGT	60
	AGCTACGGCT	GGGTGTGTAG	AAACGGGGCCG	GGGCTGGGGC	TGGGTCCCTC	AGTGGAGACC	120
	CAAGTGGCAG	AGGCAAGAAC	TCTGCAGCTT	CCTGCCTTCT	GGGTCACTTC	CTTATTCAAG	180
	TCTGCAGCCG	GCTCCACAGG	AGATCTCGGT	GGAACTTCAG	AAACGCTGGG	CAGTCTGCCT	240
	TTCAACCATG	CCCTCTGTCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCT	GGCTGTGTCT	300
	GCTGCTACTG	CTGGCATCAT	TTACAGGCCG	GTGCCCCCGG	GGTGAGCTGG	AGACCTCAGA	360
50	CGTGGTAAC	GTGGTCTCGG	GCCAGGACGC	AAAACCTGCC	TGCTTCTACC	GAGGGGAACT	420
	CGGCGAGCAA	GTGGGCAAG	TGGCATGGGC	TCGGGTGGAC	GCGGGCGAAG	GCGCCCAAGG	480
	ACTAGCGCTA	CTGCACTCCA	AATACGGGCT	TCATGTGAGC	CCGGCTTACG	AGGGCCCGGT	540
	GGAGCAGCCG	CCGCCCCCAC	GCAACCCCTC	GGACGGCTCA	GTGCTCTCTG	GCAACGCAGT	600
	GCAGGCGGAT	GAGGGCGAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCCCGCG	GCAGCTTCCA	660
55	GGCGCGGCTG	CGTCTCCGAG	TGCTGGTGCC	TCCCTGCCCC	TCACTGAATC	CTGGTCCAGC	720
	ACTAGAAGAG	GGCCAGGGCC	TGACCTCTGC	AGCCTCTCTG	ACAGCTGAGG	GCAGCCCAAG	780
	CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAG	AGGCACAAAG	TCCAGCCGTT	CCTTCAAGCA	840
	CTCCGCTCT	CGTGGCGTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
	GCAGCCCACT	ACTTGTGTGT	TGTCCCATCC	TGGCCTGCTC	CAGGACCAAA	GGATCAACCA	960
60	CATCTCTCAC	GTGTCTCTCC	TTGCTGAGGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
	GTGGCACAAT	GGCAGAGAAG	GAGCTATGCT	CAAGTGCCCT	AGTGAAGGGC	AGCCCCCTCC	1080
	CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCCACT	GGGTACGAG	TGGATGGGGA	1140
	CACTTTGGGC	TTTCCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGTCT	GCCATGTGAG	1200
	CAATGAGTTC	TCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTCTTGAACC	CCCAGGAAGA	1260
65	CTCTGGGAAG	CAGGTGGACC	TAGTGTACGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCGC	1320
	ACTCTTGTTC	TGCTTCTCTG	TGGTGGTGGT	GGTGTCTATG	TCCCGATACC	ATCGGCGCAA	1380
	GGCCACGACG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAAGG	AGAACTCCAT	1440
	CCGAGGCTG	CATTCCTATC	ACACGGACCC	CAGGAGCCAG	CCGAGGAGAG	GTGTAGGGCT	1500
	GAGAGCCGAG	GGCCACCCCT	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
70	AGAGCCCGAG	GGCCCGAGTT	ACTCCACGCT	GACCAACGGT	AGGGAGATAG	AAACAACAGC	1620
	TGAAGTCTGT	TCTCCAGGCT	CTGGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
	CAACAGGGCC	ATGAACCAAT	TTGTTCAAGG	GAATGGGACC	CTACGGGCCA	AGCCCAAGGG	1740
	CAATGGCATC	TACATCAATG	GGCGGGGACA	CCTGGTCTGA	CCCAGGCTGT	CCTCCCTTCC	1800
	CTAGGCTCTG	TCTCTCTGTG	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
75	ACACCCCTAT	TTCTTGGCGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
	AACCCCTCTG	TTTATCGGGA	GGGCTCCACC	AATGTAGTCT	CTCCCACTAT	GCATGCAGGT	1980
	CACGTGTGTG	GTGACATGTG	GCCTGTGTGA	GTGTGTGACT	ACTGTGTGTG	TGTGGAGGGG	2040
	TGACTGTCTG	TGGAGGGGGT	ACTGTGTCCG	TGCTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
	AAGTGAACCT	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACGTGTGAG	2160
80	GTITGGCGTG	TGTGTCTATG	GGCTGTGTGT	GACCTCTGCC	TGAAAAAGCA	GATATTTTCT	2220
	CAGACCCGAG	AGCAGTATTA	ATGATGCAGA	GGTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
	CAGACCCGAG	TGTGGGGGCA	TAGCTGGAGC	TGGAATCTGC	CTCGGTGTGT	AGGGAACTGT	2340
	TCTCCTACCA	CTCGGAGGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTCAAGCA	2400
	GAGGCTTGA	CTGTACAGAG	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGTGATG	2460
85	ACATATTTTC	TGTAATATATA	CATGCGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
	ACTTTTAATT	TTTTTCTTTT	TTTTTCTCTG	CCCTTTCCAT	TAGTTGTATT	TTTTTATTAT	2580
	TTTTATTTT	ATTTTTTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTGTG	2640

CTGTAAAAA ACCAAAAACC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 425 Protein sequence

Protein Accession #: AAB10423

5	1	11	21	31	41	51	
	MPLSLGAEMW	GPEAWLLLLL	LLASFTGRCP	AGELETSDDV	TVVLGDQAKL	PCFYRGDSGE	60
	QVGVAVARV	DAGBGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPRNPLDG	SVLLRNVAQA	120
10	DEGEYECRV	TFPAGSFQAR	LRLRLVLPPL	PSLNPGPAL	BQQLTLAAS	CTAEGSPAPS	180
	VTWDTVKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPGL	LQDQRITHIL	240
	HVSFLAEASV	RGLEDNLWH	IGREGAMLEK	LSEGGPPPSY	NWTRLDGFLP	SGVRVDGDTL	300
	GFPPLTFHS	GIYVCHVSNE	FSSRDSQVTV	DVLDPOEDSG	KQVDLVASAV	VVVGVIAALL	360
	PCLLVVVVVL	MSRYHRRKAQ	QMTQKYESEL	TLTRENSIRR	LHSHTDPRS	QPEESVGLRA	420
15	BGHPDSLKDN	SSCSVMSEFP	BGRSYSTLTT	VREIETQTEL	LSPGSGRAEE	EEDQDEGIKQ	480
	AMNHFVQENG	TLRAKPTGNG	IYINGRGHLV				

Seq ID NO: 426 DNA sequence

Nucleic Acid Accession #: NM_003474.2

Coding sequence: 37..3036

20	1	11	21	31	41	51	
	CACTAACGCT	CTTCTAGTCT	CCCGGGCCAA	CTCGACAGT	TTGCTCATTT	ATTGCAACGG	60
25	TCAAGCTCG	CTTGTGCCAG	AAOCCGCGCG	GCGGGAAGCA	CGCACACACA	CGGGGGGAAA	120
	CTTTTTTAAA	AATGAAGAGC	TAGAAGAGCT	CAGCGGCGGC	GCGGGCCGTG	CGCGAGGGCT	180
	CCGGAGCTGA	CTCGCGAGG	CAGGAAATCC	CTCGGTGCG	GACGCCCGGC	CCCGCTCGGC	240
	GCCCGGTGG	GATGGTCAG	CGCTGCGCGC	CGGGCCCGAG	AGCTGCTGCA	CTGAAGCGCG	300
	GCGAGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCGCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
30	GCCGGTCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGA	CGAAGGAAGA	420
	GCTGATGAAG	TTGTGAGTGC	CTCTGTTCGG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
	TTGACTCCA	AGAAATCATC	AGAAAGTCTG	AATATTGAC	TACAAAGGGA	AAGCAAAGAA	540
	CTGATCATA	ATCTGGAAG	AAATGAAGGT	CTCATTTGCC	GCAGTTTCAC	GGAAACCCAC	600
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35	TGTTACTACC	ATGGAAGATG	ACGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCACTGT	720
	TCTGGTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGCTTAGA	ACCAATGAAA	780
	AGTCAACCA	ACAGATACAC	ACTCTTCCCA	GCGAAGAAGC	TGAAAGCGT	CCGGGGATCA	840
	TGTGATCAC	ATCACAACAC	ACCAACCTC	GCTGCAAGA	ATGTTGTTCC	ACCACTCTCT	900
40	CAGACATGG	CAGAGAGGCA	TAAAGAGAG	ACCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
	GTGATGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGCGATTAA	TAGAGATTGC	TAATCACGTT	GACAAGTTT	ACAGACCAT	GAACATTGCG	1080
	ATCGTGTGG	TAGCGTTGGA	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
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45	TCCCATGACA	ATGCGCAGCT	TGTCACTGGG	GTTTATTTCC	AAGGGACAC	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCATTTCA	1320
	GACAAATCCC	TTGTGTCAGC	CGTGACCTCG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
	AATCATGACA	CATGTGACAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
	ATCATGAAGC	CTTCCACCGG	GTACCCATTT	CCCATGTTGT	TCAGCAGTTG	CAGCAGGAAG	1500
50	GACTTGGAGA	CCAGCCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACT	GCCGGAAGTC	1560
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	GACTGTGGGG	AGCCAGAGGA	ATGTATGAAT	CGCTGCTGCA	ATGCCACCAC	CTGTACCCCTG	1680
	AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
	GGAAACAGGT	GCAAGGACTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
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	CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980
	TATGGCAACT	GTGGCAAAGT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
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60	GTTTCCATAG	AAACAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
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65	GGCCCCATCC	GGCAAGCAGA	TAAACCAAGT	TTAACCATAG	GAATTCTGCT	GACCATCCTG	2460
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	CCTGCAGATC	CTCTGCCCAG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCCAAGG	2940
	CAATGGGAGA	CTTGGGCTCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
75	GTGCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCAACAG	3060
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	GCAGAAATGT	GATTACAGTG	CAGTGCCTG	TATGAGGCAT	TTTACCATC	ACTGAGTTTT	3300
	CCATGCGAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACCTGAAAT	ATCTGCTGCT	3360
80	ATGGGATCT	GGAGGATCT	TGTTTGTCTT	CTGATCAAGG	CCTTATTTGA	AAGCAGTCCC	3420
	CCAACTACCC	CCAGCTGTGC	TTATGGTACC	AGATGCAAGT	CAAGAGATCC	CAAGTAGAAT	3480
	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
	TGTGTTTGGC	TTTTCAGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGCG	GCTCCCAGGG	3600
	ACACCTGGGA	GAAATCTGGC	TTCTGGCCAG	GAAAGCTTGG	TGAGAACCTG	GGTTGCAGAC	3660
85	AGGAATCTTA	GAGTTTAGCC	ACACCAAGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCCCTGAG	CTGACCAAGC	GTGAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
	GGTCTGTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTGCTG	TCCTTCTAG	AGCACTGCCA	3840

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 ACCAAAAAAA AAAAAAAA AA

Seq ID NO: 427 Protein sequence
Protein Accession #: NP_003465

1 11 21 31 41 51
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 SHHNTPLNLA KNVFPFSSQT WARRHKRETL KATRYVELVI VADNREFORQ GKDLEKVKQR 240
 LIEIANHVDK FYRPLNIRIV LVGVEVWNDM DKCSVSQDPP TSLHEFLDWR KMKLLPRKSH 300
 DNAGLVSGVY FQGTITGMAP IMSMCTADQS GGIWMDHSDN PLGAAVTLAH ELGHNPGMNH 360
 DTLDRGCSQ MAVKGGCIM NASTGYPPPM VPSSCSRKDL ETSLEKGMV CLFNLPPEVRE 420
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 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSQDQDVG CYNGICQTHE QQCVTLMGPG 540
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 IETNIPLQGG GRILRCGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRCQC NISVFGVHEC 660
 AMQCHGRGVC NNRNKNCHCEA HWAPPFCDFK GFGGSTDGSP IRQADNQGLT IGILVTILCL 720
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Seq ID NO: 428 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 135..1043

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 TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCGGAG GGTCCCCAAG 240
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 GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG GCGTGTGTA ATGTTTCGAG AACAACTCTT 360
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5 Seq ID NO: 429 Protein sequence
Protein Accession #: NP_003705

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ISRRKPAIRB MVSQVQRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
CGEEVKBAIT HSQVQVCEQN WGSLSILSP CTSAIQKPPT APPERQPOVD RTKLSRAHHG 240
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40 GGGCTTTGTT TGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGTACCCAG CATTTGGCTC 1020
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60 ATCTCTCAA GGCATGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
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Seq ID NO: 431 Protein sequence
Protein Accession #: NP_005931

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70 LVQEQVRQM AEALKVMSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DPGGILAH 180
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YPLSLSPDCC RGQHLVYQFP WFTVTSRTPA LGPOAGIDTN EIAPLEFDAP PDACEASFDA 300
VSTIRGELEF FKAGFVWRLR GGQIQPGYPA LASRHQGLP SPVDAAPEDA QGHIWFPQGA 360
QYWVYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS 420
75 FVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKDFD VKVKALEGFP RLVGPDFFGC 480
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Coding sequence: 202..1563

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5	GGAGTCTCGG	ATTGCAAGA	CGGGGAGGAC	GAGTACCGCT	GTGTCCGGGT	GGGTGGTCAG	540
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	AAGGGTCAC	AGCAAAATGT	TGCCTGTGCC	CAACTGGGTT	TCCCAAGCTA	TGTGAGTTCA	660
	GATAACCTCA	GAGTGAGCTC	GCTGGAGGGG	CAGTTCCGGG	AGGAGTTTGT	GTCCATCGAT	720
	CACCTCTTTC	CAGATGACAA	GGTGACTGCA	TTACACCACT	CAGTATATGT	GAGGGAGGGA	780
10	TGTGCCTCTG	GCCACGTGGT	TACCTTGCAG	TGCACAGCCT	GTGGTCATAG	AAGGGGCTAC	840
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	CTTCAGTTCC	AGGGCTACCA	CCTGTGCGGG	GGCTCTGTCA	TCAAGCCCTT	GTGGATCATC	960
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	CCTCAGCTTC	CCAGTAGCT	GGGACACAG	GTGCGCGCCA	CCACACCCAA	CTAATTTTTG	1920
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	GCGGCTTTTC	CCATCTGTTC	ATCTGTGTTT	CTCTCCAGGG	GTCTTGCAAA	ATTCTCGAGG	2160
	AGATAAGCAG	TTATGTGAC	TCAGTGCACA	AGCCACCAAC	AGCCACTCAG	AAAAAGACGA	2220
	CCAGCCGACG	AGTGCCAGAAC	TGCAGTCACT	GCACTGTTTC	ATCTCTAGGG	ACCAGAACCA	2280
35	AACCCACCTT	TCTTACTTTC	AAGACTTATT	TTACATGTG	GGGAGTTTAA	TCTAGGAATG	2340
	ACTGTTTAA	GGCCTATTTT	CATGATTCTT	TTGTAGCATT	TGGTGCCTGA	CGTATTATTG	2400
	TCCTTTGATT	CCAAATAATA	TGTTTCTTTC	CCTCAAAAAA	AAAAAATAAA	AAAAAATAAA	2460
	AAAAA						

40 Seq ID NO: 433 Protein sequence
Protein Accession #: NP_076927

	1	11	21	31	41	51	
45	MGENDPPAVE	APPSFRSLFPG	LDDLKISFVA	PDADAVAAQI	LSLLPLKFFP	IIVIGIITALI	60
	LALAIGLGIH	FDCSGKYRCR	SSPKCIELIA	RCDGVSDCKD	GEDEYRCVRV	GGQNAVILQVP	120
	TAAAWKTMCS	DDWKGHYANV	ACAQLGFFSY	VSSDNLRVSS	LEGQFPREFV	SIDELLPPDX	180
	VTALHESVTV	REGCASHGVV	TLQCTACGHR	RGYSSRIVGG	NMSLLSQWPW	QASLQFQJYH	240
	LCGGSVITPL	WIITABRCVY	DLYLPKSWTI	QVGLVSLLDN	PAPSHLVEKI	VYHSKYKPKR	300
50	LGNDIALMKL	AGPLTFNEMI	QPVCLPNSEB	NFPDGKVCWT	SGWGEDGEGG	DASPLVNHAA	360
	VPLISNKNICN	HRDVGIGIIS	PSMLCAGYLT	GGVDSQCGDS	GGPLVQERR	LWLKVGATSP	420
	GIGCAEVNKP	GVYTRVTSPL	DWIHEQMERD	LKT			

55 Seq ID NO: 434 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

	1	11	21	31	41	51	
60	CACCTTCTGC	ACTGCTCATC	TGGGCAGAGG	AAGCTTCTAGA	AAGCTGCCAA	GGCACCATCT	60
	CCAGGAACTC	CCAGCACGCA	GAATCCATCT	GAGAATATGC	TGCCACAAAT	ACCCTTTTTG	120
	CTGCTAGTAT	CCTTGAACCT	GGTTCATGGA	GTGTTTTACG	CTGAACGATA	CCAAATGCCC	180
	ACAGGCATAA	AAGCCCACTT	ACCCAAACAC	AAGACACAGT	TCTTCACTCC	CTACACCATA	240
	AAGAGTAAAG	GTATAGCAGT	AAGAGGAGAG	CAAGGTACTC	CTGGTCCACC	AGGCCCTGCT	300
65	GGACCTGAG	GGCACCAGG	TCCTTCTGGA	CCACAGGAA	AACCAGGCTA	CGGAAGTCTT	360
	GGACTCCAAG	GAGAGCCAGG	GTGCCAGGA	CCACCGGAC	CATCAGCTGT	AGGGAAACCA	420
	GGTGTGCCAG	GACTCCAGG	AAAACCAAGG	GAGAGAGGAC	CATATGGACC	AAAAGGAGAT	480
	GTGGACCAAG	CTGGCTTACC	AGGACCCCGG	GGCCCAACAG	GACCACCTGG	AATCCCTGGA	540
	CCGCGCTGAA	TTTCTGTGCC	AGGAAAACCT	GGACAACAGG	GACCCACAGG	AGCCCCAGGA	600
70	CCCAGGGGCT	TTCTCTGAGA	AAAGGGTGCA	CCAGGAGTCC	CTGGTATGAA	TGGACAGAAA	660
	GGGGAAATGG	GATATGGTGC	TCCTGGTCGT	CCAGGTGAGA	GGGGTCTTCC	AGGCCCTCAG	720
	GGTCCACAG	GACCATCTGG	CCCTCCTGGA	GTGGGAAAAA	GAGGTGAAAA	TGGGGTTCCA	780
	GGACAGCCAG	GCATCAAAAG	TGATAGAGGT	TTTCCGGGAG	AAATGGGACC	AATTGGCCCCA	840
	CCAGGTCCCC	AAGGCCCTCC	TGGGAACGGA	GGGCCAGGAG	GCATTGGAAA	GCCAGGAGCT	900
	GCTGGAGCCC	CAGGCCAGCC	AGGGATTCCA	GGAAACAAAG	GTCTCCTCTG	GGCTCCAGGA	960
75	ATAGCTGGGC	CCCCAGGGCC	TCCTGGCTTT	GGGAAACCAAG	GCTTGGCCAGG	CCTGAAGGGA	1020
	GAAAGAGGAC	CTGCTGGCTC	TCCTGGGGGT	CCAGGTGCCA	AAGGGGAACA	AGGGCCAGCA	1080
	GGTCTCTCTG	GGAAGCCAGG	TCTGACTGGA	CCCCCTGGGA	ATATGGGACC	CCAAGGACCA	1140
	AAAGGCATCC	CGGGTAGCCA	TGCTCTCCCA	GGCCCTAAAG	GTGAGACAGG	GCCAGCTGGG	1200
80	CCTGCAGGAT	ACCTTGGGGC	TAAAGGTGAA	AGGGGTTCCC	CTGGGTGAGA	TGGAAAACCA	1260
	GGGTACCCAG	GAAACCCAGG	TCTCGATGGT	CCTAAGGGTA	ACCCAGGGTT	ACCAGGTCCA	1320
	AAAGGTGATC	CTGGAGTTGG	AGGACCTCCT	GGTCTCCAG	GCCCTGTGGG	CCAGCAGGGA	1380
	GCAAGGGGAA	TGCCCGGACA	CAATGGAGAG	GCTGGCCCAA	GAGGTGCCCC	TGGAAATACCA	1440
	GGTACTAGAG	GCCCTATTGG	GCCACCAGGC	ATTCCAGGAT	TCCCTGGGTC	TAAAGGGGAT	1500
	CCAGGAAGTC	CCGCTCTCTC	TGGCCAGGCT	GGCATAGCAA	CTAAGGGCCT	CAATGGAGCC	1560
85	ACCGGGCCAC	ACGGGCTCTC	AGGTCCAGGA	GGCCACTCTG	GAGAGCCTGG	TCTTCCAGGG	1620
	CCCCTGGGCG	CTCCAGGCCC	ACCAGGTCAA	GCAGTCATGC	CTGAGGGTTT	TATAAAGGCA	1680
	GGCCAAAGGC	CCAGTCTTTC	TGGGACCCCT	CTTGTTAGTG	CCAACAGGGG	GGTAACAGGA	1740

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ATGCGCTGTT CTGCTTTTAC TGTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAACTCCC 1800
ATACCAATTG ATAAAAATTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC 1860
TTTACTTTGG AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
CATGTTTGGG TAGGCGTGTA TAAGAATGGC ACCCCTGTAA TGTACACCTA TGTATGAATC 1980
ACCAAAGGCT ACCGCGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAAATGAC 2040
CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAATGGGCC TATACTCCTC TGAGTATGTC 2100
CACTCTCTCT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCAC AGAGCTAATC 2160
TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220
AGGTAGGCTG AAAAGAATGT AATTTTATT TTCTGAAATA CAGATTGAG CTATCAGACC 2280
AACAAACCTT CCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTCTT CCAATATTA AAAATATCAC 2400
CAAGAAGATC CTGCTATGTT AAAACAAAAC AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460
TAAAAAATA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTTGATTGTA GAAACTCGGC 2520
ATTTCTTTT TAAAAAGCC TGTCTTAAC TATGAATATG AGAACTCTA GGAAACATCC 2580
AGGAGGTATC ATATAACTTT GTAGAACTTA AATACTTGAA TATTCAAATT TAAAGACAC 2640
TGTATCCCCT AAAATATTTT TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTCAT 2700
CAATATCTAT TCAAAATATA AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAGC 2760
CCCAAAATAT TGAAGTTCAT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTTCAAAA 2820
CTTTCTATG ATTGACAGAA AGCTTTTAT ATACCCAGCA TAACCTGGAA ACAGTATCT 2880
GACCTATTCT TATTAGTTA ACACAAGTGT GATTAATTG ATTTCTTAA TTCCTTATG 2940
AATCTTATGT GATATGATT TCTGGATTTA CAGAACATTA GCACATGTAC CTTGTGCTC 3000
CCATTCAAGT GAAGTTATA TTTACACTGA GGGTTTCAAA ATTGACTAG AAGTGAGAT 3060
ATATTATTTA TTTATGACT GTACTGTATT TTTATATGC TGTITAAAC TTTTAAGCTG 3120
TGCTCACTT ATAAAGCAC AAAATGTTT ACCTACTCTT TATTTAAGAC ACAATAAAAT 3180
AACATCAATA GATTTTATG CTGAATTAA TTGAAAGCAG CAATTGCTG TTCTCAACCA 3240
TTCTTCAAG GCTTTTCATT CGACACATA AAATAACATC AATAG
  
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Seq ID NO: 435 Protein sequence
Protein Accession #: NP_000484.2

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1 11 21 31 41 51
| | | | |
MLPQIPFLLL VSLNLVHGVF YAERYQMPTG IKGPLPNTKT QFFIFPTIKS KGIIVRGEQG 60
TPGPPGAPAG RGHGPGSGPP GKPGYGSFGL QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120
GPYGPKGDVG PAGLPGPRGP PGPPGIPGPA GISVPGKPOQ QGPTGAPGPR GPPGKGAAG 180
VPMNGNGKGE MGYGAPGRGP ERGLPGPGP TGSPGPPGVG KRGENGVPQ PGIKGDRGFP 240
GEMGPIGPPG PQGPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300
PGLPGLGERG GPAGLPGGGP AKGEQGPAGL PGKPLGTGFP GNMGPQGPKG IPGSHGLPGP 360
KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLDGFK GNPGLPGPKG DRVGVPGL 420
PGPVGPAGAK GMPGNGEAG PRGAPGIPGT RGPFGPPGIP GPPGSKDGP SPGPPGAGI 480
ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
SANQGVGTGP VSAFTVILSK AXPALGTFIP FDKILYNRQQ HYDPRGTIPT CQIPGIYFS 600
YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
GLYSSEVHVS SPSGFLVAPM
  
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Seq ID NO: 436 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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 55
 60
 65

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1 11 21 31 41 51
| | | | |
ATGTGGGGGG CTGCGCGCTC GTCCGCTCTC TCATCTCGGA ACGCGGCTTC GCTCCTGCAG 60
CTGCTGTCTG CTGCGCTGCT GGCGGCGGGG GCGAGGGCCA GCGCGAGTA CTGCCACGGC 120
TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 180
GGCGACGCCA CCATCTGCTG CGGCAGCTCG GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 240
GGCGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 300
CGGGCGGACA AAGACGGGCC CGAOGGCTCG GCAGTGCCCA TCTACGTGCC GTTCTCTATT 360
GTGTGCTCGG TGTTTGTGCG CTTTATCATC TTGGGCTCCC TGTGTGCAGC CTGTGCTGTC 420
AGATGTCTCC GGCTTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
ATGGAGACCA TCCCATGAT CCCCAGTGCC AGCACTCTCC GGGGTCGCTC CTCAGCCAG 540
TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCGCACTCAG GGGCCCGGGC GCGCCCAACA 600
AGGTACAGCA CCAACTGTTG CTTGCCGGA GGGACCATGA ACAACGTGTA TGTCAACATG 660
CCCACGAATT TCTCTGTGCT GAACTGTGAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
GCTGTGCCAC CTTTCATGGA CGGCTGTCAG CTTGGCTACA GGCAGATTCA GTCCCCCTTC 840
CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA
  
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Seq ID NO: 437 Protein sequence
Protein Accession #: XP_062811

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1 11 21 31 41 51
| | | | |
MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQGGAGEPG RADKDGPDGS AVPIYVPLFI 120
VGSVFVAFII LGLSLAACCC RCLRPKQDPQ QSRAPGGRNL METIPMIPSA STSRGSSSRQ 180
SSTAASSSSS ANSGARAPPT RSQTNCLLPE GTMNNVYVNM PTNPSVLNCQ QATQIVPQQG 240
QYLHPYVGY TVQHDSVPMF AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV
  
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Seq ID NO: 438 DNA sequence
Nucleic Acid Accession #: NM_004004.1
Coding sequence: 1..681

80
 85

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1 11 21 31 41 51
| | | | |
ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACTCTC CACCAGCATT 60
GGAAAGATCT GGCTCACCGT CTTCTTCATT TTTCGCAITA TGATCTCTGT TGTGGCTGCA 120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180
  
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AAGAACGTGT GCTACGATCA CTA CTCTCCCC ATCTCCCCA TCCGCTATG GGCCTGCG 240
CTGATCTTGG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
GAGAAGAGGA GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG 360
ATCAAAACCC AGAAGGTCCG CATCGAAGGC TCCTGTGGT GGACCTACAC AAGCAGCATC 420
TTCTTCGGGG TCATCTTCGA AGCCGCCCTT ATGTACGTCT TCTATGTCAT GTACGACGGC 480
TTCTCCATGC AGCGGTGGT GAAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGAGTCG 540
TTTGTGTCCC GGCACACGGA GAAGACTGTC TTCACAGTGT TCATGATGTC AGTGTCTGGA 600
ATTTCATCC TGCTGAATGT CACTGAATTG TGTATTATGC TAATTAGATA TTGTTCTGGG 660
AAGTCAAAA AGCCAGTTTA A

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Seq ID NO: 439 Protein sequence
Protein Accession #: NP_003995.1

1 11 21 31 41 51
MDWGLTQTIL GGVNKHSTSI GKILWTVLPI PRIMILVVAA KEVWGDQAD FVNTLQPGC 60
KNVCYDHYFP ISHRLWALQ LIFVSSPALL VAMHVAYRRH EKKRKFIDGE IKSEFDIEE 120
IKTQKVRIEG SLNWTYSSSI FFRVIFEAAP MYVFYVMYDG FSMQLVKCN ANPCFNTVDC 180
FVSRPTEKTV FTFPMIAVSG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 440 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

1 11 21 31 41 51
ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTGGC TTCTCCAAGA GCCGCCCGGG 60
CACCGAGGCG TGGTGGCGCG TCTCCTTCGG GTGAGTCCCA GCCCGAGATT GGCTCTGGCG 120
CCCGGATACC CGCCAGTGCC GCGTGGCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
GTTGGGAAGC CTCCTTTTGA GGCAAAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
ATTTACAGTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTGTGTA 360
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCATT TGCCATCACA 420
GTCTGTGACG GTCTGGACAT CAGCCCGGAG AGGGTCAGAG TGGGAGCATT CCAGTTCACT 480
TCCACTCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCAACAGGA AGTGAAGGCA 540
AGAATCAAGA GGATGTTTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
GGTGTCACTG GTTTGCTGTG GGGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCACATG 780
GCCAGCGAGC CTAGAGGGCA GCACTGCTG TTGGCTGAGC AGTGGAGGA TGCCACCAAC 840
GGCCTCTTCA GCACCTTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
CCCGAGCTTG TCTTCATGGA GGGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCCTC 1020
TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
GTGACCTCC TCTTCTGCTT GGACAGCTCT GCGGGCACA CTCTGGACGG CTTCCTGCGG 1140
GCCAAGTCT TCGTGAAGCG GTTTGTGCGG GCGGTGCTGA GCGAGGACTC TCGGGCCGGA 1200
GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGGGG TGCTGTGGGG GGAGTACCAG 1260
GATGTGCTG ACCTGTGCTG GAGCCTCGAT GGCATTCCCT TCGGTGGTGG CCCCACCTTG 1320
ACGGGCACTG CTTTGGCGCA GCGCGCAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGCG 1380
CAGGACCGGC CAGCTAGAGT GGTGTTTGT CTCACTGAGT CACATCCGA GGATGAGGTT 1440
GCGGGCCCG CCGCTCACGC AAGGGCCGGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG 1620
CGGCCAGGT AGAGGGGTGC AGCCCTGGAC CTGCTCTTCA TGTGGACAC CTCTGCTTCA 1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC OCTCCAGTTT 1740
GAGGTGAACC CTGAGTGAC ACAGGTCCGC CTGTTGGTGT ATGSCAGCCA GGTGCAGACT 1800
GCCTTCGGGG TGGACACCAA ACCACCCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGACATCTA TGACAAAGTG 1920
ATGACCGTTC AGAGGGGTGC CCGGCTGGT GTCCCAAGC CTGTGGTGGT GCTCACAGCG 1980
GGGAGAGGCG CAGAGGATGC AGCCGTTCTT GCCCAGAGC TGAGGAACAA TGGCATCTCT 2040
GTCTTGGTTC TGGGGTGGG GCCTGTCCTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC 2100
CGGGATTCCC TGATCCAGT GGCAGCTTAC GCGACCTGC GGTACCCACA GGACGTGCTC 2160
ATTGAGTGGC TGTGTGAGA AGCCAGCAG CCACTCAACC TCTGCAACC CAGCCCGTGC 2220
ATGAATGAGG GCAGCTGGCT CCGCAGAAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
GGATGGAATC TTGAGAGGCC CCGTGGGAC ATGGCTCCCG TGCGAGAGGG CAGCAGCCGT 2400
ACCCCTCCCA GCAACTACAG AGAAGGCGCT GGCAGTGAAA TGTGCTTAC CTCTGGAAT 2460
GTCTGTGCCC CAGGTCTCTA G

Seq ID NO: 441 Protein sequence
Protein Accession #: XP_061091.1

1 11 21 31 41 51
MPNTSGTTRI EIWLQEPGP HRLVAALLP VSPSPALALA PGYFPVPAAD DRPTLFMIGG 60
QMHGKVDLW SLGLVCEYFL VGRPPFEANE VHSKETIGK ISAASMMNC SAAVDIMFLL 120
QSNVSVKGS PERSKHFAIT VCDGLDISPE RVRVGAFQPS STPHLEPLD SPSTQOEKVA 180
RIKRMVFKGG RTETELALKY LLHRLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
GTFVFAVGR FTRWELHAL ASEPRGQHV LABQVEDATN GLFSTLSSA ICSSATPAGS 300
PELVFMERLM GISLIGPCDS QPCQNGGTCV PBGLDGYQCL CPLAFGGEAN CALKLSLECR 360
VDLLFLDSS AGTTLDDGLR ARVFKRFVR AVLSRDRAR VGVATYSREL LVAVPVGLEYQ 420
DVPDLVSLD GIPFRGGPTL TGSALRQAAE RGFSAATRG QDRPRVVVL LTSHSEDEV 480
AGPARHARAR ELLLLGVGE AVRAELEBIT GSPKHMVYS DPQDLFNQIP ELQKLCRSQ 540
RPGCRTQALD LVFMILDSAS VGPENFAQM PYLGGVGSAG TALLHYDEV MTVQRGARPG VPKAVVVLTG 600
AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHYDEV MTVQRGARPG VPKAVVVLTG 660
GRGAEDAAVP AQRLRNNGIS VLVVGVGPVL SEGLRLRAGP RDSLIHVAAY ADLRYHQDVL 720

IEWLGEAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780
GWILETFLRH MAPVQEGSSR TTPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 442 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

1 11 21 31 41 51
10 ATGCCCCCTT TCCTGTGTCT GGAGGCGGTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180
AGCGTCGGGA AAGGGAGCTT TGAAGGTTC AAGCACTTTG CCATCAGAGT CTGTGAOCSGT 240
CTGGACATCA GCCCCGAGAG GGTGAGAGTG GAGCAITTC AGTTCACTTC CACTCTCAT 300
15 CTGGAATTTC CTTGATTTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
ATGGTTTTCA AAGAGGGGCG CACGGAGACG GAACCTTGCTC TGAATACCT TCTGCACAGA 420
GGGTGCTCGT GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480
AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
20 AGAGGGCAGC ACGTGCTGTT GGTGAGCAG GTGGAGGATG CCAACCAAGG CCTCTTCAGC 660
ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGAGTTTGG CTGGCAATGC CCCATGCTGG 780
AGAGGATCGC GCGGACCCTT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
AGAGTGTTC TAAACCAACC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900
25 TOGCAGCGCT GCCAGATGTT AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCACTGC 960
CTCTGCGCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CTGGAATGC 1020
AGGTGAGC TCTCTTCTCT GCTGGACAGC TCTGGGGCA CCACTCTGGA CGGCTTCTG 1080
CGGGCCAAAG TCTTCTGTAA CCGGTTTGTG CCGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCTGTG GGGGGAGTAC 1200
30 CAGGATGTGC TAGCTCTGTT CTGAGCCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC 1260
CTGACGGGCA GTGCTTGGG CAGGCGGCA GAGCGTGGCT TCGGAGCGCG CACCAAGACA 1320
GGCCAGGACC GGCACGATAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CAGGATGAG 1380
GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
35 TCGGATCCTC TAGGTCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
CAGCGGCGAG GGTGCGGAGC ACAAGCCCTG GACCTGTGCT TCATGTTGGA CACCTCTGCC 1620
TCAGTAGGCG CCGAATATT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGTGCAG 1740
ACTGCTTTC GGTGTGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
40 GCCCCTTACC TAGGTGGGTG GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920
GGCGGAGAG GCGCAGAGA TGCAGCGGTT CCGCCAGAG AGCTGAGGAA CAATGGCATC 1980
TCTGTCTTGG TCGTGGCGGT GGGGCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
CCCCGGGATT CCCTGATCCA CTGCGCAGCT TACGCGAGCC TGCGGTACCA CCAGGACGTG 2100
45 CTGATTGAGT GCGTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
TGATGAAATG AGGGCAGCTG GTCCTGCGAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
GGCTGGGAGG GCCCCCACTG CGAGAACCCT GAGTGAGGCT CTTGCTCTGT ATGTGTGAGC 2280
CAGGATGGA TTCTTGAGAG GCCCCTGAGG CACATGGCTC CCGTGACAGG GGGCAGCAGC 2340
50 GTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTG 2400
AATGTCTGTG CCCAGGTCC TTAG

Seq ID NO: 443 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
55 MPPFLLEAV CVPLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
SVKGSGPERS KHPAIVTCVG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIK 120
60 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSGQDVALPS KQLKERVTV 180
FAVGVRPFRH EELHALASEP RQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFYSWK RVFLTHPATC YRTCTCPGCD 300
SQPQNGGTC VPBGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVPVKRPV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPLDVNSL DGIPFRGGPT 420
65 LTGSALRQAA ERGPGSATRT QDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLVGS 480
EAVRAELEBI TGSPKHMVYV SDPDQLFNQI PELQKLCRS QRPGRCTQAL DLVFMIDTSA 540
SVGPENFAQM QSFVRSQALQ FEVNPDVTOV GLVVYGSQVQ TAFGLDTPKT RAAMLRAISQ 600
APYLGVGGA GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQLKRNNGI 660
SVLVVGVGVV LSEGLRLLAG PRDSLHVAA YADLRVHQDV LIEMLGEAK QPVNLCKPSP 720
70 CMNEGSCVLQ NGSYRCKCRD WNEGPHCENR ENSSCSVCVS QGWILETFLR HMAPVQEGSS 780
RTPPSNYREGL LGTEMVPTFW NVCAPGP

Seq ID NO: 444 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 89..2356

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80 TGTTCCTCTG TTTCCAGAG TGCCCCATC TCTCCTCTC CAGGAAGTCC ATGTAAGCAA 180
AGAAACCATC GGAAGATTTC CAGCTGCCAG CAAATGATG TGGTCTCGG CTGCACTGGA 240
CATCATGTTT CTGTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGTCCAA 300
GCACITTGCC ATCAGCTCT GTGACGGTCT GGACATCAGC CCGAGAGGGT TCAGAGTGGG 360
85 AGCATTCCAG TTAGTTCCA CTCTCATCT GGAATTCCTC TTGATTTCAT TTTCAACCCA 420
ACAGGAAGT AAGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CCGAGAGCGA 480
ACTTGTCTCTG AAATACCTTC TGACACAGAG GTTGCTCTGA GGCAGAAATG CTTCTGTGCC 540
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	GCAGCTGAAG	GAAGGGGGT	TCACTGTGTT	TGCTGTGGGG	GTGAGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTTGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAAGGGCC	TCTTCAGCAC	CCTCAGCAGC	TGGCCATCT	GCTCCAGCGC	780
5	CACGCCAGAC	TGGGGGTGG	AGGCTCACCC	CTGTGAGCAC	AGGAGCCTGG	AGATGGTCCG	840
	GGAGTTGCT	GGCAATGCC	CATGCTGGAG	AGGATGCGGG	CGGACCTTGG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCTTG	CCACCTGCTA	960
	CAGGACCAAC	TGCCAGGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAAATGGAG	GCACATGTGT	1020
	TCCAGAAAGG	CTGGAAGGCT	ACCAGTGCTT	CTGCCCCGTG	GCCTTTGGAG	GGGAGGCTAA	1080
10	CTGTGCTCT	AAGCTGAGCC	TGGAATGCAG	GGTGAACCTC	CTCTCTCTGC	TGACAGCTCT	1140
	TGCGGGCACC	ACTCTGGAAG	GCTTCTCTGG	GGCCAAAGTC	TTCTGGAAGC	GGTTTGTGGC	1200
	GGCGTGTCT	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGGTGGCG	GTGCTGTGG	GGGAGTACCA	GGATGTGCTT	GACCTGGTCT	GGAGCTCTGA	1320
	TGGCATTCCC	TTCCGTGGTG	GCCCCACCTT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
	GGGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
15	GCTCACTGAG	TCACTACTCC	AGGATGAGGT	TGCGGGCCCA	GCGCGTCAAG	CAAGGGCGCG	1500
	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGGGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCGAGCCA	AAGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTTC	ACCAATATCC	1620
	TGAGCTGCAG	GGGAAGCTGT	GCAGCCGGCA	GCGGCCAGGG	TGCGGCAGAC	AAGCCTCTGA	1680
20	CCTGCTCTTC	ATGTTGGACA	CCTCTGCTTC	AGTAGGGCCC	GAGAA'TTTG	CTCAGATGCA	1740
	GAGCTTTTGT	AGAAAGCTGT	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTGG	1800
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	GGCTGCGATG	CTGGCGGCCA	TTAGCCAGGC	CCCTTACCTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCGCCTTG	CTGCACATCT	ATGACAAAGT	GATGAACGTC	CAGAGGGGTG	CCCGCCTTGG	1980
25	TGTCGCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCGGTTC	2040
	TGCCCAGAA	CTGAGGAACA	ATGGCATCTC	TGCTTTGGTC	GTGGGCGTGG	GGCCTGTCT	2100
	AAGTGAGGGT	CTGCGGAGGC	TTGCAGGTCC	CCGGGATTC	CTGATCCACG	TGGCAGCTTA	2160
	CGCGAGCCCA	CGGTACCAAC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAAGCA	2220
	GCCAGTCAAC	CTCTGCAAAC	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCTCTCAGAA	2280
30	TGGGAGCTAC	CGCTGCAAGT	GTGCGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCGATT	2340
	CTTGAGAGCG	CTTGAGGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCGG	TACCCCTCCC	2400
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	CCAGGTCCCT	AGAATGTCTA	CTTCCCGCCG	TGGCCAGGAC	CATTATTCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTACCCAC	2580
35	AAACGATGTT	GTTGAAAAGT	TTTGTATGTT	AAGTAAATAC	CCACTTTCTG	TACCTGTGTT	2640
	GCCTTGTGTA	GGCTATGTCA	TCTGCCACCT	TTCCCTTGAG	GATAAACAA	GGGTCTCGAA	2700
	GACTTAAATT	TAGCGGCTG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
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Seq ID NO: 445 Protein sequence
Protein Accession #: Bos sequence

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	MVFKGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFPWR	EELHALASEP	RQGHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCERHRTLEW	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCCPGCD	300
	SQPCQNGGCT	VPEGLDGYQC	LCPLAPGGEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
50	RAKVPVRRFV	RVLSSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVDPVLVWSL	DGIPFRGGPT	420
	LTGSALRQAA	ERGPSASATR	QGDPRPRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEBI	TGSPKHMVVI	SDPQDLFNQI	PELQGLKCSR	QRPGRCTQAL	DLVFMLDISA	540
	SVGPENFAQM	QSFVRSALCQ	FEVNPVDVTQ	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
	APYLGGVGA	GATLLHIYDK	VMTVQRGARP	GVPKAVVVL	GGRGAEADA	PAQLKRNNGI	660
55	SVLVVGVGVF	LSEGLRLLAG	PRDSLIVHAA	YADLRYEQDV	LIEWLOGEAK	QPVNLCKPSP	720
	CHNBGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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	CGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCCGG	TGCCGAGAA	AGATCTCAGA	180
	GTAAGAAGA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAAC	GAGGCTGCAG	300
	TCAGTTGGGG	AAGGCTGTAG	GACCCGAGC	CAGTGCAAGC	ACTCTGGACC	TCTCAGGGTG	360
70	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCGC	420
	CAGCCCTCAG	AGAAATCTGT	GACTGATTCC	AACTCCGATT	CAGAAGATGA	AAGTGAATG	480
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	ATGTCGTGA	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGSA	GACATCCCC	CCCAGGCTCC	600
	GACTCACAAT	CAAGGAGACC	GCGAAGCGGT	ACATTCOCGG	GTGTTGCTTC	CAGGAGAAAC	660
75	CCTGAACGGA	GAGCTGTGTC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCCGAG	GOOGTCGCTC	CAGATCATCC	840
	GTGACCTCTC	CGCATATAAT	TGCCCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTGGAGAAAC	900
	GTCTGCAGCA	ATTCTGAGGA	GAAGATATAT	AACCGTTTAC	TGGGCTCTAC	TTGTTCATCA	960
80	TGCGGTCAAG	AGACTATTTGA	TACCAAAACA	AACCTGCAG	ACCCAGACTG	CTGGGGGCTT	1020
	CGAGGCCAGT	TCTGTGGCCC	CTGCCCTTGA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTGGCA	TTGCCCGCCT	TGTGAGAGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGACGCGAG	ATGAGCGGTG	TGCGACTGGG	GTCCCTGTGT	ATTAGCCAA	ATATCATGGC	1200
	TTTGGGAATG	TGCACTGCTA	CTTGAAAAGC	CTGAAAACAG	AATTGTGAAT	GCAAGCATAA	1260
85	TATCTGAAA	ATTGTCTGCC	TGCCTTCTAC	TTCTCAAAATC	TTTCTGTGTA	AAGTTTCCAA	1320
	TTTTTTCACT	GAACCTGAG	TTAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

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GAAACACAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
CTTGTTTACA CAAAAACGAG TATGATTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
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Seq ID NO: 447 Protein sequence
Protein Accession #: NP_114148.1

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NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRPR RRTFFGVASR RNPERRARPL 180
TRSRRIIGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR 240
PVEBITTEEL ENVCNSNREK IYNRSLGSTC HQCRQKTIDT KTNCRNPDCW GVRGQPCGPG 300
LRNRYGEEVR DALLDPNWHC PRCRGICNCS PCRQDGRCA TGVLVYLAKY HGFPGNVHAYL 360
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Seq ID NO: 448 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

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TACTTCTCTCT CGCGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTCT CTTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
GGGAACCTGGT TCTCTGCCTG TTTGACAAC TTACAGAAAG CTCTGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
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TTCAACCCCA TGTAACCCCA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCCTC 900
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GCCACCCGCT TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACCTG TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGCTGCAA TGCAGACGAT 1080
GCGTACCAGG GGGAGGTCAC CGAGAAGATG ATGTGTGTCAG GCATCCCGGA AGGGGGTGTG 1140
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GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCCG GCACCCGAGG AGTATACACC 1260
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Seq ID NO: 449 Protein sequence
Protein Accession #: NP_063947.1

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GNWFSACFDN FTEALAEATC RQMGSYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GFLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWPMQV SIQYDKQHV GGSILDPHWV 240
LTAACFRKH TDFPMWVRA GSDKLGFFS LAVAKIIIE FNPMPKMD IALMKLQFPL 300
TFSGTVRPIC LPFFDEELTP ATPLWIIIGW FTKQNGGMS DILLQASVQV IDSTRNADD 360
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Seq ID NO: 450 DNA sequence
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Coding sequence: 52..3042

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CCCAAACTCA CAGTCACCAT TGACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT 240
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5	AAGTTTGTCT	TGGGATTATA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTACGTA	CCCGATTTCAC	TTCCACCTGG	COGGTGATGT	AGACGAAAGG	660
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	AACCACACAG	CTAAGGGAGG	GCCTGGGGAG	CCCCACCTTA	GGCCTTGGTG	CCACACACCA	4440
70	TTGCCCTAAC	AACCGGCCCC	AGAGTGCCCA	GGCACTCCTG	AGGTAGCTTC	TGGAAATGGG	4500
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	CCCTCTCTGT	CCAGCGGCAC	ACAAACCCGC	CCTCCCTTTG	GTGTTGGCGG	TCCCTGTGGC	4620
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	TGTTGCTACC	TGGCTCTCCT	GTCTCTGACG	CTCTACAGGT	GAGGCCACAG	AGAGGGAGTA	4740
75	GGGCTCGGCA	TGTTTCTGGT	GAGCCAATTT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTT	AGCTGCTGCT	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
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Seq ID NO: 451 Protein sequence
 Protein Accession #: XP_051860.2

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Seq ID NO: 453 Protein sequence
Protein Accession #: Eos sequence

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ERSWGHGRVI VHVLDPKSGT VIHSDRFDTY RSKKESERLV QYLNAPVDR ILISVAVNDEG 240
SRNLDDMARK AMTLGSKSEF LHLGFRHPWS FLTUKGNPSS SVEDHIEYHG HRGSAAARVF 300
KLQTERGEY PNVLSSSEW QDVWENTWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR PLCGKPVVRPK LVTVIDTNVN 420
STIINLEDNV QSWKPGDTLV IASTDYSMYQ AEFQVLPSCR SCAPNQVKVA GKPMYLHIGE 480
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LGKPYNNRAH SNYRAGMIID NGVKTTASA KDKRFLFSII SARYSPHQDA DPLKPREPAI 780
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Seq ID NO: 454 DNA sequence
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35 Seq ID NO: 455 Protein sequence
Protein Accession #: NP_037414.2

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55 Seq ID NO: 456 DNA sequence
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Coding sequence: 325..1514

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Seq ID NO: 457 Protein sequence
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Seq ID NO: 459 Protein sequence
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ASCLNIPGSP KCSREBHWIG NGIKCIDLDE CSNTHQCSI NAQCVNTPGS YRCACSEBPT 1440
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VSGTCNLTND MFHICIDGTY ELDRGTGNCT DIDECAFPIN CVNGLCVNTP GRVENCNPPD 1560
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QBNADCNINP GSYRCECAAG FKLSFNGACV DRNECLEIPN VCSHGLCVDL QGSYQCICHN 1920
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SKNPNYNGS NTEGGYLCG PPGYRVGQG HCVSGMGFNK GQYLSLDETV DEENALSPEA 2760
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Seq ID NO: 460 DNA sequence
Nucleic Acid Accession #: NM_013372.1
Coding sequence: 63..617

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ATGGGTGCTT GTGGGTGTTT TTAGACACCA GAGAAAACAC AGTCTCTGCT AGAGAGCACT 840
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5	CTTTCTCTCT	CCTCCTCACA	ATCCATCTCT	TCTTAAAGTG	ATAGTGACTA	TGTCAGTCTA	1140
	ATCTCTTGTT	TGCCAAGGTT	CCTAAATTAA	TTCACTTAAC	CATGATGCAA	ATGTTTTTCA	1200
	TTTTTGTAAG	ACCCTCCAGA	CTCTGGGAGA	GGCTGGTGTG	GGCAAGGACA	AGCAGGATAG	1260
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10	ATTAACCTTG	GCCCTTGCAA	TCTGCTCAAA	CCTAACACCA	AACTGAAAAC	ATAAATACTG	1500
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	RAGAGAGAGC	GACGAGAGTG	AGGAAATAAA	GGGRATTGCC	TCTGGCTAGA	GAGTAAGTTA	1920
	GGTGTAAATA	CCTGGTAGAA	ATGTAAGGGA	TATGAOCTCC	CTTTCTTTAT	GTGCTCACTG	1980
	AGGATCTGAG	GGGACCCCTG	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCACTCTG	2040
20	CTACTGTTTG	GATGACATA	ACTATTGTAA	CTATTGAGTA	TTTACTGGTA	GGCACTGTCC	2100
	TCTGATTAAA	CTTGCCCTAC	TGGCAATGGC	TACTTAGGAT	TGATCTAAGG	GCCAAAGTGC	2160
	AGGGTGGGTG	AACCTTATTG	TACTTTGGAT	TTGGTTAAAC	TGTTTTCTCT	AAGCCTGAGG	2220
	TTTTATATAC	AACTCCCTG	AATACTCTTT	TTGCCTTGTA	TCTTCTCAGC	CTCCTAGCCA	2280
25	AGTCCTATGT	AATATGAAA	ACAAACACTG	CAGACTTGAG	ATTCAGTTGC	CGATCAAGGC	2340
	TCTGGCATTG	AGAGAACCTC	TGCAACTCGA	GAAGCTGTTT	TTATTTGCTT	TTTGTTTTGA	2400
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30	CCAAATCTTT	GTATTTGCCA	CATTCTCCAA	CAATAAAGCA	CAGAGTGGAT	TTAATTAAGC	2640
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	ATGTAAACCC	ACACCAGGGA	GGAAAAATGA	CATTGAGAAC	CAGCAACAC	TGAATTTCTC	2760
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	AGCAGTAATC	TTCTTTTAGG	AGCTTGTAAC	ACAGTCTTGC	ACATAAGTGC	AGATTTGGCT	2880
35	CAAGTAAGA	GAATTTCCCT	AACACTAACT	TCACTGGGAT	AATCAGCAGC	GTAACCTACC	2940
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	GACTAGTACA	AAATGGGTGT	GTCTTCCAAC	TTCAATTGAA	AATGCCATAT	CTATACCATA	3060
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	TTATGGCAAG	ATATTTGTGG	TCTTGATCAT	ACCTATTAAA	ATAATGCCAA	ACACCAAATA	3180
	TGAATTTTAT	GATGTACACT	TTGTGCTTGG	CATTAAAGAA	AAAAAACACA	CATCCTGGAA	3240
40	GTCTGTAAGT	TGTTTTTTGT	TACTGTAGGT	CTTCAAAGTT	AAGAGTGTAA	GTGAAAAATC	3300
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45	GAGTCAGTGC	CTGAATCTTT	ATTTTTTAAA	TGAAATGTTT	CTTAAAGGTT	AACATTTCTA	3600
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50	AAATCATTTA	AAAACGGCAA	AGAAATTATAT	AGACTATGAG	GTACCTTGCT	GTGTAGGAGG	3900
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Seq ID NO: 461 Protein sequence
Protein Accession #: NP_037504.1

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Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2733

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	CATCTAGGCC	CAGTCGAAGA	ATATCAGCTG	CTGCTTCAGG	TGACCTATAG	AGATTCCAAG	180
	GAGAAAGAGG	ATTTGAGAAA	TTTTCTGAAG	CTCTTGAAGC	CTCCATTATT	ATGGTCACAT	240
75	GGGCTAAATTA	GAATTATCAG	AGCAAGGCT	ACCAAGAGCT	GCAACAGCCT	GAATGGAGTC	300
	CTGCAAGTGA	CCTGTGAAGA	CAGCTACACC	TGGTTTCCTC	CCTCATGCCT	TGATCCCCAG	360
	AACCTGTACC	TTCACACGGC	TGGAGCACTC	CCAAGCTGTG	AATGTCTATCT	CAACAACCTC	420
	AGCCAGAGTG	TCAATTTCTG	TGAGAGAAACA	AAGATTTGGG	GCACTTTCAA	AATTAATGAA	480
	AGGTTTACAA	ATGACCTTTT	GAATTCATCT	TCTGCTATAT	ACTOCAAATA	TGCAAAATGGA	540
80	ATTGAAATTC	AACTTAAAAA	AGCATATGAA	AGAATTCAAG	GTTTGTAGTC	GSTTCAGGTC	600
	ACCCAATTTT	GAATGGAAG	CATCGTTGCT	GGGTATGAAG	TTGTTGGCTC	CAGCAGTGCA	660
	TCTGAACCTG	TGTCAGCCAT	TGAACATGTT	GCGAGAGAAG	CTAAGACAGC	CCTTCACAAG	720
	CTGTTTCCAT	TAGAGAGCGG	CTCTTTCAGA	GTGTTTCGAA	AAGCCAGTGT	TAATGACATT	780
	GTCTTTGGAT	TTGGGTCCAA	GGATGATGAA	TATACCTTGC	CCTGCAGCAG	TGGCTACAGG	840
85	GGAAACATCA	CAGCCAGTGT	TGAGTCTCTT	GGGTGGCAGG	TCAACAGGGA	GACTTGTGTG	900
	CTCTCTCTGC	TTGAAGAACT	GAACAAGAA	TTCAGTATGA	TTGTAGGCAA	TGCCACTGAG	960
	GCAGCTGTGT	CATCCTTCGT	GCAAAATCTT	TCTGTATCA	TTGGGCAAAA	CCCATCAACC	1020

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	CTCAAAAGGG	GTTACAGCTA	TCAGATTAAA	ATGTGTCCCC	AAAATACATC	TATTCCTCAT	1380
	AGAGGCCGTG	TGTTAATTGG	GTCAGACCAA	TTCCAGAGAT	CCCTTCCAGA	AACTATTATC	1440
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10	GTCAATGGAC	CTGTGATATC	CACGGTTATT	CAAAACTATT	CCATAAATGA	AGTTTCTCTA	1560
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	GTGTTCTTTA	CACACTTCTT	CTACCTCTCT	TGTTTCTTCT	GGATGCTCAT	GCTTGGCATC	2040
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	GTGGTGTCTG	TAGTTCTCAC	AAAGCTCTGG	AGGCGGACTG	TTGGGGAAG	ACTGAGTGGG	2340
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25	GTTATTTTGG	CTTTACTCAA	TGCATTCCAG	GGATTTTATA	TCTTATGCTT	TGGAATACTC	2520
	TTGGACAGTA	AGCTGCGACA	ACTTCTGTTC	AACAAGTTGT	CTGCCCTAAG	TTCTTGGGAG	2580
	CAAAACAGAA	AGCAAAACTC	ATCAGATTTA	TCGTCCAAAC	CCAAATTCCT	AAAGCCTTTT	2640
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Seq ID NO: 463 Protein sequence
Protein Accession #: Eos sequence

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	NCYLHTAGAL	PSCECHLNLL	SQSVNFCERT	KIWGTFKLINE	RPTNDLLNSS	SAIYSKYANG	180
	IEIQLKKAYE	RIQGFESVQV	TQPRNGSIVA	GVEVVGSSSA	SELLSAIEHV	AEKAKTALHK	240
40	LFPLEDGSPR	VFGKAQCNDI	VFGPGSKDDE	YTLPCSSGYR	GNITAKCESS	GWQVIRETCV	300
	LSLLEELNKN	PSMIVGNATE	AAVSSPVQNL	SVIIRQNPST	TVGNLASVVS	ILSNISLSL	360
	ASHFRVNSGT	MEDVISIADN	ILNASVNTW	TVLLREEKYA	SSRLLETLEN	ISTLVPP TAL	420
	PLNFSRKFID	WKGI PVNKSQ	LKRGYSYQIK	MCPQNTSIPI	RGRVLIGSDQ	FORSLPETII	480
	SMASLTGNI	LPVSKNGNAQ	VNGPVISTVI	QNYISINEVFL	FFSKIESNLS	QPHCVFMDPS	540
45	HLQWNDAGCH	LVNETQDQIV	CQCTHLTSFS	ILMSPPFPST	IPFVVKMITY	VGLGISIGSL	600
	ILCLIIELALF	WKQIKKSQTS	HTRRICMVNI	ALSLLIADVW	FIVGATVDTT	VNPSGVCTAA	660
	VFPFTHFYLS	LFPWMLMGI	LLAYRIILVP	HEMAQHLMAA	VGFCLGYGCP	LIISVITIAV	720
	TQPSNTYKRR	DVCLNWSNG	SKPLLAFFVP	ALAIIVAVNFV	VVLLVLTCLW	RPTVGERLSR	780
	DDKATIIIRVG	KSLILILPLL	GLTWGPGIGT	IVDSQNLAMH	VIFALLNAFQ	GFIFLCPGIL	840
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Seq ID NO: 464 DNA sequence
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Coding sequence: 9845..10219

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	TTGGTTTGAA	AGCATACAGT	AAATATGATG	TCTGTCCCTG	GCAGTGTGGT	CAGAGTAGGA	240
	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACGTG	ACTTACATAT	300
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75	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCAATTTT	AGTTAGTACC	TTTCTTAAAG	1020
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	ATAGGCAAT	CCATAGAAAAC	AGGAGGTAGA	TTCTGGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
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	GATGATAGCA	CAACTTTGTG	AATATAATAA	AATCATTTGAA	TTGTACAGTT	GAATTTATGG	2280
10	TATATAAAT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTGAGGAG	ATATTGGATT	AAATGGCCTT	GGACAAACAC	CCCTCTCCCT	GGCCACAGAC	2400
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	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGGATCT	CCTGAGGCTT	2820
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	TGAGTAACCT	CAATACTAA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTCATTTCCA	CAGACACACA	CAGCCTCTCT	CCCCACCTCT	GCTTCTCTTA	3720
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Seq ID NO: 465 Protein sequence
Protein Accession #: BAB21525.1

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	DAIKKFPQTS	VESTDFANAP	EESRKKINSW	VESQTNELIK	NLFPDGTIGN	DTTLVLVNAI	180
	YFKQGWENKF	KKENTKEEKF	WPNKNTYKSV	QMMRQYNSFN	FALLEDDVQAK	VLEIPYKGGD	240

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50 Seq ID NO: 467 Protein sequence
Protein Accession #: NP_001901.1

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FDGILGLGYP SLAVGGVTFV FDNMMAQNLV DLPMSVYMS SNPEGGAGSE LIPGGYDHS 240
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75 AACTTCTTT TCCACAACCG GGGCGATGGC ACCTTTGTGG ACGCTGCGGC CAGTGTGGT 540
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AAAGTGAGCA TGTCTATGG CAACTGGAAT GGCCCCACCC GCCTCTATCT GCAATGAGC 660
ACCATGGGA AGGTCCGCTT CCGGACATC GCCTCAACCA AGTCTCCTAT GCCTCCCTT 720
GTCGCGACGG TCATCACCGC CCACTTTGAC AATGAACAGG AGCTGGAGAT CTTCTTCAAC 780
80 AACATTGCTT ACCGAGCTC CTCAGCCAAC GCCTCTTCC GCGTCATCCG TAGAGAGCAC 840
GGAGACCCCC TCATCGAGGA GCTCAATCCC GGGACGCGCT TGGAGCCTGA GGGCCGGGC 900
ACAGGGGGTG TGGTGAACGA CTTGACGGA GACGGGATGC TGGACCTCAT CTGTGCCAT 960
GGAGAGTCCA TGGCTCAGCC GCTGTCTGTC TTCCGGGCA ATCAGGGCTT CAACAAAC 1020
TGGCTGAGAG TGGTGCCAGC CACCCGGGTT GGGGCTTTG CCAGGGGAGC TAAGTGTGG 1080
85 CTCTACACCA AGAAGAGTGG GGGCCACTG AGGATCATCG ACGGGGGCTC AGGCTACCTG 1140
TGTGAGATGG AGCCCGTGGC ACACTTTGGC CTGGGGAAGG ATGAAGCCAG CAGTGTGGAG 1200
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	GTGCTGGAGA	TCCTCTACCC	CCGGGATGAG	GACACACTTC	AGGACCCAGC	CCCACTGSGAG	1320
	ACACCAATGA	ATGCATCCAG	TTCCCATTCG	TGTGCCCTCG	AGACAAGCCC	GTATGTGTCA	1380
	ACACCTATGG	AAGCTACAGG	TGCCGGACCA	ACAAGAAGTG	CAGTGGGGCC	TACGAGCCCA	1440
	ACGAGGATGG	CACAGCCTGC	GTGGGGACTC	TGGGCCAGTC	ACCGGGCCCC	CGCCCCACCA	1500
5	CCCCCACCGC	TGCTGCTGCC	ACTGCCGCTG	CTGCTGCCGC	TGCTGGAGCT	GCCACTGCTG	1560
	CACCGGTCTC	CGTAGATGGA	GATCTCAATC	TGGGGTCGGT	GGTTAAGGAG	AGCTGCGAGC	1620
	CCAGCTGCTG	AGCAGGGGTG	GGACATGAAC	CAGCGGATGG	AGTCCAGCAG	GGGAGTGGGA	1680
	AAGTGGGCTT	GTGCTGCTGC	CTAGACAGTA	GGGATGTAAA	GGCCTGGGAG	CTAGACCCCTC	1740
	CCCAAGCCCA	TCCATGACCA	TTACTTAGCT	AACAATTAGG	GAGACTCGTA	AGGCCAGGCC	1800
10	CTGTGCTGGG	CACATAGCTG	TGATCAGAGC	AGACAGGGTC	GCTGCCCTGA	TGGCGCTTAC	1860
	ATTCCAGTGG	GTCTAATGAC	CATATCTTAG	GACACAGATG	TGCCCAGGGA	GGTGGTGTCA	1920
	CTGCACAGGA	AGTATGAGGA	CTTTAGTGTC	CTGAGTTCAA	ATCCTGATTTC	AGGAACTCAC	1980
	AAAGCTATGT	GACCTTACAC	CAGTCACTTA	ACTTGTTAGC	CATCCATTAT	CGCATCTGCA	2040
	AAATGGGGAT	TAAGAAATAGA	ATCTTGGGGT	TAGTGTGGAG	ATTAGATTAA	ATGTATGTAA	2100
15	GACACTTGGC	ACAAAACCTG	GCACATAGTA	AAGGCTCAAT	AAAAACAGT	GCCTCTCACT	2160
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Seq ID NO: 469 Protein sequence
Protein Accession #: NP_060528.1

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	RGDGTFFVDA	ASAGVDDPHQ	HGRGVALADF	NRDGKVDIVY	GNWNGPHRLY	LQMSTHGKVR	120
25	FRDIASPKFS	MPSPVRTVIT	ADFDNDQELE	IFPNNIAYRS	SSANRLPRVI	RREHGDPLIE	180
	ELNPGDALSF	EGRGTGGVVT	DFDGDGMLDL	ILSHGSEMAQ	PLSVFRGNQG	PNNNWLVRVP	240
	RTRVGAFARG	AKVLYTKKS	GAHLRIIDGG	SGYLCEMEFV	AHFPLGKDEA	SSVEVTWPDG	300
	KMVSRRVASG	EMNSVLBIILY	PRDEDTLQDP	APLETFMNAS	SSHSCALETG	FVYSTFMEAT	360
	GAGPTRSAVG	ATSPTRMAQF	ANGLSASHRA	PAPPPPPLLL	PLFLLPLLE	LPILLRHS	
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Seq ID NO: 470 DNA sequence
Nucleic Acid Accession #: AJ279016
Coding sequence: 1..1962

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	CAGCGGGCTG	AACCCATGTT	CACTGCAGTC	ACCAACTCAG	TTCTGCCTCC	TGACTATGAC	120
	AGTAATCCCA	CCCAGCTCAA	CTATGGTGTG	GCAGTTACTG	ATGTGGACCA	TGATGGGGAC	180
40	TTTGAGATGG	TGCTGGCGGG	GTACAATGGA	CCCAACCTGG	TTCTGAAGTA	TGACCGGGCC	240
	CAGAAGCGGC	TGGTGAACAT	CGCGTCCGAT	GAGCGCAGCT	CACCCCTACTA	CGCGCTGCGG	300
	GACCGGCAGG	GGAAACCCAT	CGGGGTCACT	GCTTGCAGCA	TGCAAGGGGA	CGGCGGGGAG	360
	GAGATCTACT	TCCTCAACAC	CAATAATGCC	TTCTCGGGGG	TGGCCACGTA	CACCGACAG	420
	TTGTTCAAGT	TCCGCAATAA	CCGGTGGGAA	GACATCTCTA	GCGATGAGGT	CAACGTGGCC	480
45	CGTGGTGTGG	CCAGCTCTCT	TGCCGGACGC	CTCTGGGCTT	GTGTGGACAG	AAAGGGCTCT	540
	GGAGCTACT	CTATCTACAT	TGCCAATTAC	GCTTACGGTA	ATGTGGGCCC	TGATGCCCTC	600
	ATTGAAATGG	ACCTTGAGGC	CAGTGACCTC	TCCCGGGGCA	TTCTGGCGCT	CAGAGATGTG	660
	GCTGCTGAGG	CTGGGGTCAG	CAAAATATACA	GGGGGCGGAG	GCGTCAGCGT	GGGCCCCATC	720
	CTCAGCAGCA	GTGCTCGGGA	TATCTTCTGC	GACAATGAGA	ATGGGCTTAA	CTTCTCTTTC	780
50	CACAACCGGG	GCGATGGCAC	CTTTGTGGAC	GCTGGGGCCA	GTGCTGGTGT	GGAGCAACCC	840
	CACCAGCATG	GGCGAGGTGT	CGCCCTGGCT	GACTTCAACC	GTGATGGCAA	AGTGGACATC	900
	GTCTATGGCA	ACTGGAATGG	CCCCCACCGC	CTCTATCTGC	AAATGAGCAC	CCATGGGAAG	960
	GTCCGCTTCC	GGGACATGCG	CTCACCCAAG	TTCTCCATGC	CCTCCCTGTG	CCGCAACGTC	1020
	ATCACCGCGG	ACTTTGACAA	TGACCCAGGAG	CTGGAGATCT	TCTTCAACAA	CATTGCCCTAC	1080
55	CGCAGCTCCT	CAGCCAAACG	CCTCTTCCGG	GTCAATCCGT	GAGAGCACCG	AGACCCCTCT	1140
	ATCGAGGAGC	TCAATCCCGG	CGACGCTTGG	GAGCCTGAGG	GCCGGGGCAC	AGGGGGTGTG	1200
	GTGACCGACT	TGACCGGAGT	CGGGATGCTG	GACCTCATCT	TGTCCCATGG	AGAGTCCATG	1260
	GCTCAGCCCG	TGTCCTGTCT	CGGGGGCAAT	CAGGGCTTCA	ACAACAACCTG	GCTGGAGATG	1320
	GTGCCACGCA	CCCGGTTTGG	GGCCTTTGCC	AGGGGAGCTA	AGGTCTGTCT	CTACACCAAG	1380
60	AAGAGTGGGG	CCCACTGAGG	GATCATCGAC	GGGGGCTCAG	GCTACCTGTG	TGAGATGGAG	1440
	CCCGTGGCAC	ACTTTGGCCT	GGGGAAGGAT	GAAGCCAGCA	GTGTGGAGGT	GACGTGGCCA	1500
	GATGGCAGAA	TGGTGAAGCG	GAACGTGGCC	AGCGGGGAGA	TGAACTCAGT	GCTGGAGATC	1560
	CTCTACCCCC	GGGATGAGGA	CACACTTCAG	GACCCAGCCC	CAGTGGAGTG	TGGCCAAGGA	1620
	TTCTCCACAG	AGGAAAATGG	CCATTGCAATG	GACACCAATG	AATGCATCCA	GTTCCCATTC	1680
65	GTGTGCCCTC	GAGACAAGCC	CGTATGTGTC	AACACCTATG	GAAGCTACAG	GTGCCGGACC	1740
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	CTCGGCCAGT	CACCGGGCCC	CGGCCCCACC	ACCCCCACCG	CTGCTGTGTC	CAGTCCCGCT	1860
	GCTGCTGCCG	CTGCTGGAGC	TGCCACTGCT	GCAACGGTTC	TGTAGATGAG	AGATCTCAAT	1920
	CTGGGGTCCG	TGGTTAAGGA	GAGCTGCGAG	CCGAGCTGCT	GAGCAGGGGT	GGGACATGAA	1980
70	CCAGCGGATG	GAGTCCAGCA	GGGGAGTGGG	AAAGTGGGCT	TGTGCTGCTG	CCTAGACAGT	2040
	AGGGATGTAA	AGGCTGGGA	GCTAGACCTT	CCCCAAGCCC	ATCCATGCAC	ATTACTTAGC	2100
	TAACAATTAG	GGAGACTCGT	AAGGCCAGGC	CCTGTGCTGG	GCACATAGCT	GTGATCAGAG	2160
	CAGACAGGGT	CGCTGCCCTG	ATGGCGCTTA	CATTCCAGTG	GGTCTAATGA	CCATATCTTA	2220
	GGACACAGAT	GTGCCCAGGG	AGGTGGTGTG	ACTGCACAGG	AAGTATGAGG	ACTTTAGTGT	2280
75	CCTGAGTTCA	AATCCTGATT	CAGGAACCTCA	CAAAGCTATG	TGACCTTACA	CCAGTCACTT	2340
	AACCTTGTAG	CCATCCATTA	TCCCATCTGC	AAAATGGGGA	TTAAGAAATAG	AATCTTGGGG	2400
	TTAGTGTGGA	GATTAGATTA	AATGTATGTA	AGACACTTGG	CACAAAACCT	GGCACATAGT	2460
	AAAGGCTCAA	TAAAAACAAG	TGCCTCTCAC	TGGGCTTTGT	CAACACG		

Seq ID NO: 471 Protein sequence
Protein Accession #: CAC08451

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	EIYFLNTNNA	PSGVATYTDK	LPKFRNNRWE	DILSDEVNVA	RGVASLFAGR	SVACVDRKGS	180

	GRYSIYIANY	AYGNVGPDL	ISEMDPEASDL	SRGILALRDV	AAEAGVSKYT	GGRGVSVGPI	240
	LSSASDIFC	DNENGFNPLF	HNREGDTFVD	AAASAGVDDP	HQHGRGVALA	DFNRDGKVDI	300
	VYGNWNGPFR	LYLQMSHFGK	VRFRDIASPK	FSMPSPVTV	ITADFDNDQE	LEIPFNLIAY	360
	RSSSANRFLP	VIRREHGDPL	IEELNPGDAL	EPDGRGTGGV	VTDFDGDMGL	DLILSHGESM	420
5	AQPLSVFRGN	QGFNNNWLVR	VPRTRFGAPA	RGAKVVLYTK	KSGAHLRIID	GGSGVLCEME	480
	PVAHFGLGKD	EASSVEVTWP	DGMVSRNVA	SGEMNSVLEI	LYPRDEDTLQ	DPAPLECOQG	540
	PSQQENGHCM	DTNECIQFPF	VCPRDKPVCV	NTYGSYRCRT	NKKCSRGYEP	NEDGTACVGT	600
	LQSPGPRPT	TPTAAAAATA	AAAAAGAATA	APVLVDGDLN	LGSVVKESCB	PSC	

10 Seq ID NO: 472 DNA sequence
Nucleic Acid Accession #: FGENESH
Coding sequence: 1..4794

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	GTTCTGAAGT	ATGACCGGGC	CCAGAAGCGG	CTGGTGAACA	TCGGGTCGA	TGAGCGCAGC	180
	TCACCTACT	ACGCGCTGCG	GGACCGSCAG	GGGAACGCCA	TCGGGTCAC	AGCCTCGAC	240
20	ATCGACGGGG	ACGGCCGGGA	GGAGATCTAC	TTCTCAACA	CCAATAATGC	CTTCTGGGCG	300
	CACAGCAGCT	CAGCGCAGGT	CCCTCTGGG	CTCCACAGAA	ACAGGCTGT	GCTGAAGCCT	360
	CCACCTACAA	CCCTGCGAGG	CCTCCTGGGT	CTGCCTCCAC	TCAGCGGAAG	GGACTTTTCC	420
	TCCTCCCTGG	GTCAGGCTTC	TCGGACAGC	AGGCAGGGAG	AGAGGGTGCC	GGTTCCTGTC	480
	TGTGGGGTG	GACTGAGACC	TACCCATGAA	CCAGAACCAT	TTCTTCTGAG	ACCCAAATCA	540
25	GGGGTGGCCA	CGTACCCGA	CAAGTTGTTC	AAGTTCGGCA	ATAACGGTG	GGAGAGCATC	600
	CTGAGCGATG	AGGTCAACGT	GGCCCGTGGT	GTGGCCAGCC	TCTTTGCCGG	ACGCTCTGTG	660
	GCTGTGTGG	ACAGAAAGGG	CTCTGGACGC	TACTCTATCT	ACATTGCCAA	TTACGCTTAC	720
	GGTAATGTGG	GCCTGTATGC	CCTCATTGAA	ATGGACCTTG	AGGCCAGTGA	CCTCTCCCGG	780
	GGCAATCTCG	CGCTCAGAGA	TGTGGCTGCT	GAGGCTGGGG	TCAGCAATA	TACAGAAGGC	840
30	TTCTCCCACT	CTGCTCTCC	AAGCATTGGT	GAGATATCTG	GCAGAACCGA	GGAGCGGGAA	900
	GGAGGAGACG	CAGAGGAGGC	AGATGAGGAG	CACAGTGGGG	ATGGAAGCAC	CAGCCAACTG	960
	TGCGGCTGG	GTCGGAAGCA	CGGGCAGTTC	AAGGAAGAAG	CAGCAGCTTT	GGTGAGGAA	1020
	CAGAGGGAGG	CTGGGGCAGC	TGGCTGCCCC	AGAGSACCTG	TTGSAACAGC	TCTGCAGACT	1080
	TCCAAAGGCC	ATTGGGCTGA	CAAGAACTTA	TTTGGCCCAT	CATGTTACTA	TTCTGTCTCG	1140
35	GCGCCTTCTC	CAGCCCACTC	TTTCCCTGCC	CGCCAAAGCC	CCCAACACTA	GGCCTGTAGC	1200
	CCCTCTGTCA	CTCAGCTAAT	GACACATGGA	CGTCTGGCTG	GAATACTAGC	CCGAGGTGTC	1260
	CCCAACCCCC	GAGCCCGAGG	AATGGACCCC	AAATGTAAGG	GCGCCATGTC	TGAGCCCGGC	1320
	CTGATGGCTG	AGGCTTTGGG	CGGCTGGCCA	GCGCTCAGCA	CCACTGTGCT	GCCAGGGGGC	1380
40	CTGAGAAAGT	GGGAGGAAAG	CAGGCAGAA	GGGCAGGCCA	TGTCCAGATG	TGCACCTCAG	1440
	GAGCTGGGAG	GTCCCTGGAG	CCAAGCCACA	CAGCACCTGC	CTGCTAGAGA	GCTGTATGAC	1500
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	CCCAAGGTCA	CACAGAGTGC	CCATCTAGTG	GCCACCATGC	CAGCTCTCGG	GGGACTCGAG	1620
	GGCCCCGGGA	GGGTGGCCAA	GCGAGAGATT	GGGAGAGAGA	CTGGGGCAGT	AGGAAGACCA	1680
45	CTCTCCCATC	CCCTGTGCCC	CAACTTCCCC	AGCTGCTTGA	GGCCTCTTGA	AGCCGGGACA	1740
	GTGCGGGAGC	CTGCCCTGCG	TGGGAATCCT	GGGAACCTGG	TTCTGGACAT	GGCCAAAGCC	1800
	CTGGCGTGA	ACCAGATGGA	AAAAGAGGAG	GGGAAGATTC	ATGGAGACCA	TGAGCCACGA	1860
	TTTAGGCTCA	GGAAAGCAG	GGAAGCAGAA	TTCCCCCAG	GCTCCTCTGA	GGAGCCTCTG	1920
	CTGCAAGTTC	CCTCAGGCTC	CAGAGGCAGC	CCTGTCTCTC	AGGTGGGCTT	GGGCTTGTCT	1980
50	TCTGCCACTC	ACTGTGGGTC	GATGTCTTTT	CTAGGGGGCC	GAGGCGTCAG	CGTGGGCCCC	2040
	ATCCTCAGCA	GCACTGCTTC	GGATATCTTC	TGCGACAATG	AGAAATGGCC	TAACTCTCTT	2100
	TTCCACAACC	GGGGGATGGA	CACCTTTGTG	GACGCTGCGG	CCAGTGTCTGA	ACGTGCTTTA	2160
	GCCCTTCATG	TTCACTCAA	ATATCACCTC	TGCAGAGATT	TTCTCTACTC	CCTGTGCCAC	2220
	CTAGCAGAAA	CTGCTCTCTC	CTCCTCTGTC	TGCCGCTGGC	ATGCACGTCT	TCTTCAGGCT	2280
55	CCACATTGCC	ATCATGTTTT	GTCTATGAGC	TTTACAAGGA	CCGGGTCAAG	GTCTTATTCA	2340
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	CAGGGGGCCC	CACCTGCTCT	TCTGGCAAGA	GCTCCCTGTG	TCCTGGGGTC	TCTGATCCCC	2460
	ACTGCCTATT	ACATTGTCTT	GTGGTCTGCC	ATCCCAAGAG	GCCTGATGAC	CCACAGCTAT	2520
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60	GCCCTGGCTG	ACTTCAACCG	TGATGGCAAA	GTGGACATCG	TCTATGGCAA	CTGGAATGGC	2640
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	GACCAGSAGC	TGGAGATCTT	CTTCAACAC	ATTGCCTACC	GCAGCTCCTC	AGCCAAACCG	2820
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	GGTCAGGGAG	AAGGTTTAAG	AATCAGAAAG	GGAGGGTTCC	CAGGGCCAGG	GGGTGAGGCC	2940
65	AAGGTCAACA	CAGGTCCCTC	GATGAAGAAA	CAGAAAGGAA	GGAAAGGAGA	GGACTGGGCA	3000
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70	CGGGGTCCAA	TCACTACCAG	GAAAAGGGGC	TACGGGGTCC	AATCACTACC	AGGAAAAGGG	3300
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75	ACTACAGGGA	AAAGGGGCTA	CGGGCTCCAA	TCACTACCAG	GAAAAGGGGC	TACGGGGTCC	3600
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	GGCTACCTGT	GTGAGATGGA	GCCCGTGGCA	CACCTTTGGC	TGGGGAAGGA	TGAAGCCAGC	4260
	AGTGTGGAGG	TGAAGTGGCC	AGATGGCAAG	ATGGTGAGCC	GGAACTGTGC	CAGCGGGGAG	4320

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Protein Accession #: FGENESH predicted

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AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAGGCAC CACCATCGCC 480
AATGTGTTGT CTGGCTCTCT CAGCATTTC TCTGGCATCC TGACCTCGT CGGCATGGGT 540
CTGGCACCTC TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
ATCACAGCGG CTTTGACCGG GATTACCAGC AGTACCATTG ACTACGGAAA GAAGTGGTGG 660
ACACAAGCCC AAGCCACAGA CCTGGTCATC AAAAGCCTTG ACAAAATTGA GGAGGTGAGG 720
GAGTTTTTGG GTGAGAACAT ATCCAACTTT CTTTCTTTAG CTGGCAATAC TTACCAACTC 780
ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
GTACCGCATG CCTCAGCCTC ACGCCCCCGG GTCACTGAGC CAATCTCAGC TGAAGCGGT 900
GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCTCGGAAA TGAGCAGAGG AGTCAAGCTC 960
ACGAGTGTGG CCCCTGTAAG CTCTTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020
TCAAAGCACT TACATGAGGG GGCAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080
CAGGAGCTGG AGGAGAGCT AAACATTCTC AACATAATT ATAAGATTCT GCAGGCGGAC 1140
CAAGAACTGT GA
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Seq ID NO: 475 Protein sequence
Protein Accession #: NP_003652.1

1 11 21 31 41 51
75
80
85

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KEKVSTQNL LLLTDNEAWN GFVAAELPR NEADELRKAL DNLARQIMK DQNWEDKQQ 120
YRWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLST SGILTLVGMG 180
LAPFTGGSL VLEPMEWG ITAALTGITS STMDYGKXW TQAQADLVI KSLDKLKEVR 240
EPLGENISNP LSLAGNYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISABSG 300
EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVYE SKHLHEGAKS ETABELKKVA 360
QELREKGLNL NNNYKILQAD QEL
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Seq ID NO: 476 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

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5	GCTCAGCGAG	AACGAAGGG	CTCGAATCTC	ATTGGCACAT	ACGCCCATGT	TGACCGGTGCC	180
	ACCGGCCAGG	TGCTAACCTG	TGACAAGTGT	CCAGCAGGAA	CCTATGCTCT	TGAGCATTGT	240
	ACCAACACAA	GCTGCGCGCT	CTGCAGCAGT	TGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
	AATGGCATAG	AGAAATGCCA	TGACTGTAGT	CAGCCATGCC	CATGGCCAAT	GATTGAGAAA	360
	TTACCTTTGT	CTGCCTTGAC	TGACCGAGAA	TGCACCTGCC	CACCTGGCAT	GTTCCAGTCT	420
10	AACGCTACTT	GTGCCCCCCA	TACGGTGTGT	CCTGTGGGTT	GGGTGTGGG	GAAGAAAGGG	480
	ACAGAGACTG	AGGATGTGGG	GTGTAAGCAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCCT	540
	TCTAGTGTGA	TGAAATGCAA	AGCATACACA	GACTGTCTGA	GTGAGAACCT	GGTGGTGATC	600
	AAGCCGGGGA	CCAAGGAGAC	AGACAACGTC	TGTGGCACAC	TCCCGTCTCT	CTCCAGCTCC	660
	ACCTCAGCTT	CCCTTGGCAC	AGCCATCTTT	CCAACGCTCT	AGCACATGGA	AACCCATGAA	720
15	GTCCCTTCTT	CCACTTATGT	TCCCAAAGGC	ATGAACTCAA	CAGAAATCAA	CTCTTCTGCC	780
	TCTGTAGAC	CAAAGGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAAGC	840
	TCAGCAAGGG	GGAAAGGAGA	CGTGAACAG	ACCTTCCCAA	ACCTTCAGGT	AGTCAACCCAC	900
	CAGCAAGGCC	CCCAAGGAGC	ACACATCCTG	AAGCTGCTGC	CGTCCATGGA	GGCCACTGGG	960
	GGCGAGAAAT	CCAGCAGGCC	CATCAAGGGC	CCCAAGAGGG	GACATCTTAG	ACAGAAACCTA	1020
20	CACAGACCTT	TTGACATCAA	TGAGCAATTG	CCCTGGATGA	TTGTGCTTTT	CCTGCTGCTG	1080
	GTGCTTGTGG	TGATGTGGT	GTGCAGTATC	CGGAAAGCT	CGAGGACTCT	GAAAAAGGGG	1140
	CCCGGGCAGG	ATCCAGTGC	CATTGTGGAA	AAGGCAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGAGGC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCCTGAAG	1260
	CTTGTAGCAG	CCCAAGTGGG	AAGCCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
25	AGTGAGAGGG	AGGTTGCTGC	TTTCTCCAAT	GGGTACACAG	CCGACCACGA	CGGGGCTTAC	1380
	GCAGCTCTGC	AGCAGTGGAC	CATCCGGGGC	CCCGAGGCCA	GCCTCGCCCA	GCTAATTAGC	1440
	GCCTCTGGCC	AGCAGCGGAG	AAACGATGTT	GTGGAGAGAA	TTGGTGGGCT	GATGGAAGAC	1500
	ACCAACCCAG	TGGAACCTGA	CAAACTAGCT	CTCCCGATGA	GCCCCAGCCC	GCTTAGCCCG	1560
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30	TCCCCACAG	ACAAGAACA	GGGCTTCTTC	GTGGATGAGT	CGGAGCCCTT	TCTCCGCTGT	1680
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	AAGAAGGACA	CAGTGTGGG	GCAGGTACGC	CTGGACCCCT	GTGACTTGCA	GCCTATCTTT	1800
	GATGACATGC	TCCACTTTCT	AAATCCTGAG	GAGCTGCGGG	TGATTGAAGA	GATTCCCCAG	1860
35	GCTGAGGACA	AACTAGACCG	GCTATTGAAA	ATTATTGGAG	TCAAGAGCCA	GGAAGCCAGC	1920
	CAGACCTCC	TGGACTCTGT	TTATAGCCAT	CTTCTGACC	TGCTGTAG		

Seq ID NO: 477 Protein sequence
Protein Accession #: NP_055267.1

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	LPCAALTDRE	CTCPPMFQS	NATCAPHTVC	PVGWGVKRG	TETEDVRCKQ	CARGTFSDVP	180
	SSVMKCKAYT	DCLSQLNLI	KPOTKETDNV	CGTLPSFSSS	TSPSPGTAIP	PRPEHMETHE	240
45	VPSSTYYPKG	MNSTYESSA	SVRPKVLSSI	QBGTYPDNTS	SARGKEDVNK	TLNLIQVNNH	300
	QGGPHRHLL	KLPLSMEATG	GEKSSTPIKG	PKRGHPRQNL	HKHPTINEHL	PWMLVFLILL	360
	VLVVIIVCSI	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNRKWIYY	CNHGIDILK	420
	LVAAGVGSQW	KDIYQPLCNA	SEREVAAPSN	GYTADHERAY	AALQHWITRG	PEASLAQLIS	480
50	ALRQHRNDV	VEKIRGLMED	TTQLETDKLA	LPMSPSPLSP	SPIPSFNAKL	ENSALLTVEP	540
	SPQDKNGKPF	DESEPLRLRC	DSTSSGSSAL	SRNGSFITKE	KKDTVLRLQVR	LDPCDLQPIF	600
	DDMLHPLNPE	ELRVIEEIPQ	AEDKLDRLPE	IIGVKSQEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 478 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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	GGAGGCGGGG	GCCCGCGGGG	CGACTCGGGG	GCGGACCGGG	GGGCGGAGCT	GCCCGCCGTG	180
	AGTCCGGCGG	AGCCACCTGA	GCCCGAGCGG	CGGGACACCG	TGCTCTCTGC	TCTCGAATG	240
	CTGCGCACCG	CGATGGCGCT	GAGGAGCTGG	CTGCGCGCCC	CATGGGCGGC	GCTGCGGCTT	300
65	CGGCCACCGG	TGCTGCTGCT	CCTGCTGCTG	CTGCTCTGCG	TGCAGCCGCC	GCTTCCGACC	360
	TGGGCGCTCA	GCCCCCGGAT	CAGCCTGCGT	CTGGGCTCTG	AAGAGCGGCG	ATTCTCTAGA	420
	TTCGAAGCTG	AACACATCTC	CAACTACACA	GCCCCCTGCG	TGAGCAGGGA	TGGCAGGACC	480
	CTGTAGCTGG	GTGCTCGAGA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCTTGCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCAG	AGAAGAAACA	GCAGTGCAGC	600
70	TTCAAGGGCA	AGGACCCACA	GCGGAGCTGT	CAAAACTACA	TCAAGATCCT	CCTGCGGCTC	660
	AGCGGCGATC	ACCTGTTTCA	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACCTACATC	720
	AACATGAGGA	ACTTCAACCT	GGCAAGGGAC	GAGAAGGGGA	ATGCTCTCTT	GGAGATGGC	780
	AAGGGCGGTT	GTCCTTGA	CCCGAATTC	AAGTCCACTG	CCCTGGTGGT	TGATGGGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
75	AGCCTTGCGC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
	GCCTCAGCCT	ACATTCTGAG	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCCTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TCTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGAGC	1140
	TCCTTCTCTA	AGGCCAGAGT	GCTGTGCTCA	CGGCCGAGCG	ATGGCTTCCC	CTTCAACGTG	1200
80	CTGCAGGATG	TCTTCAAGCT	GAGCCCCAGC	CCCCAGGACT	GGCGTGACAC	CCTTTCTTAT	1260
	GGGGTCTTCA	CTTCCAGTGG	GCACAGGGGA	ACTACAGAA	GCTCTGCGGT	CTGTGCTTTC	1320
	ACAATGAAGG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CGGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCCGGTG	CCCAACCCCG	GGCCTGAGAG	GTGCATCAC	1440
	AACAGTGCCC	GGGAAGGAA	GATCAACTCA	TCCCTGCAGC	TCCAGACCG	CGTGTGTAAC	1500
85	TTCTCAAGG	ACCACTTCTT	GATGGACGGG	CAGGTTCGAA	GCCCATGTCT	GCTGTCTGAC	1560
	CCCCAGGCTC	GCTACAGCG	CGTGGCTGTA	CACCGCGTCC	CTGGCCTGCA	CCACACCTAC	1620
	GATGTCTCTT	TCCTGGGCAC	TGCTGACGGC	CGGCTCCACA	AGGCACTGAG	CGTGGGCCCC	1680
	CGGTGCACA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAAGATCTG	1740

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5 ACCAGGCGGT GGATCCAGGA CATCGAGGA GCCAGCGCA AGGACCTTG CAGCGGTCT 1980
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10 CAAACAGATG AGGGTGGCAG TGTACCGTTC ATTATCAGCA CATCGCGTGT GAGTGCACCA 2340
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15 CTGATCAGC GAGGTACCA GTCCCTGTCA GACAGCCCC CGGGTCCCG AGTCTTCACT 2640
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20 GGCCAGTCTG CAGTGTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACC AGACCCCAA 2940
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25 TGGCTCTCTC ACCTTCCACT TTATCCGCT GCCACCGCT GCCTGTCTC ACTGCAGATT 3240
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CTGCGCTGCT CCCACCACT CAGGGAACAG AGGGCTAGGT TGGCACTGG GCCCTACCA 3360
GGTCTGCGC TCGGACCCAA CTCTGGACC TTTCCAGCT GTATCAGCT GTGSCACAC 3420
GAGAGGACAG CCGAGCTCA GGAGAGATT CTGTGCAATG TAGCCTTTC CCTCAGAAAT 3480
30 CAGGGAAGAG ACTGTGCGCT GCCTTCTCTC GTTGTGCGT GAGAACCGT GTGCCCTTC 3540
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GTCCTCTCCC CAGTCCCGAG TTCACCTCC ATCCCTCAC TTCTCCACT CTAAGGATA 3660
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35 ATGCACCTTA TGTCACTTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 479 Protein sequence
Protein Accession #: XP_044533.3

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SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180
45 GKGRCPDPFN FKSTALVVDG ELYTGTVSSP QGNDFPISRS QSLRPTKTBS SLNWLQDPAP 240
VASAYIPESL GSLQDDDKI YFFPSETGQE FEFFENTIVS RIARICKGDE GGERVLOQRW 300
TSFLKAQLLC SRPDDGPPFN VLQDVFTLSP SPQDWRDTLP YGVFTSQWHR GTTEGSAVCV 360
FTMKDVQRVF SGLYKEVNR TQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
NFLKDHFLMD GQVRSRMLLL QPQARYQOVA VHRVPLGHT YDVLFLGTGD GRLEKAVSVG 480
50 PRVHIIEELQ IPSSQPVQVN LLLDTHRGLL YASHSQVQV VPMANCSLYR SCGDCLLARD 540
PYCANSSSC KHVSLYQPL ATRPWIQDIE GASAKDLCSA SSVVSPSPVP TGEKPCBQVQ 600
PQPNVTNTLA CPILLSNLATR LMLRNGAPVN ASASCHVLEP GDLLLVTGTO LGEFQWLSLE 660
EGPQQLVASV CEPVEVDGVA DQTEGGSVV VIISTSRVSA PAGGKASWGA DRSYWKEFLV 720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPSTR FLNGLGPPST 780
55 PLDBERGQSL SDSPGSRVP TESEKRPLSI QDSFVEVSPV CPRPRVRLGS BIRDSV

Seq ID NO: 480 DNA sequence
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Coding sequence: 58..1092

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65 ATGAGCGGCT CCAATGTCCA GCCACAGCT GCCCTGGCC AGAAGGTGAT GGAGAATAGC 240
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CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
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70 CTGCGCAGAG AGATCGAAAT CCAGGCCAC CTGCAACCAT CCAACATCCT GGTCTCTTAC 480
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Seq ID NO: 481 Protein sequence
Protein Accession #: NP_004208

85 1 11 21 31 41 51

5 MAQKENSYPW PYGRQTAPSG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60
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 QLRREIEIOA HLHHPNLRRL VNYFYDRRI YLILEYAPRG ELYKELOKSC TFDEQRTATI 180
 MEELADALMY CHGKKVIHRD IKPENLLGL KGELKIADPG WSVHAPSLRR KTMCGTLDYL 240
 PPENIEGRMH NEKVDLWICG VLCEYELLVGN PPFESASHNE TYRRIVKVDL KPPASVPTGA 300
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10 Seq ID NO: 482 DNA sequence
 Nucleic Acid Accession #: AK055663
 Coding sequence: 38..1423

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Seq ID NO: 483 Protein sequence
 Protein Accession #: BAB70980.1

60 1 11 21 31 41 51
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 ESAERFLEQP EIHTGRLLVG TFVALCFNLF TMLSRNKPF AYVSEAASTS WLQEHVADLS 180
 RSLCGIIPGL SSIFLPRMNP FVLIDLGAFA ALCITYMLIE INNYFAVDTA SAIALALMTF 240
 GTMYPMVSYS GKVLQQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GPGSLAGSVH 300
 VRIRRDANEQ MVLAEVNTNL YTLVSTLTVQ IFKDDWIRPA LLSGPFVAANV LMFSDHVVIP 360
 MPILLKGTDL NPVTSTPAKP SSPPEFSFN TPGKNVNPVI LLNTQTRPYG PGLNHGHTPY 420
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70 Seq ID NO: 484 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..900

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 ATGCCGCGGC GGGAGCTGAG CGAGGCGGAG CCGCCCGCGC TCCGGGCCCC GACCCCTCCC 60
 CCGGCGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTCTGTGT GGGCGACGGC 120
 CCGGTGGGCA AGAGCAGCCT CATGCTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCGCACTG CGCTGGACAC CTTCTGTGT ACGTACGTTA AATCGCCGCT GGGCGCGCT 240
 GGCCTGCGGG GGCCTGTGCA CGGGGAGCT GGGCGCGGG TCTCGCGGG AGGGCGCAGA 300
 GGACCCCGGG GAGGAGACTG GAGCAGGCC CGAGGTGGCG CTGGTGGGG CCAGGACGCT 360
 CTTCTAATCT CAGCTCTCC CCGCCCGGCC CCGCAGTGC AAGTCTGTGT GGATGGAGCT 420
 CCGGTGCGCA TTGAGCTCTG GGCACAGCG GGCACAGAGG ATTTTACCG ACTTCTTCC 480
 CTTTGTCTAC CGGATACGA TGTCTTCTG GCGTCTTCA GCGTGTGCA GCCCAGCTCC 540
 TTTCAAACA TCACAGAGAA ATGGCTGCCC GAGATCCGCA CGCACACCC CCAGGCGCCT 600
 GTGCTGCTGG TGGGCACCCA GGCAGACCTG AGGGACGATG TCAAGTACT AATTGAGCTG 660

GACCAGGGG GCGGAGGG CCGGTGCC CAACCCAGG CTCAGGGTCT GGCGAGAAG 720
 ATCCGAGCTT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAAGT GAAGGAAGTA 780
 TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAGGTG TGGCACCT CTCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA

Seq ID NO: 485 Protein sequence

Protein Accession #: PGENESH predicted

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPFRLAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTPSG TYVQSPVRRP GCGGAVERGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120
 LPNNGSPRPA PAVQVLVDGA PVRIELMDTA GQEDFDRLRS LCYPDTDVFL ACPVSVQPS 180
 FQNIETKWL P BIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGPVP QPQAQGLAEK 240
 IRACCYLECS ALTQKMLKEV FDSAILSAIE HKARLEKRLN AKGVRTL SRC RWKFFCFV

Seq ID NO: 486 DNA sequence

Nucleic Acid Accession #: XM_063832.2

Coding sequence: 1..711

1 11 21 31 41 51
 | | | | |
 ATGCCGCGCG GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGCGCGG GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGGAGACGG 120
 GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTCTCTCTGT CAAGTCTCTG TGGATGGAGC TCCGGTGC 240
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTGTCT CTTTGTCTAC 300
 COGATACCG ATGTCTTCTT GCGGTGCTTC AGCGTGTGTC AGCCAGCTC CTTTCAAAC 360
 ATCAGAGAGA AATGGCTGCC CGAGATCCGC ACGCACACCC CCCAGGCGCC TGTGTCTGT 420
 GTGGGCACCC AGGCCGACCT GAGGAGCAT GTCAACGTAC TAATTCAGCT GGACGAGGG 480
 GGCGGGAGG GCCCGTGCC CCAACCCAG GCTCAGGCTC TGGCCGAGAA GATCCGAGCC 540
 TGCTGTCTAC TTGAGTGCTC AGCCTTGAGC CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAACTGAA TGCCAAAGGT 660
 GTGCGCACC TCCTCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTGTGTTG A

Seq ID NO: 487 Protein sequence

Protein Accession #: XP_063832.1

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPFRLAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTPSV QVLVDGAPVR IELMDTAGQE DFDRLRLSLCY PDDTVFLACF SVVQPSFQ 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPP AQGLAEKIRA 180
 CCYLECSALT QKMLKEVPDS AILSAIEHKA RLEKGLNAGK VRTLSCRWK KPF CFV

Seq ID NO: 488 DNA sequence

Nucleic Acid Accession #: NM_014398.1

Coding sequence: 64..1314

1 11 21 31 41 51
 | | | | |
 GGCACCGATT CGGGGCTGCG CCGGACTTCG CCGCAOGCTG CAGAACCTCG CCCAGCGCCC 60
 ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
 CAGATGGGCA GTCAATAGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
 ACTGCAGCAG CACAGCTACA GGACATAAAA AAACCTGTCC AGCAACCCAGC TAAGCAAGCA 240
 CCTCACAAA CTTTAGCAGC AAGATTATG GATGGTCATA TCACCTTTCA AACACGGGCC 300
 ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA AACTGCAAC CACCAGCCCC 360
 ATTACTTACA CCGTGTCTAC AACCCAGGCC ACACCCAAACA ACTCACACAC AGCTCCTCCA 420
 GTTACTGAAG TTACAGTGGG CCCTAGCTTA GCCCCTTAT CACTGCCACC CACCATCACC 480
 CCACAGCTC ATACAGCTGG AACCACTTCA TCAACGCTG GCCACAAAC TGGGAACACC 540
 ACTCAACCCA GTAACAGAG CACCCCTTCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
 ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAAAGGC AGCTGCCACC 660
 AATAACACCC GCACAGCTGC ACCTGCCTCC ACAGTTCTCG GGCACACCTC TGCACCTCAG 720
 CCATGCTCAG TCAAGACTGG AATTATCAG GTTCTAAAGG GAAGCAGACT CTGTATAAAA 780
 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
 TACTTCAACA TCGAACCCTA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
 AACCTTCTGT TGAATTTTCA GGGGCGATT GTGAATCTCA CATTACCAA GGATGAAGAA 960
 TCATATTATA TCAAGTGAAT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
 CAAGGAATCA AACATCGGCT GGTGATGTTT CAGACAGCAG TCGGGCATT CTTCAAGTGC 1080
 GTGAGTGAAC AGAGCCTCCA GTTGTACGCC CACCTGCAGG TGAACAAAC CGATGTCCAA 1140
 CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTGCTCTGAC 1200
 TACACAATTG TGCTTCTGT GATTGGGGCC ATCGTGGTGT GTCTCTGCCT TATGGGTATG 1260
 GGTGTCTATA AAATCGGCT AAGGTGTCAA TCATCTGAT ACCAGAGAAT CTAATTGTTG 1320
 CCGGGGGGGA ATGAAATAAA TGGAAATTAG AGAACTCTT CATCCCTTCC AGGATGGATG 1380
 TTGGGAAATT CCTCAGAGT GTGGGTCTCT CAAACAATGT AAACCACTT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500
 GTTTATTTTA TGAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCTTTTA GAATATTTTA 1560
 GCCACTCAA GTCAACATT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAA TTATAAACCA AGGTCAATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680
 ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCCTTG TTATCAAATG GACTTTCACT 1740
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATAA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAG GGAGTTTAC TCTTGTCAAC 1860
 CAGGCTGGAG TCAGTGGCA CGATCTCGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAAG 1920
 TGATTTCTCT GCTTCAGCTT CCGGAGTAGC TGGGATTACA GGCACACACT ACCAGCCTG 1980
 GCTAATTTTT GTATTTTAT TATAGACGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGCG CCGGCTCTTA AATGTTTTT TTAATCATCA AAAAGAACAA CATATCTCAG 2160

5 GTTGTCTAAG TGTITTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220
CTTGATGACT CTGCTCCAG AATGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
CTAAACAATA AGCAAGAGAC AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340
TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
ACTGAGACTT AAGGGAACCTG AATCACTTAA ATGTACACCTG GCTAACTGAT GGCAGAGCCA 2460
GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTCTCCCTA CACCAAGTTA 2520
CCTACAAGAA CAATGACACC ACACCTCGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
AGCTTTGAGC ATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
10 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTGCT TAGCTGGGCT 2760
GTAAGATGA AGSCATCAAA TAAACTCAA GTATTTTTAA ATTTTTTTGA TAATAGAGAA 2820
ACTTGCTTAA CCAACTGTTC TTTCTTGAGT GTATAGCCCC ATCTTGTGTT AACTTGCTGC 2880
TTCTGCACCT CATATCCATA TTTCTTATG TTCACCTTAT TCTGTAGAGC AGCCTGCCAA 2940
15 GAATTTTAT TCTGCTGTT TTTTGTGTC TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000
AGAAAGTCC ACATAACCTC AGAATCTTCA GTCAAGGAAT AATTCAGTC AGCCTAGAGA 3060
CCATGTTGAC TTTCTCATG TGTTCCTTCA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
TAGTCTTAAT AAAACATTGA ATGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 489 Protein sequence
Protein Accession #: NP_055213.1

20 1 11 21 31 41 51
| | | | | |
25 MPROLSAAAA LPASLAVILH DGSQMRAP PETRDYSQPT AAATVQDIKK FVQOPAKQAP 60
HQTLAARFMD GHITPQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTQAT PNNSHTPFV 120
TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTTLPA TLSIALHKST 180
TGKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNSRLCICA 240
EMGIQLIVQD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLLNPGGPFV NLFTTDEES 300
YVISVGAYL TVSDPETVYQ GIKHAVVMFO TAVGHSFKCV SEQSLQLSAE LQVKTIDVQL 360
30 QAFDFEDDFH GNVDECSSDY TIIVLPVIGAI VVGLCLMGAG VYKIRLRQCS SGYQRI

Seq ID NO: 490 DNA sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

35 1 11 21 31 41 51
| | | | | |
40 TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
TTGGCTGTGA TATGTGTGTC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
ATAATGTACC CAGTAACAAA CTGTGACAAA ATAGAAGTGA TTATTACCTC GAAAGAAAAAT 300
AAAGGACAAAC GATGCTTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGATT 360
45 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420
AACCTAGAAC AAGTTTAACT GTGACTACTG AATGACAAG AATTCTACAG TAGGAAACTG 480
AGACTTTTCT ATGGTTTGTG GACTTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCTGGAAT GAATGACRAAT CAGAATTCCA 600
CTGCCCAAGG GAGTCCAGCA ATTAATATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
50 GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTTGTATT ATACATTCTAT 720
GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
GAGAAACATT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
CTGTGGTTAC AGTGAGAGCA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
CATCTATGTG TGTAAAGCA TTCTTCAAC ATTTTTCAT GCAAATACAC ACTTCTTTCC 960
55 CCAAAATATCA TGTAGCACA CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
TTTATAACCA AATCTTAAAT TGTAAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
TGGGATCTG GCAACAGTGC ACATATTCCA TAACCAAAAT AGCAGCACC GTCTTAATTT 1140
GATGTTTTTC AACTTTTATC CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAT 1200
TGTACTTTTT GTTTGTATCC GTTTGTATTA ATGATAGCAA TATCTTGGAC ACATTTGAAA 1260
TACAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAAT TATACCTAGC 1320
60 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
TTGTTATGTC CTATATATCTG TAAAATTTAG GTATACTCAA GACTAGTTTA AAGAAATCAA 1440
GTCAATTTTT TCTCTAATAA ACTACCACAA CCTTCTTTTT TTAATAAAAA AAA

Seq ID NO: 491 Protein sequence
Protein Accession #: NP_005400.1

65 1 11 21 31 41 51
| | | | | |
70 MSVKGMAIAL AVILCATVVQ GPFMPKRGRC LCIGPGVKAV KVADIEKASI MYPNNNDKRI 60
EVIITLKENK GQRCLNPKSK QARLIIEKVE RKNF

Seq ID NO: 492 DNA sequence
Nucleic Acid Accession #: NM_000577.1
Coding sequence: 41..520

75 1 11 21 31 41 51
| | | | | |
80 GGCACGAGGG GAAGACCTCC TGTCTTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
CCGACCTCTT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAATGT 180
CAATTAGAAA GAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCTTT 360
CATCGCTCA GACATGGGCC CCACCACAG TTTTGTAGTCT GCGGCTGCCC CCGGTTGGTT 420
85 CCTCTGCACA CGCATGGAAG CTGACCAGCC CGTCAACCTC ACCAATATGC CTGACGAAGG 480
CGTCATGTGC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCAGC GCCTGCCTGT 540
TCCCATTTCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCGTGCCTCC AGGGCTCCCG 600

GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
 CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCAGAAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTGSCA CAAAGCCCTT CCATGTGCGC 780
 TCTGCATTCA GGATCAAACC CCGACCACCT GCCCAACCTG CTCTCTCTT GCCACTGCGT 840
 5 CTCTCTCCCT CATTCACCT TCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCA 900
 ACCAAGTGGC TCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
 TTTAAGSGTT TGTGAAAAT GAAAATTAGG ATTTTCATGAT TTTTTTTTTT CAGTCCCGT 1020
 GAAGGAGAGC CCTTCATTG GAGATTATGT TCTTTGGGG AGAGGCTGAG GACTTAAAA 1080
 ATTCTGCAAT TGTGAAAAT ATGGTGAAG TAAGTGGTAG CTTTCCCTT CTTTCTTC 1140
 10 TTTTTTTGTT ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
 ATTTTTTTTT TCCTTTTAAA ACACCTCCAT AATCTGGACT CCTCTGTCCA GGCAGTCTGT 1260
 CCCAGCTCC AAGCTCCATC TCCACTCCAG ATTTTITACA GCTGCTGCA GTACTTTACC 1320
 TCCTATCAGA AGTTTCTCAG CTCCTAAGGC TCTGAGCAAA TGTGGCTCT GGGGGTCTT 1380
 TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTCTG GCACTTGGAG 1440
 15 ACTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
 GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
 CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAAT TCCTACTTTC 1620
 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAATAA GCCTAAAAAA AAAAAA 1680
 20 AAAAAA AAAAAA AAAAAA AAAAAA

Seq ID NO: 493 Protein sequence
 Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGFNVNLE EKIDVVPPIEP 60
 HALFLGHHG KMCLSCVKSG DETRLQLEAV NITDLSENK QDERFAFIRS DSGPTTSPES 120
 AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDF

Seq ID NO: 494 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

1 11 21 31 41 51
 GGCTGCCCGA GCGAGCGTTC GGACCTGCA CCGCGCGCGC CCGCGCGCGC CGCGCGCGCC 60
 GGCTTTTGTGT GTCTCCGCTT CCTCGCGCGC CGCGCGCTCT GGACCGGAG CGCGCGCGCG 120
 CGGACCTTGG GCTCTGCGCT TCGCGGGCGG GAACCTGCGA GGACCGGCGC AGGATCCGAG 180
 AGAGGCGCGG GCGGGTGGCC GGGGGGCGCG CCGGCGCGCG CATGGAGCTC CGGGCGCGAG 240
 40 GCTGGTGGCT GCTATGTGCG GCGCGAGCGC TGGTGGCTGT CGCGCGCGG GACCGGCGCA 300
 GCAAGAGCGG GAGCTGCGGC GAGGTCCGCC AGATCTACGG AGCCAAGGCG TTGAGCTCTGA 360
 GCGAGCTGCC CCAGCGGAG ATCTCGGGTG AGCACTTGG GATCTGTCCC CAGGGCTACA 420
 CCTGCTGCAC CAGCGAGATG GAGGAGAAC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 CCGCGCTCGG GGACAGCAGC CGCGTCTTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540
 45 TCGATGACCA CTGCTGACAC CTGCTGAACG ACTCGAGCG GACGCTGCAG GCCACCTTCC 600
 CCGGCGCTTT CCGAGAGCTG TACAGCAGA ACGGAGGGC CTTCCGGGAC CTGTACTCAG 660
 AGCTGCGCCT GTACTACCGG GGTGCCAAC TGCACCTGGA GGAGACGCTG GCGGATCTCT 720
 GGGCGCGCTT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCTCTGATG 780
 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGCGCTGCGG GCGCTTGGGG GAGGCGCGCA 840
 50 GAGAGCTGCG CCGCGGGGCC ACCCGTGCCT TGGTGGCTGT TGGTGGCTTT GTGCGAGGCC 900
 TGGGCGTGGC CAGCGAGCTG GTCCGGAAG TGGCTCAGGT CCGCTTGGGC CCGGAGTGTCT 960
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCTT GGGAGTCCCC GCGCGCAGGC 1020
 CCTGCCCTGA CTATTGCGGA AATGTGCTCA AGGGCTGCCT TGCCAACCG GCGGACCTGG 1080
 ACGCGAGTGT GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140
 55 CATCGGCTGT CAGGAGTGTG ATCGGAGCG TGACACGCTG GCTGGGCGAG GCCATCAAG 1200
 CCTCCAGGA CAACAGGGAC ACGCTCAGCG CCAAGGTCTT CCAGGGCTGC GGGAAACCCA 1260
 AGGTCAACCC CCAGGGCCCT GGGCTGAGG AGAAGCGCG CCGGGCAAG CTGGCCCGCG 1320
 GGGAGAGGCC ACCTTCAGGC ACGCTGGAGA AGCTGGTCTC TGAAGCTAAG GCCCAGCTCC 1380
 GCGACGTCGA GGACTTCTGG ATCAGCTTCC CAGGGCACT GTGCACTGAG AAGATGGCCC 1440
 60 TGAGCACTGC CAGTGTATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCGCG TACCTCCCCG 1500
 AGGTATGGG TGAAGGCTG GCCAACAGA TCAACAACCC CGAGGTGGAG GTGGACATCA 1560
 CCAAGCCGGA CATGACATC CCGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCGGC 1620
 TCGCAGCGC CTACAACGG AACGAAGTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG 1680
 GCTCGGCGAG CGGTGATGGC TGTCTGGATG ACCTCTGCG CCGGAAGGTC AGCAGGAAGA 1740
 65 GCTCCAGCTC CCGGAAGCCC TTGACCCATG CCCTCCAGG CCTGTGAG CAGGAAGGAC 1800
 AGAAGACCTC GGTCTCCAGC TGCCCCAGC CCGGACCTT CTCTCTGCCC CTCTCTCTCT 1860
 TCTTGGCCCT TACAGTAGCC AGGCCCGGT GGGGTAACT GCCCAAGGC CCCAGGACA 1920
 GAGGCCAAGG ACTGACTTTG CCAAAATAC AACACAGAAG ATATTTAAT CACTCAGCC 1980
 TGGAGAGGCC TGGGGTGGGA CAGGGAGGCG CGCGGCTCT GAGCAGGGCG AGGCGCAGAG 2040
 70 GTCCAGCCC CAGGCTGGC CTGCGCTGCC TTTCTGCTT TTAATTTTGT ATGAGGTCTT 2100
 CAGGTGAGCT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCAAC 2160
 TCCGGCTGCC TAGCCCTTCC CCCAGCTCCC TGCAAGCGG CAGAAGCAGC CCCTGAGGC 2220
 CTACAGAGGA GGCCTCAAAG CAACCGCTG GAGCCACAG CGAGCTGTG CCTTCTCTCC 2280
 OGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACAGCC AGCCCTGGCC CACCCCCAG 2340
 75 CCTCCAGAGA AGCCCGCAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400
 TCTGAGATGA TGCATGATGC CCTCCCTCA GCGCAGGCTG CAGAGCCCGG CCCCACCTCC 2460
 CTGCGCCCTT GAGGGGCCCC AGGCTGTGCA GGGTGACGCC TGAGACAGCA CCACTGTCTGA 2520
 GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCAGTGAAG GGCCTCCAT GCGCAGATGA 2580
 GGGGCACTG ACCACCTGCT GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAG 2640
 80 GGAGGAGCG TGGCTCTGCT CAATGTGGGC TGCCCTCGC ACACAGGGCT CACAGGGCAG 2700
 GCCTTGTCTG GGTCCAGGGC TGTGGAGGA CCGCGAGGCG TGAGGAGCAG CCAGGACCCG 2760
 CCTGTCTCCA TCCTCACCCA GATCAGGAAC CAGGGGCTCC CTGTTCAAG TGACACAGGT 2820
 CAGGGCTCAG AGCTGTCTCT GCGTGTCAAG TGTCTCAGG GATGCTGGTG GCTGGTGA 2880
 CCGCGCACTG CACACGGGAA TGCTTAGTCT CCTTCCGAC CCAGCCAGCT GCACTGCAAG 2940
 85 GCAAGGGAC CTGATAGTT AAGGGCTTTT CCAACATGAC ATCCATTAC TGACACTTCC 3000
 TGTCTTGTG CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTGGAGGC CCGCAGGGCC 3060
 CACCTTGAGC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGGCC TGCCCCAGGC 3120

5 CTGAGCGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180
TGTGGTGTG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGCTCTG GGGGCAGCTG 3240
TCCTGAACCG ACTGACCCCTG AGGAGGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCCTCC 3300
CGCACAGTGG ACGGAGGTCC CGGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360
CTGACTTTAG ATGTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
CCTGCCAGT GCCAGGGTGG GCTGGGACT CTGGCACAGT GATGCGGGC GCCAGGACAG 3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTAC TGGTCAGGGC AGTGGCCAAG CTTGCTGTGT 3600
10 CCTTCTCCA CAAGGTCCCC CCACCGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTTGG 3660
TCCTGTATG AATAAAGGC TGAACCTA AA

Seq ID NO: 495 Protein sequence
Protein Accession #: NP_002072.1

15 1 11 21 31 41 51
| | | | | |
MELRARGWNL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSLDPV QAEISGEHLR 60
ICPGYTCCT SEMEENLANR SHALETALR DSSRVLAQML ATQLRSPDDH PQHLNDSESR 120
20 TLQATPFGAF GELYTQARA FRDLYSELRL YRGNLHLE ETLAEFWARL LERLFKQLHP 180
QLLLPDDYLD CLGQAQALR PFGEAPRELRL LRATRAFVAA RSPVQGLGVA SDVVRKVAQV 240
PLGPECSRVA MLYVYCAHCL GVPGARPCPD YCRNVLKCL ANQADLDAEW RNLLDSMVLII 300
TDFKFWGTSV ESVGTSVETW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 360
RGKLAPRERF PSGLTEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMAALSTA SDDRWNWMA 420
25 RGRYLPVWNG DGLANQINNRP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDPDQD 480
ASDDGSGSGS

Seq ID NO: 496 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

30 1 11 21 31 41 51
| | | | | |
GGGGCAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCAGAGCA 60
AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCCTTCAAA 120
35 GGGGTCTGGA CTCAGCTTTT CTGGAAGGCA GTCACAGCGG AATTTCTGGC CATGCTTATT 180
TTTGTCTCCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
GTGACATGG TTCTCATCTC CCTTTGCTTT GGAATCAGCA TTGCAACCAT GGTGCACTGC 300
TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCAAC 360
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45 GAAAACCATT GGATATATTG GGTGGGCCCC ATCATAGGAG CTGTCTCTCG TGGTGGCCTT 780
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50 CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCTCTAG ATTTCTCTCC ACCCATTAA 1080
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Seq ID NO: 497 Protein sequence
Protein Accession #: NP_001641.1

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| | | | | |
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65 AQCLGAIIGA GILYLVTPPS VVGLGVMTV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
KRTDVTGSIA LAIGFSVAIG HLPALNTGA SMNPARSFGP AVIMGNWENH WIYWVGPIIG 240
AVLAGGLYBY VFPCPDVEFKR RFKEAPSKAA QQTKGSYMEV EDNRSQVETD DLILKPGVVH 300
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Seq ID NO: 498 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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CAGCCAGGA GAGGAGCTCT GGCAGGCTTC TTCAGATTG TGGCCACTGT TTCTCATTTG 3480
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TAGGGAGGCC AGTTTGGAGC AGAGGCGCTGA AGGTCCCTGC TATGCAGCGG TGGCCACAGC 4020
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TTGCTACAC ATTTTCGAAA ACAGAGTTGG GGCTGTATT CTTTAAAGAG ATAAGCTCT 4260
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Seq ID NO: 499 Protein sequence
Protein Accession #: BAA74900.1

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1 11 21 31 41 51
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PLVINTLKRF NLYPEVILAS WYRIYTKIMD LIGIQTKICW TVTRGEGLSP IESCBGLGDP 60
ACFPVAVIFI LNLGMMALFF IYGTLYSGSR LGGLVTVLCF FPNHGECTRV MWTPLPRESP 120
SYFPLVLQML LVTHILRATK LYRGSLLALC ISNVFFMLPW QFAQFVLLTQ IASLFAVYVV 180
GYIDICKLRK IYIHIMSLA LCFVLMFGNS MLLTSYASS LVIIWGLIAM KPHFLKINVS 240
ELSLWVIQGC PWLEGTIVLK YLTSKIPGIA DDAHIGNLLT SKFPYSYKDFD TLLYTCAAEF 300
DFMEKETPLR YTKLTLPLVV LVVPVAIVRK IISDMWGLVA RQQTTHVRKHQ FDHGLVYHA 360
LQLLAYTAGL ILIMRLKPLF TPHMCMVASL ICSROLPGWL PCKVHPGATV FAILAAMSIQ 420
GSANLQTQWN IVGEFSNLPO EELIEWIKYS TKPDAVFAGA MPTMASVKLS ALRPIVNHPEH 480
YEDAGLRART KIVYSMSYRK AAEEVKRELI KLKVNYYILE ESWCVRRSKP GCSMPEDWDV 540
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Seq ID NO: 500 DNA sequence
Nucleic Acid Accession #: NM_001276.1
Coding sequence: 127..1278

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GCCAGAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGCT GCTCCAGTGC 180
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GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGG ATGATGTGAC GCTCTACGGC 360
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CCCCCTCTGG CTCCAGCTGG CCGGAGCGCT GATCACTGCG CTGCTGAGT CCCAGGCTGA 1380
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ACTTCCCTCT CCTAATTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAAC AGTGTGTTGG 1800
CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCGCCCATC 1860
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Seq ID NO: 501 Protein sequence
Protein Accession #: NP_001267.1

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ISNDHIDTWE WNDVTLYGML NTLKRNPNL KTLISVGGWN PGSQRFPSKLA SNTQSRRTFI 120
KSVPPPLRTH GFDGLDLAWL YPGRRDKQHF TTLIKEMKAE FIKEAQPGKK QLLLSAALSA 180
GKVTIDSSYD IAKISQLDF ISIMTYDFHG AWRGTTGHHG PLFRGQEDAS PDRPSNTDYA 240
VGVMLRLGAP ASKLVGMGIP FGRSFTLASS ETGVGAPISG PGIPGRPTKE AGTLAYYRIC 300
DPLRGATVHR TLQQQVPIAT KGNQWVGYYD QESVKSIVQY LKDRQLAGAM VMLDLDDPQ 360
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Seq ID NO: 502 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

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TTCCCCCAGC TCAGAACTCT GCTGCTCGGC CCCGAGGAGA GCAACAATC AACCGGAAAG 180
ATGTGGAAGG TGTCACTCT GCTCTTGGT TTGGGAAGCG CGTGCCTGT GGTCTGGGCA 240
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GCCATCGGTT TCATTGGTGG AATCATGCTT GTGGTTATGC GAAAAATGTC GGGAAAGGTAC 660
TCGCCCTAAA AAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACGCT 720
TTCGACTCT GTGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCCCT GGAACATTGT 780
CGGGCCCAAT CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840
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Seq ID NO: 503 Protein sequence
Protein Accession #: NP_006465.1

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KSLGLTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVVDGDTQTT 120
VERDGLSTVT LVGIIVGVLL AIGFIGGIIV VVMRKMSGRY SP
  
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Seq ID NO: 504 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

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CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCCAG 180
AGAAGCAGCG TCTGGCAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT 240
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	TGTCGTGCT	GCTGGATGGA	TGGCTAAGGG	CAGAGTTGGA	TACCCCATG	TGAAGCCAGG	360
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	TGAAAGATGG	GATGCCTATT	GCTACAAACC	ACACGCAAGG	GAGTGTGGTG	GGGCTCTTAC	480
5	AGATCCAAAG	CAATTTTAA	AATCTCCAGG	CTTCCCAAT	GAGTACGAAG	ATAACCAAT	540
	CTGCTACTGG	CACATTAGAC	TCAAGTATGG	TCAGCGTATT	CACCTGAGTT	TTTTAGATT	600
	TGACCTTGAA	GATGACCCAG	GTGTCTGGC	TGATTATGTT	GAAATATATG	ACAGTTACGA	660
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10	CCAAATCAA	TATGTTGCAA	TGGATCCTGT	ATCCAAATCC	AGTCAAGGAA	AAAAACAAG	840
	TACTACTTCT	ACTGGAATA	AAAACCTTTT	AGCTGGAAGA	TTTAGCCACT	TATAAAAAA	900
	AAAAAAGGA	TGATCAAAAC	ACACAGTGT	TATGTTGGAA	TCCTTTGGAA	CTCCTTTGAT	960
	CTCACTGTTA	TTATTAACAT	TTATTTATTA	TTTTTCTAAA	TGTGAAAGCA	ATACATAATT	1020
	TAGGGAAT	TGGAAATAT	AGGAACTTT	AAACGAGAAA	ATGAAACCTC	TCATAATCCC	1080
	ACTGCATAGA	AATAACAAGC	GTTAACATTT	TCATATTTT	TTCTTTTCAGT	CATTTTTCTA	1140
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	TCATTGATTA	TTCTACAAA	ACATGATTTT	AAACAGCTGT	AAAATATTCT	ATGATATGAA	1320
	TGTTTATGTC	ATTATTTAAG	CCTGTCTCTA	TTGTGGAAT	TTCAGTTCAT	TTTCATAAAT	1380
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Seq ID NO: 505 Protein sequence
Protein Accession #: Eos sequence

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	EGGHLATYKQ	LEAARKIGFPH	VCAAGWMAKG	RVGYPIVKPG	PNCXFGKTGI	IDYGIRLNRS	120
	ERWDAYCYNP	HAKCCGVFT	DPKQIFKSPG	PFNEYEDNQI	CYWHIRLKYG	QRIHLSFLDP	180
30	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELFPDDIIS	TGNVMTLKFL	SDASVTAGGF	240
	QIKYVAMDPV	SKSSQKNTS	TTSTGNKNFL	AGRPSHL			

Seq ID NO: 506 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

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40	GGGGAITCAA	GGATGGAATT	TTTCATAACT	CCATATGGCT	TGAACGAGCA	GCCGGTGTGT	180
	ACCACAGAGA	AGCAGCGTCT	GGCAAATACA	AGCTCACCTA	CGCAGAAGCT	AAGGCGGTGT	240
	GTGAATTGGA	AGGCGGCCAT	CTCGCAACTT	ACAAGCAGCT	AGAGGCAGCC	AGAAAAATTG	300
	GATTTTCATGT	CTGTGCTGCT	GGATGGATGG	CTAAGGGCAG	AGTTGGATAC	CCCATTTGTA	360
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45	ATAGGAGTGA	AAGATGGGAT	GCCTATTGCT	ACAAOCCACA	CGCAAAGSAG	TGTGGTGGCG	480
	TCTTTACAGA	TCCAAGCGGA	ATTTTAAAT	CTCCAGGCTT	CCCAAATGAG	TACGAAGATA	540
	ACCAAATCTG	CTACTGGCAC	ATTAGACTCA	AGTATGGTCA	GCGTATTCAC	CTGAGTTTTT	600
	TAGATTTTGA	CCTTGAAGAT	GACCCAGGTT	GCTTGGCTGA	TTATGTTGAA	ATATATGACA	660
	GTTACGATGA	TGTCCATGGC	TTTGTGGGAA	GATACTGTGG	AGATGAGCTT	CCAGATGACA	720
50	TCATCAGTAC	AGGAATGTCT	ATGACCTTGA	AGTTTCTAAG	TGATGCTTCA	GTGACAGCTG	780
	GAGGTTTCCA	AATCAAATAT	GTTGCAATGG	ATCCTGTATC	CAAATCCAGT	CAAGGAAAAA	840
	ATACAAGTAC	TACTTCTACT	GGAAATAAAA	ACTTTTTAGC	TGGAAGATTT	AGCCACTTAT	900
	AAAAAATAAA	AAGGATGATC	AAAACACACA	GTGTTTATGT	TGGAATCTTT	TGGAATCCTC	960
	TTGATCTCAC	TGTTATTATT	AACATTTATT	TATTATTTTT	CTAAATGTGA	AAGAAATACA	1020
55	TAAATTAGGG	AAATTTGGA	AATATAGGAA	ACTTTAAACG	AGAAAAATGAA	ACCTCTCATA	1080
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60	ATGAATGTTT	TATGCAATTAT	TTAAGCCTGT	CTCTATTGTT	GGAAITTCAG	GTCATTTTCA	1380
	TAAATATTGT	TGCAATAAAT	ATCCTTCGGA	ATTC			

Seq ID NO: 507 Protein sequence
Protein Accession #: NP_009046.1

	1	11	21	31	41	51	
65							
	MIILYLFLL	LWEDTQGWGF	KDGIFHNSIW	LERAAGVYHR	EARSQKYKLT	YAEAKAVCEP	60
	EGGHLATYKQ	LEAARKIGFPH	VCAAGWMAKG	RVGYPIVKPG	PNCXFGKTGI	IDYGIRLNRS	120
70	ERWDAYCYNP	HAKCCGVFT	DPKQIFKSPG	PFNEYEDNQI	CYWHIRLKYG	QRIHLSFLDP	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELFPDDIIS	TGNVMTLKFL	SDASVTAGGF	240
	QIKYVAMDPV	SKSSQKNTS	TTSTGNKNFL	AGRPSHL			

Seq ID NO: 508 DNA sequence
Nucleic Acid Accession #: NM_001044.1
Coding sequence: 129..1991

	1	11	21	31	41	51	
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	AAAGCCAGG	CCGCGGGCGC	CAGACCAAGA	GGGAAGAAGC	ACAGAATTCC	TCAACTCCCA	120
	GTGTGCCCAT	GAGTAAGAGC	AAATGCTCCG	TGGGACTCAT	GTCTTCCGTG	GTGGCCCCGG	180
	CTAAGGAGCC	CAATGCCGTG	GGCCCGAAGG	AGGTGGAGCT	CATCCTTGTC	AAGGAGCAGA	240
85	ACGGAGTGCA	GCTCACCAGC	TCCACCCCTCA	CCAACCCCGC	GCAGAGCCCC	GTGGAGGCCC	300
	AGGATCGGGA	GACCTGGGGC	AAGAAGATCG	ACTTTCTCCT	GTCCGTTCATT	GGCTTTGCTG	360
	TGGACCTGGC	CAACGCTCGG	CGGTTCCCTT	ACCTGTGCTA	CAAAAAATGGT	GGCGGTGCTT	420

	TCCCTGGTCCC	CTACCTGCTC	TTTCATGGTCA	TTGCTGGGAT	GCCACTTTTC	TACATGGAGC	480
	TGGCCCTCGG	CCAGTTCAC	AGGGAAGGGG	COGCTGGTGT	CTGGAAGATC	TGCCCCATAC	540
	TGAAAGGTGT	GGGCTTCACG	GTTCATCTCT	TCTCACTGTA	TGTGGGCTTC	TTCTACAAAG	600
5	TCACTATCGC	CTGGGGCTGT	CACATCTCT	TCTCTCTCT	CACCAAGGAG	CTCCCCGGA	660
	TCCACTGCAA	CACTCTCTGG	AACAGCCCCA	ACTGCTCGGA	TGCCCATCCT	GGTGACTCCA	720
	GTGGAGACAG	CTCGGGCTTC	AACGACACTT	TTGGGACCAC	ACCTGCTGCC	GAGTACTTTG	780
	AACGTGGCGT	GCTGCACCTC	CACCAAGACC	ATGGCATCGA	CGACCTGGGG	CCTCCGCGGT	840
	GGCAGCTCAC	AGGCTGCTGT	GTGCTGGTCA	TGCTGCTGCT	CTACTTCAGC	CTCTGGGAAG	900
10	GGGTGAAGAC	CTCAGGGAAG	GTGGTATGGA	TCACAGCCAC	CATGCCATAC	GTGGTCTCTA	960
	CTGCCCTGCT	CCTGGGTGGG	GTACCCCTCC	CTGGAGCCAT	AGACGGCATC	AGAGCATACC	1020
	TGAGGGTGA	CTTCTACCGG	CTCTGGGAGG	CGTCTGTTTG	GATTGACGGG	GCCACCCAGG	1080
	TGTGCTTCTC	CCTGGGCGTG	GGGTTGCGGG	TGCTGATCGC	CTTCTCCAGC	TACAAACAGT	1140
	TCACCAACAA	CTGCTACAGG	GACGCGATTG	TCACCACTCC	CATCAACTCC	CTGACGAGCT	1200
15	TCTCTCTCGG	CTTCTCTCTC	TTCTCTCTCC	TGGGGTACAT	GGCACAGAAG	CACAGTGTGC	1260
	CCATCGGGGA	CGTGGCCAAG	GACGGGCCAG	GGCTGATCTT	CATCATCTAC	CCGGAAGCCA	1320
	TGCGCAAGCT	CCCTCTGTCC	TCAGGCTGGG	CGGTGGTCTT	CTTCATCATG	CTGCTCACCC	1380
	TGGGTATCGA	CAGGCGCATG	GGTGGTATGG	AGTCACTGAT	CACCGGGCTC	ATCGATGAGT	1440
	TCCAGCTGCT	GCACAGACAC	CGTGAGCTCT	TCACTGCTCT	CATGCTGCTG	GCGACCTTCC	1500
20	TCTGTCCCTT	GTCTCTGCTC	ACCAACGGTG	GCATCTACGT	CTTCACGCTC	CTGACCAATT	1560
	TTGCGAGCCG	CACGTCCATC	CTCTTTGGAG	TGCTCATCGA	AGCCATCGGA	GTGGCCTGGT	1620
	TCTATGGTGT	TGGGAGTTCG	AGGAGACACA	TCCAGCAGAT	GACCGGGCAG	CGGCCAGGCC	1680
	TGTACTGGTG	GCTGTGCTGG	AAGCTGGTCA	GCCCCGCTTT	TCTCTGTGTC	GTGGTCTGTG	1740
	TCAGCATTTG	GACCTTCAGA	CCCCCCCACT	ACGGAGCCTA	CATCTTCCCC	GACTGGGCCA	1800
25	ACGCGCTGGG	CTGGGTCATC	GCCACATCCT	CCATGGCCAT	GGTGCCCATC	TATGCGGCTT	1860
	ACAAGTTCTG	CAGCTTGCCT	GGGTCTCTTC	GAGAGAAATC	GGCCTACGCC	ATTGCACCCG	1920
	AGAAGGACCG	TGAGCTGGTG	GACAGAGGGG	AGGTGCGCCA	GTTCAAGCTC	CGCCACTGGC	1980
	TCAGGTGTGA	GAGGAGCAG	AGAAGAAAGC	CCAGGAAGT	CATCTGCAAA	TGGGAGAGAC	2040
	ACGAACAAC	CAAGAAATC	TAAAGTTTGA	GAGAAAGGAG	GGCACTTCT	ACTCTTCAAC	2100
30	CTCTACTGAA	AACCAAAACA	ACAAAGCAGA	AGACTCTCTT	CTTCTGACTG	TTTACACCTT	2160
	TCCGTGCGCG	GAGCGCACCT	CGCCGTGTCT	TGTGTGTCTG	TAATAAGCAC	GTAGATCTGT	2220
	GCAGCGAGGT	CCACCCCGTT	GTGTCTCCCTG	CAGGGCAGAA	AAAGCTCTAA	CTTCATGCTG	2280
	TCTGTGTGAG	GCTCTCTCTC	TCCCTGCTCC	CTGCTCCCGG	CTCTGAGGCT	GCCCCAGGGG	2340
	CACGTGTGTC	TCAGGCGGGG	ATCAGATCC	TTGTAGACGC	ACCTGCTGAG	AATCCCGGTG	2400
35	CTCACAGTAG	CTTCTAGAC	CATTTACTTT	GCCCATATTA	AAAAGCCAAG	TGTCTCTGCT	2460
	GGTTAGCTG	TGAGAAAGGT	GAAATGGAGG	AAACCAACAA	TTATGCAAA	GTCTTTTCCC	2520
	GATGCGTGGC	TCCAGCAGA	GGCCGTAAAT	TGAGCGTTCA	GTTGACACAT	TGCACACACA	2580
	GTCTGTTCAG	AGGCATTGGA	GGATGGGGGT	CCTGGTATGT	CTCACCAGGA	AATTCTGTTT	2640
	ATGTTCTTGC	AGCAGAGAGA	AATAAACTC	CTTGAACCA	GCTCAGGCTA	CTGCCACTCA	2700
40	GGCAGCTGTT	GGGTCTCTGT	GGTGTAGGGA	ACGGCTGAG	AGGAGCGTGT	CCTATCCCCG	2760
	GAGCATGCA	GGGCCCCAC	AGGAGCGTGT	CCTATCCCCG	GAGCATGCA	GGGCCCCAC	2820
	AGGAGCATGT	CCTATCCCCG	GAGCATGCA	GGGCCCCAC	AGGAGCGTGT	ACTACCCAC	2880
	AAGCATGCA	GGGCCCCAC	AGGAGCGTGT	ACTACCCAC	GAGCATGCA	GGGCCCCAC	2940
	TGGAGCGTGT	ACTACCCAC	GAGCATGCA	GGGCCCCAC	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCGAGCGC	CTGACGGGCC	CCCACAGGAG	CGTGACTAC	CCCAGGAGCG	ATGACGGGCC	3060
	CCCACAGGAG	CGTGACTAC	CCCAGGAGCG	ATGACGGGCC	CCCACAGGAG	CGTGACTAC	3120
	CCCAGGAGCG	ATGACGGGCC	CCCAGGAGCG	CAGCCTGCAG	ACCAACACTC	TGCCCTGGCT	3180
	TGAGCGGTGA	CCTCAGGAA	GGGACCCAC	TGGAATTTTA	TTTCTCTCAG	GTGCGTGCCA	3240
	CATCAATAAC	AACAGTTTTT	ATGTTTGGGA	ATGGCTTTTT	AAAATCATAT	TTACCTGTGA	3300
50	ATCAAAACAA	ATTCAAGAA	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTTTG	3360
	TTTACAGAA	TAATTAGCAA	TACTGAGTGA	AGGATGTTGG	CCAAAGCTGT	CTTTCCATGG	3420
	CACACTGGCC	TCTGCCACTG	ACAGGAAAGT	GGATGCCATA	GTTTGAATTC	ATGCTCTCAAG	3480
	TOGGTGGGCC	TGCTACCTGT	CTGCGCGAGG	GCAGGGGCCG	TGCAGGGCCA	GTCTATGGCTG	3540
	TCCCTTGCAA	GTGGACGTGG	GCTCCAGGGA	CTGGAGTGTA	ATGCTCGGTG	GGAGCCGTCA	3600
55	GCCTGTGAAC	TGCCAGGCGC	CTGCAGTTAG	CACAGAGGAT	GGCTTCCCCA	TTCCTTCTG	3660
	GGGAGGGACA	CAGAGACCGG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAATC	AGCACAGAGA	3720
	CGGCTTCCG	CATTGCTCTC	TGGGGAGGGA	CACAGAGGAT	AGTTTCCCCA	TGCGCTTCTG	3780
	GTGTGTTAAG	ACAGCACAGA	GAGCGGCTTC	CCCATCGCCT	TCTGGGAGG	GGCTCCGTGT	3840
	AGCAACCCAG	GTGTGTTCCG	TGTCTGTTGA	CCAATCTCTA	TTGAGCATCG	TGTGGGTCCC	3900
60	TAAACCAAT	AAAGACATC	CACAATGGA	AAAAAAAAG	GAATTC		

Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

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	MSKSKCSVGL	MSSVVAPEKE	PNAVGPKEVE	LILVKEQNGV	QLTSSTLTNP	RQSPVBAQDR	60
	ETWGGKIDPL	LSVIGFAVDL	ANVWRFPYLC	YKNGGGAFLV	PYLLFWVIAG	MPLPYMELAL	120
	GQFNREGAAG	VWIKICPILKG	VGPTVILISL	YVGFYINVII	AWALHYLPSS	FTTELPWIHC	180
70	NNSWNPNPNC	DAHFGDSSGD	SSGLNDTFTG	TPAAEYFERG	VLHLHQSHGI	DDLGPFRWQL	240
	TACLVLVIVL	LYFSLWKGVK	TSGLVWNITA	TMPIYVLTAL	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV	WIDAATQVCF	SLGVGPVGLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
	GFVVPSFLGY	MAQKHSVPFG	DVARDGPGLI	FIIYPEALAT	LPLSSANAVV	PFIMLLTLGI	420
	DSAMGMESV	ITGLIDEPQL	LHRHRELFTL	FIVLATFLLS	LPCVTNGGIY	VFTLLDHFAA	480
75	GTSLFGLVLI	EAIGVAVFYG	VGQFSDDIQQ	MTGQRPSLYW	RLCNKLVSPC	FLLFVVVVS	540
	VTFRPFYGA	YIFPDWANAL	GWVIATSSMA	MVPIYAAYKF	CSLPGPSFEX	LAYALAPEKD	600
	RELVDREGEV	QFTLRHRLKV					

Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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85	AGCCCTTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240

	AGTGAAGAG	ATTACCCAG	AGAGGAGGAT	CCACCCCGAG	AGGAGGATCT	ACCTGGAGAG	300
	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCAGC	420
5	AATAATGCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGGGAC	480
	CCGCCCCG	CCCGGGTGTC	CCCAGCCTGC	GCGGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCCAGC	TGCGCGCCTT	CTGCCCCGCC	CTGCGCCCCC	TGGAATCCTT	GGGCTTCCAG	600
	CTCCCGCCGC	TCCCAGAACT	GCGCCTGCGC	AACAATGGCC	ACAGTGTGCA	ACTGACCCCTG	660
	CCTCCTGGGC	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGGCTCT	GCAGCTGCAT	720
10	CTGCACTGGG	GGGCTGCAGG	TGCTCCGGGC	TGGAGCACAC	CTGTGGAAAG	CCACCGTTTC	780
	CCTGCCGAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCTTG	840
	GGGCGCCCGG	GAGGCTTGGC	CGTGTGGGCC	GCCTTTCTGG	AGGAGGGCCC	GGAGAAAAC	900
	AGTGCCCTATG	AGCAGTTGCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
	CAGGTCCAGT	GACTGGACAT	ATCTGCACTC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
15	TATGAGGGGT	CTCTGACTAC	ACCGCCTGT	GCCAGGGGTG	TCATCTGGAC	TGTGTTTAAC	1080
	CAGACAGTGA	TGCTGAGTGC	TAAGCAGCTC	CACACCTCTT	CTGACACCCT	GTGGGGACCT	1140
	GGTGACTCTC	GGCTACAGCT	GAACCTCCGA	GCGAGCGAGC	CTTTGAATGG	GCGAGTGATT	1200
	GAGGCTCCTC	TCCCTGCTGG	AGTGGACAGC	AGTCTCGGG	CTGCTGAGCC	AGTCCAGCTG	1260
	AATTCTGTCC	TGGCTGCTGG	TGACATCCTA	GCCCTGGTTT	TTGGCCTCCT	TTTGTCTGTC	1320
20	ACCAGCGTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCAC	GAAGGGGAAC	CAAGGGGGT	1380
	GTGAGCTACC	GCCAGCAGCA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGAGAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA	ACTGTCTGT	CCTGCTCATT	1500
	ATGCCACTTC	CTTTAACTG	CCAAGAAATT	TTTTAAATA	AATATTATA	AT	

25 Seq ID NO: 511 Protein sequence
Protein Accession #: NP_001207.1

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30	MAPLCPSFWL	PLLIPAPAPG	LTVQLLLSL	LLMPVHPQRL	PRMQEDSPLG	GGSGEDDFL	60
	GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPVVKP	KSEEEGSLKL	EDLPTEAPG	120
	DPQEPQNNAH	RDKEGDDQSH	WRYGGDPFWP	RVPSPACAGRF	QSPVDIRPQL	AAPCFALRPL	180
	ELLGFLPPL	PELRLRNNGH	SVQLTLPPGL	EMALGPGREY	RALQLHLHWG	AAGRPGSEHT	240
	VEGHRFAEI	HVVHLSTAPA	RVDEALGRPG	GLAVLAFLFE	EGPEENSAYB	QLLSRLIEIA	300
35	EEGSETQVPG	LDISALLPSD	FSRYFYEGSS	LITPPCAQGV	IWTVFNQTVM	LSAKQLHTLS	360
	DTLMGPGDSR	LQLNFRATQP	LNGRVIRASP	PAGVDSSPRA	AEPPQLNSCL	AAGDILALVF	420
	GLLFAVTSVA	FLVQMRQRHR	RGTGGVSYR	PAEVAETGA			

40 Seq ID NO: 512 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3978

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	TTAGCACCCA	ACCGGGTGGG	TGATGCCGGG	CTACTCTCCT	TGCCCACATT	TTCTTGGCTC	180
	ACGCGCATATG	TGGTGAAGG	CTACCGGCAA	AGGCTGACCG	TAGACACCCCT	GCCCCATTG	240
	TGACATATG	ACTCATCTGA	CACCAATGCC	AAAAGATTTC	GAGTCCCTTG	GGATGAAGAG	300
	GTAGCAAGGG	TGGGTCTCTG	GAAGGCCTCT	CTGAGCCACG	TGGTGTGGAA	ATTCCAGAGG	360
50	ACACGCGTGT	TGTCAGACAT	CGTGGCCAAAC	ATCCTGTGCA	TCATCATGGC	AGCCATAGGG	420
	CCGACAGTTC	TCATTACCA	AATCTCCAG	CAGACTGAGA	GGACCTCTGG	GAAAGTCTGG	480
	GTTGGCATTG	GACTGTGCAT	AGCCTTTTTT	GCCACCGAGT	TTACCAAAGT	CTTCTTTTGG	540
	GCCCTTGCCCT	GGGCCATCAA	CTACCGCAGG	GCCATCCGGT	TGAAGGTGGC	GCTCTCCACC	600
	TGGTCTTTTG	AAAACCTAGT	GTCTTCAAG	ACATTGACCC	ACATCTCTGT	TGGCGAGGTG	660
55	CTCAATATAC	TGTCAGTGA	TAGCTATTCT	TTGTTTGAAG	CTGCCTTGTT	TTGCTCTTGG	720
	CCAGCCACCA	TCCGATCTCT	AATGGTCTTT	TGTGGCGGCT	AGCCTTTTTT	CATTCTGGGG	780
	CCCACAGCTC	TCATCAGGAT	ATCAGTGTAT	GTCAATATCA	TACCCGTCCA	GATGTTTATG	840
	GCCAGACTCA	ATTGAGCTTT	CGAAGGTGCA	GCAATTTTGG	TGACAGACAA	GCGAGTTTCT	900
60	ACAATGATAT	AGTTTCTGAC	CTGCATCAGG	CTGATCAAAA	TGTATGCCCTG	GGAGAAATCT	960
	TTTACCAACA	PCLTCCAGGA	TATAAGAAAG	AGGGAAGAAA	AATTACTGGA	AAAAGCTGGA	1020
	TTTGCCAAA	GTGGAACCTC	TGCCCTGGCC	CCCATCGTGT	CCACCATAGC	CATCGTGTCTG	1080
	ACATTATCCT	GCCACATCCT	CCTGAGACGC	AAACTCACCG	CACCCGTGGC	ATTAGTGTG	1140
	ATTGCCATGT	TTAATGTAAAT	GAAATTTTCC	ATTGCAATCT	TGCCCTTCTC	CATCAAAGCA	1200
	ATGGCTGAAG	CGAATGTCTC	TCTAAGGAGA	ATGAAGAAAA	TTCTCATAGA	TAAAAGCCCC	1260
65	CCATCTTACA	TCACCCAAAC	AGAAGACCCA	GATACTGTCT	TGCTTTTAGC	AAATGCCACC	1320
	TTGACATGGG	AGCATGAAGC	CAGCAGGAAA	AGTACCCCAA	AGAAATTGCA	GAACAGAAA	1380
	AGGCATTAT	GCAAGAAACA	GAGGTCAGAG	GCATACAGTG	AGAGGAGTCC	ACCAGCCAAG	1440
	GGAGCCACTG	GCCAGAGGGA	GCAAAAGTGAC	AGCCTCAAAAT	CGGTTCTGCA	CAGCATAAGC	1500
70	TTTGTGTGTA	GAAAGTTATG	TGGTATATCC	GAAAGCCAGC	TCTTGGCTTG	GAGGTGGCCA	1560
	GCAGTGTGTT	TGGGAGAAT	CATCAGAGGA	TACAGGCCTC	ATGGATTTTC	TGCTAAAGAC	1620
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	GCCAAATACC	TGGGGAAGAT	CTTGGGAATA	TGTGGGAATG	TGGGAAGTGG	AAAGAGCTCC	1740
	CTCCTTGCGAG	CTCTCTTAGG	ACAGATGCAG	CTGCAGAAAG	GGGTGGTGGC	AGTCAATGGA	1800
75	ACTTTGGCCT	ACGTTTCAAC	GCAGGCAATG	ATCTTTCTATG	GAAATGTGAG	AGAAACACATA	1860
	CTCTTTGGAG	AAAAGTATGA	TCACCAAAGG	TATCAGCACA	CAGTCCGCGT	CTGTGGCCTC	1920
	CAGAAGGACC	TGAGCAACCT	CCCCTATGGA	GACCTGACTG	AGATTGGGGA	GCGGGGCTTC	1980
	AACCTCTCTG	GGGGGCGAGG	GCAGAGGATT	AGCCTGGCCC	GCGCTGTCTA	CTCGACCGT	2040
	CAGCTCTTACC	TGCTGGACGA	CCCCCTGTGG	GCGGTGGAGC	CCCACGTGGG	GAGCAGCTC	2100
	TTTGAGGAGT	GCATTAAAGAA	GACGCTCAGG	GGAAGAGCAG	TGCTCTCTGT	GACCCACAGG	2160
80	CTACAGTCTT	TAGAGTCTTG	TGATGAAGTT	ATTTTATTAG	AAGATGGAGA	GATTGTGAA	2220
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	CTGCGAGGAT	TGCAAGTTCAA	GGATCCTGAA	CACCTTTACA	ATGCAGCAAT	GGTGGAAGCC	2340
	TTCAAGGAGA	GCCCTGCTGA	GAGAGAGGAA	GATGCTGGTA	TAATCGGGTA	CCTCTTTCT	2400
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85	CTGGGTCTCT	GGTGGACCAA	GGGCTCACGG	ATGACCTGTG	GGCCCCAGGG	CAACAGGACC	2520
	ATGTGTGAGG	TGGGCGCGGT	GCTGGCAGAC	ATCGTGCAGC	ATGTGTACCA	GTGGGTGTAC	2580
	ACTGCAAGCA	TGGTGTTCAT	GCTGTGTGTT	GGGTGCACCA	AAGGCTTCGT	CTTCAACCAAG	2640

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TTTGACAAGC CTGAAGTCTT TGCAGAGAAG CCAGATTCTG CATTTGCGAT GTTACTAGCA 3960
GCAGAAGTCA GATTGTAG
  
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Seq ID NO: 513 Protein sequence
 Protein Accession #: Eos sequence

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1 11 21 31 41 51
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TRVLMDIVAN ILCIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEPTKVFVW 180
ALAWAINYRT AIRLKVALST LVFENLVSKF TLTHISVGEV LNILSSDSYS LFEALPCPL 240
PATIPILMVF CAAYAPFILG PTALIGISVY VIPFVQMFM AKLNSAFRRS AILVTDKRVQ 300
TMEFTCTIR LKMYAWEEKS PTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360
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GATGPBQSD SLKSVLHSIS PVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSKD 540
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Seq ID NO: 514 DNA sequence
 Nucleic Acid Accession #: Z31560
 Coding sequence: 1-966

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1 11 21 31 41 51
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AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGTCCTCG CCGGACGCGG 180
CGCAAGATGG CCGAGAGAA CCCCAGATG CACAACTCGG AGATCAGCAA GCGCTAGCGG 240
CGCGAGTGA AACTTTTGTG GGAGACGGAG AAGCGGCGCT TCATCGACGA GCGTAAGCGG 300
CTGCGAGCGC TGACATGAA GGAGCACCGG GATTATAAAT ACCGGCCCCG GCGGAAAAAC 360
AAGACGCTCA TGAAGAAGGA TAAGTACAG CTGCGCGGCG GCGTGTCTGC CCGCGGCGGC 420
AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCGGCGCTGG GCGGCGGCGT GAACGAGCGC 480
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CAGCTGGGCT ACCCGCAGCA CCGCGGCTC AATGCGCAG GCGCAGCGCA GATGAGCCCC 600
ATGCACCGCT ACGAGTGGAG CGCCCTGCAG TACAACTCCA TGACAGCTC GCAGACCTAC 660
ATGAACGGCT CGCCCACTTA CAGCATGTCC TACTCGCAGC AGGCAACCCC TGGCATGTCT 720
CTTGGCTCCA TGGGTTCCGT GGTCAAGTCC GAGGCGAGCT CCAGCCCCCT TGTGTTACC 780
TCTTCTCTCC ACTCCAGGGC GCGCTGCCAG GCGGGGACG TCGGGACAT GATCAGCATG 840
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CACTACACGA GCGGCGCGGT GCGCGCACG GCCATTAAAG GCACACTGCC CCTCTCACG 960
ATGTAGGGGC CGACAGCGGA ACTGGAGGGG GGAGAAATTT TCAAGAAAAA ACGAGGGAAA 1020
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Seq ID NO: 515 Protein sequence
 Protein Accession #: CAA83435

80
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1 11 21 31 41 51
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RDMQEMPIQ HNSEISKRLG AEWKLLSETE KRPFIDRAK LRALEMKRHP DYKVRPREKT 120
KTLAKKDKYT LPQGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGSYSMQD 180
  
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QLGYPQHPGL NAHGAQMOP MHRVDVSALQ YNSMTSSQTY MNGSPTYSMS YSQQGTGMA 240
 LGSMSVVKV SASSSPVVT SSSSRAPCQ AGDLRDMISM YLPGAIEVPEP AAPSRHMSQ 300
 HYQSGPVPVT AINGTLPLSH M

5 Seq ID NO: 516 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29..541

10 1 11 21 31 41 51
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 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 15 AGCTGAGGAA ACAGGAGAAG TTCAATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GGCTTTAGCT TGGAAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAATT CCTATATTC TGAACCGCA 480
 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 20 AGAGAATAAA TCATTATATT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTTG TGTGAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGTTT 660
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 TCTTCAAAA AAAAAAAA AAATGGGGCC GCAATT

25 Seq ID NO: 517 Protein sequence
 Protein Accession #: AAB50564

30 1 11 21 31 41 51
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 LIQEDILDG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSEYV

35 Seq ID NO: 518 DNA sequence
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 Coding sequence: 109..2940

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 GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAACAT TAAGGAAATG 300
 45 ATAACTGAAG CTTCAATTTA CCTATTAAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT 360
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 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTTGAA 1140
 ATTCAATCT TGTGGGCTAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCACGCTA 1200
 60 CACCAAAATG ACAGCAATGA TGAATGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
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 75 GTTATAAAAA ATGATGGAAT TTACTGAGG TATTTTTTCT CCTTGTCTGC AAATGGTAGA 2160
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 80 CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2460
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5 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATTA 2940
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Seq ID NO: 519 Protein sequence
Protein Accession #: NP_006527.1

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 GDDPYTLQYR GCGKEGKYIH PTPNPLNDN LTAGVGSRRG VFWHEAHLR WGVDFEYND 180
 25 KPFIYINGNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTPIY NSTQMATASI 240
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 TFSLVQAGDK VVCLVLVDVSS KMAEADRLLO LQQAEEFYLM QIVIEHTFVG IASFDSKEGI 360
 RAQLHQINSN DDKRLVSVL PTTVSAKTDI SICSLKKGFP EVVEKLNGKA YGSVMILVTS 420
 GDDKLLGNCL PTVLSGSGTI HSIALGSSAA PNLELSRLT GGLKFPVPDI SNSNSMIDAF 480
 30 SRISSTGDI PQHQIQUEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPPIIL 540
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 AVPPATVEAF VERDSLHFPF PVMYIANVKQ GFYPIILNATV TATVEPETGD PVTLRLLDDG 660
 AGADVINKNG IYSRYFSPFA ANGRYSLKVE VNHSPISTP AHSIPGSHAM YVPGYTANGN 720
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 35 LTLSWTAPGE FDPQGGATSY BIRMSKSLQN IQDDFNAIL VNTSKRNPPQ AGIREIFTFS 840
 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
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Seq ID NO: 520 DNA sequence
Nucleic Acid Accession #: NM_000228.1
Coding sequence: 82..3600

40 1 11 21 31 41 51
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 50 CCTCACAATC ACTACAGTCA CCGAGTAGAG AATGTGGCTT CATCTCCGG CCCCATGCGC 360
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 TTCCAGCTTC AAGAGTTCAT GATGGAGTTC CAGGGGCCCA TGCCCGCGCG CATGCTGATT 480
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 55 CAGTCCCTGC CTCAGAGGCC TAATGCACGC CTAATGGGG GGAAGGTCCA ACTTAAACCTT 660
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5	GAGGCGGTGC	TGGCCCTGTG	GCTGCCCA	GACTCAGCTA	CTGTTCTGCA	GAAGATGAAT	2880
	GAGATCCAGG	CCATTGTCAGC	CAGGCTCCCC	AACGTGGACT	TGGTGTCTGC	CCAGACCAAG	2940
	CAGGACATTG	CCGCTGCCCG	CCGTTGTCAG	GCTGAGGCTG	AGGAAGCCAG	GAGCCGAGCC	3000
	CATGTCAGTG	AGGGCCAGTG	GGAGATGTG	GTTGGGAACC	TGCGGCAGGG	GACAGTGGCA	3060
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10	AGGGTTGCTG	AGGTTTCAGC	GGTACTGCGG	CCAGCAGAAA	AGCTGGTGAC	AAGCATGACC	3180
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	GGGGCAGAGG	CAGTCCAGGC	CCAGCAGCTT	GCGGAAGGTG	CCAGCGAGCA	GGCATTGAGT	3300
	GCCCAAGAGG	GATTITGAGG	AATAAAACAA	AAGTATGCTG	AGTTGAAGGA	CCGGTTGGGT	3360
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15	CTGCGGGGCA	GCCAGGCCAT	CATGCTGCGC	TCCGGGGACC	TGACAGGACT	GGAGAAGCGT	3540
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	GATTGGGTGT	GAATGCTTTC	CATCTCCAGG	AGACTTTTAT	GCAGCCTAAA	GTACAGCCTG	3720
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20	GGGACAGTTA	CACCTTGACAG	ACAAAGATGG	TGGAGATTGG	CATGCCATTG	AAACTAAGAG	3840
	CTCTCAAGTC	AAGGAAGCTG	GGCTGGGCAG	TATCCCCCGC	CTTTAGTTCT	CCACTGGGGA	3900
	GGAACTCTGG	ACCAAGCACA	AAAACTTAAC	AAAAGTGATG	TAAAAATGAA	AAGCCAAATA	3960
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25 Seq ID NO: 521 Protein sequence
Protein Accession #: NP_000219.1

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	MEPQGPMPAG	MLIERSSDPG	KTWRYVQYLA	ADCTSTFPRV	RQGRPSQWQD	VRCQSLPQRP	180
	NARLNGGKVQ	LNLMDLVSGI	PATQSQKIQE	VGBITNLRVN	FTRLAPVPQR	GYPHPSAYYA	240
	VSQRLRQSGC	FCHGHADRC	PKPGASAGPS	TAVQVHDCV	COHNTAGFNC	ERCAFFYNNR	300
35	PWRPAEQDGA	HECQRCDCNG	HSETCHFDPA	VFAASQGAAG	GVCNCRDHT	BGNKNCERQL	360
	HYFRNRFPGA	SIQTCTISCE	CDPDGAVPGA	PCDPVTGQCV	CKEHVQGERC	DLCKPGFTGL	420
	TYANPQCHRR	CDCNILGSR	DMPCEESGR	CLCLFNVVGP	KCDQCAPHYW	KLASGQGCPE	480
	CACDPENSPQ	PTVQPVHRAV	PCREGFGLM	CSAAAIROCP	DRTYGDVATG	CRACDCDFRG	540
	TEGPGCDKAS	GRCLCRPGLT	GPBCDQCQRG	YCNRYPCVVA	CHPCPQTYDA	DLREQUALRFG	600
40	RLRNATASLW	SGPGLDRLG	ASRILDAKSK	IEQIRAVLSS	PAVTEQEVQA	VASAILSLRR	660
	TLQGLQLDLF	LEEBTSLRPL	DLESILDRSFN	GLLTMYQRKR	EQFEKISSAD	PSGAFRMLST	720
	AYEQSAQAAG	QVSDSSRLLD	QLRDSRREAE	RLVRQAGGGG	GTGSPKLVAL	RLEMSLFDL	780
	TPTFNKLCGN	SRQMACTPIS	CPGELCPQDN	GTACGSRRCR	VLPRAAGAFI	MAGQVABQLR	840
	GFNAQLQRTR	QMIRAABESA	SQIQSSAQR	ETQVSASRSQ	MEEDVRRTRL	LIQQVRDFLT	900
45	DPDIDAATIQ	EVSEAVLALM	LPTDSATVLQ	KMNEIQALIA	RLPNVDLVLS	QTKQDIARAR	960
	RLQAEAEER	SRHAHVEGQV	EDVVGNLRQG	TVALQEAQDT	MQGTSRSLRL	IQDRVAEVQQ	1020
	VLRPAEKLVF	SMTRQLGDFW	TRMEELRHOA	RQQAQAEVQA	QQLABGASEQ	ALSAQEGFER	1080
	IKQKYAELKD	RLGQSSMLGE	QGARIQSVKT	BAEELFGETH	EMDMRMKDME	LELLRGSQAI	1140
50	MLRSADLTGL	EKRVEQIRDH	INGRVLYYAT	CK			

Seq ID NO: 522 DNA sequence
Nucleic Acid Accession #: NM_001944.1
Coding sequence: 84..3083

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	CCATCTTCGT	GGTGGTCATA	TTGGTTTCATG	GAGAATTGGG	AATAGAGACT	AAAGGTCAAT	180
60	ATGATGAAGA	AGAGATGACT	ATGCAACAAG	CTAAAGAAG	GCAAAAACGT	GAATGGGTGA	240
	AATTTGCCAA	ACCCTGCAGA	GAAGGAGAAG	ATAACTCAA	AAGAAACCCA	ATTGCCAAGA	300
	TTACTTCAGA	TTACCAAGCA	ACCCAGAAAA	TCACCTACCG	AATCTCTGGA	GTGGGAATCG	360
	ATCAGCCGCC	TTTTGGAATC	TTTGTGTTTG	ACAAAAACAC	TGGAGATATT	AACATAACAG	420
	CTATAGTCGA	CCGGGAGGAA	ACTCCAAGCT	TCCTGATCAC	ATGTGGGGCT	CTAATGCCCC	480
65	AAGGACTAGA	TGTAGAGAAA	CCACTTATAC	TAACGGTTAA	AATTTTGGAT	ATTAATGATA	540
	ATCCTCCAGT	ATTTTCACAA	CAAAATTTCA	TGGGTGAAT	TGAAGAAAAT	AGTGCTCAA	600
	ACTCACTGGT	GATGATACTA	AATGCCACAG	ATGCAGATGA	ACCAAAACCAC	TTGAATTCTA	660
	AAATTGCCCT	CAAAATGTGC	TCTCAGGAAC	CAGCAGGCAC	ACCATATGTC	CTCCTAAGCA	720
70	GAAACACTGG	GGAAAGTCCG	ACTTTGACCA	ATTTCTTTGA	CCGAGAGCAA	GCTAGCAGCT	780
	ATCGTCTGGT	TGTGAGTGGT	GCAGACAAAG	ATGGAGAAGG	ACTATCAACT	CAATGTGAAT	840
	GTAATATTAA	AGTGAAGAT	GTCACGATA	ACTTCCCAAT	GTTTAGAGAC	TCTCAGTATT	900
	CAGCAOGTAT	TGAAGAAAAT	ATTTTAAGTT	CTGAATTACT	TCGATTTCAA	GTAACAGATT	960
	TGGATGAAGA	TACACAGAT	AATTGGCTTG	CAGTATATTT	CTTTACCTCT	GGGAATGAAG	1020
	GAAATTGGTT	TGAAATACAA	ACTGATCCTA	GAACTAATGA	AGGCATCCTG	AAAGTGGTGA	1080
75	AGGCTCTAGA	TTATGAACAA	CTACAAAGCG	TGAAACTTAG	TATTGCTGTC	AAAAACAAAG	1140
	CTGAATTCCA	CCATCATGTT	ATCTCTCGAT	ACCGAGTTCA	GTCACCCCA	GTCACAAATC	1200
	AGGTAATAAA	TGTAAGAGAA	GGAATTGCAT	TCCGTCTCTG	TTCCAAGACA	TTTACTGTGC	1260
	AAAAAGCAAT	AAGTAGCAAA	AAATTGGTGG	ATTATATCCT	GGGAACATAT	CAAGCCATCG	1320
	ATGAGGACAC	TAACAAGCT	GCCTCAAAAT	TCAAAATATG	CATGGGAAGT	AACGATGGTG	1380
80	GATACCTAAT	GATTGATTCA	AAAACCTGCT	AAATCAAAAT	TGTCAAAAT	ATGAACOGAG	1440
	ATTCTACTTT	CATAGTTAAC	AAAACATCA	CAGCTGAGGT	TCTGGCCATA	GATGAATACA	1500
	CGGGTAAAA	TCTACAGGC	ACGGTATATG	TTAGAGTACC	CGATTTCAT	GACAAATGTC	1560
	CAACAGCTGT	CTCGAAAAA	GATGCACTTT	GCAGTTCTTC	ACCTTCCTGT	GTTGTCTCGG	1620
	CTAGAACATC	GAATAATAGA	TACACTGGCC	CCTATACATT	TGCACTGGAA	GATCAACCTG	1680
85	TAAAGTTGCC	TGCGTATGG	AGTATCAAA	CCCTCAATGC	TACCTGGCCG	CTCCTCAGAG	1740
	CCAGGAACA	GATACCTCT	GGAGTATACC	ACATCTCCCT	GGTACTTACA	GACAGTCAGA	1800
	ACAATCGGTG	TGAGATGCCA	CGCAGCTTGA	CAGTGGAAGT	CTGTGAGTGT	GACAAACAGG	1860

	GCATCTGTGG	AACCTCTTAC	CCAACCACAA	GCCCTGGGAC	CAGGTATGGC	AGGCCGCACT	1920
	CAGGGAGGCT	GGGGCCTGCC	GCCATCGGCC	TGCTGCTCCT	TGGTCTCCTG	CTGCTGCTGT	1980
	TGGCCCCCTC	TCTGCTGTGG	ACCTGTGACT	GTGGGGCAGG	TTCTACTGGG	GGAGTGACAG	2040
5	GTGGTTTTAT	CCAGTTCTCT	GATGGCTCAG	AAGGAACAA	TCATCAGTGG	GGAAATTGAAG	2100
	GAGCCCATCC	TGAAGACAAG	GAAATCACAA	ATATTTGTGT	GCCTCCTGTA	ACAGCCAAATG	2160
	GAGCCGATTT	CATGGAAGTT	TCTGAAGTTT	GTACAAATAC	GTATGCCAGA	GGCAGAGCGG	2220
	TGGAAGGCAT	TTCAAGGAATG	GAAATGACCA	CTAAGCTTGG	AGCAGCCACT	GAATCTGGAG	2280
	GTGCTGCAGC	CTTTGCAACA	GGGACAGTGT	CAGGAGCTGC	TTGAGGATTC	GGAGCAGCCA	2340
10	CTGGAGTTGG	CATCTGTCTC	TCAGGGCAGT	CTGGAACCAT	GAGAACAAAG	CATTCCACTG	2400
	GAGGAACCAA	TAAGGACTAC	GCTGATGGGG	CGATAAGCAT	GAATTTCTCT	GACTCCTACT	2460
	TTTCTCAGAA	AGCATTGGCC	TGTGCGGAGG	AAGACGATGG	CCAGGAAGCA	AATGACTGCT	2520
	TGTTGATCTA	TGATAATGAA	GGCGCAGATG	CCACTGGTTC	TCTGTGGGGC	TCCGTGGGTT	2580
	GTTGCAGTTT	TATTGCTGAT	GACCTGGATG	ACAGCTTCTT	GGACTCACTT	GGACCCAAAT	2640
	TTAAAAAAT	TGCAGAGATA	AGCCTTGGTG	TTGATGGTGA	AGGCAAGAA	GTTCCGCCAC	2700
15	CCTCTAAGA	CAGCGGTTAT	GGGATTGAAT	CCTGTGGCCA	TCCCATAGAA	GTTCCAGCAG	2760
	CAGGATTGTT	TAAGTGCCAG	ACTTTGTCTG	GAAGTCAAGG	AGCTTCTGCT	TTGTCCGCCT	2820
	CTGGGTCTGT	CCAGCCAGCT	GTTTCCATCC	CTGACCTCTT	GCAGCATGGT	AACTATTTAG	2880
	TAAAGGAGAC	TTACTCGGCT	TCTGGTTCCT	TCTGCAACCC	TTCACTGCA	GGCTTTGATC	2940
	CACCTTCTAC	ACAAAATGTT	ATAGTGACAG	AAAGGGTGAT	CTGTCCCAT	TCCAGTGTTC	3000
20	CTGGCAACTC	AGCTGGGCCA	ACGCAGCTAC	GAGGGTCACA	TACTATGCTC	TGTACAGAGG	3060
	ATCCTTGCTC	CCGTCTAATA	TGACCCAGAT	GAGCTGGAA	ACCACACTGA	CCAAATCTGG	3120
	ATCTTTGGAC	TAAAGTATTC	AAAATAGCAT	AGCAAAGCTC	ACTGTATTGG	GCTAATAAAT	3180
	TGGCACTTAT	TAGCTTCTCT	CATAAACTGA	TCAAGATTAT	AAATTAAATG	TTTGGGTTCA	3240
25	TACCCCAAAA	GCAATATGTT	GTCACCTCTA	ATTCTCAAGT	ACTATTCAAA	TTGTAGTAAA	3300
	TCTTAAAGTT	TTTCAAAACC	CTAAAATCAT	ATTCCG			

Seq ID NO: 523 Protein sequence
Protein Accession #: NP_001935.1

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	GEDNSKRNPI	AKITSDYQAT	QKITRISGV	GIDQPPFGIF	VVDKNTGDI	ITAIVDREET	120
	PSFLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVFSQQ	IPMGEIENS	ASNSLVMILN	180
35	ATDADEPNHL	NSKTAIFKIV	QEPAGTMMFL	LSRNTGEVRT	LTSNLDREQA	SSYRLVVSGA	240
	DKDGEGLSTQ	CECNIKVKDV	NDNPFMFRTS	QYSARIEENI	LSSELLRPQV	TDLDEEYTDN	300
	WLAVYFTTSG	NEGNMFELQT	DPRTNEGILK	VVKALDYBOL	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSKK	LVDYILGTQY	AIDEDTNKAA	420
	SNVKYVMGRN	DGGYLMIDSK	TAEIKFVNKM	NRDSTFIVNK	TITAEVLAI	EYTGKTSSTG	480
40	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPTYPALED	QPVKLPVNS	540
	ITTLNATSL	LRAQEQIPPG	VYHISLVLT	SONNRCMPR	SLTLEVQCCD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPA	IGLLLLGLLL	LLLAFLLLLT	CDGAGSTGG	VTGGFIPVFD	660
	GSEGTIHQWG	IEGAHPEDKE	ITNICVPPVT	ANGADFMESS	EVCTNTYARG	TAVEGTSGBE	720
	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	QSGTMRTRH	STGGTNKDYA	780
45	DGAISMNPLD	SYFSQKAFAC	AEEDDQGEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDDSFLLSLG	PKFKLAEIS	LGVDGEGKEV	QPPSKDSGYG	IESGHPFIEV	QQTGFVKCQT	900
	LSSGSQASAL	SASGSVQPAV	SIPDPLQHGN	YLVTTYSAS	GSLVQPSLAG	FDPLLTQWVI	960
	VTERVICPIS	SVFPGNLAPG	QLRGSHTMLC	TEDPCSRLI			

Seq ID NO: 524 DNA sequence
Nucleic Acid Accession #: XM_058069.2
Coding sequence: 1..1413

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	AGCTCTACAA	GCCTGGAAAA	AAATAATGTT	CTATTGGTGG	AAGATACACT	AGAAAAATTT	120
	TATGGCCCTG	AGATAAACAA	ACTTCCAGTG	ACAAAAATGA	AATATAGTGG	AAACTTAATG	180
	AAGGAAAAAA	TCCAGAAAT	GCAGCACTTC	TTGGGTCTGA	AAGTGACCGG	GCAACTGGAC	240
60	ACATCTACCC	TGGAGATGAT	GCACGCACCT	CGATGTGGAG	TCCCGATGT	CCATCAATTC	300
	AGGGAAATGC	CAGGGGGGCC	CGTATGGAGG	AAACATTATA	TCACTACAG	AATCAATAAT	360
	TACACACCTG	ACATGAACCG	TGAGGATGTT	GACTACGCAA	TCCGAAAGC	TTTCCAAGTA	420
	TGGAGTAATG	TTACCCCTCT	GAAATTGAGC	AAGATTAAAC	CAGGCATGGC	TGACATTTTG	480
	GTGGTTTTTG	CCCGTGGAGC	TGATGGAGAC	TTCCATGCTT	TTGATGGCAA	AGGTGGAATC	540
65	CTAGCCCATG	CTTTTGAGAC	TGGATCTGGC	ATTGGAGGGG	ATGCACATT	CGATGAGGAC	600
	GAATTCCTGA	CTACACATTC	AGGAGGCACA	AACTGTGTCC	TCACTGCTGT	TCAAGAGATT	660
	GGCCATTCCT	TAGGCTCTTG	CCATTCTAGT	GATCCAAAGG	CGTAATGTT	CCCCACCTAC	720
	AAATATGTTG	ACATCAACAC	ATTTGCGCTC	TCTGCTGATG	ACATACGTTG	CATTGAGTCC	780
	CTGTATGGAG	ACCCAAAGAA	GAACCAACGC	TTGCCAAATC	CTGACAAATC	AGAACAGCTG	840
70	CTCTGTGAAC	CCAATTTGAG	TTTTGATGCT	GTCACACCG	TGGGAAATAA	GATCTTTTTT	900
	TTCAAAGACA	GTTTCTCTCT	GCTGAAGGTT	TCTGAGAGAC	CAAAGACAG	TGTTAATTTA	960
	ATTTCTTCCT	TATGGCCAA	CTTGCCATCT	GGCATTGAAG	CTGCTTATGA	AATTGAAGCC	1020
	AGAAATCAAG	TTTTTCTTTT	TAAAGATGAC	AAATACTGGT	TAATTAGCAA	TTTAAGACCA	1080
	GAGCCAAATG	ATCCCAAGAG	CATACATTCT	TTTGGTTTTT	CTAACTTTGT	GAAAAAAAT	1140
75	GATGCAAGCT	TTTTTAACCC	ACGTTTTTAT	AGGACCTACT	TCTTTGTAGA	TAACCAATAT	1200
	TGGAGGTATG	ATGAAGGAG	ACAGATGATG	GACCTCTGTT	ATCCCAACT	GATTACCAAG	1260
	AACTTCCAAG	GAATCGGGCC	TAAAATTGAT	GCAGTCTTCT	ACTCTAAAA	CAATACTAC	1320
	TATTTCTTCC	AAGGATCTAA	CCAATTTGAA	TATGACTTCC	TACTCCAACG	TATCACCAAA	1380
80	ACACTGAAAA	GCAATAGCTG	GTTTGGTGTG	TGA			

Seq ID NO: 525 Protein sequence
Protein Accession #: P39900

85	1	11	21	31	41	51	
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	KEKIQEMQHF	LGLKVTGQLD	TSTLEMMHAP	RCGVDPDVHF	REMPGGPVWR	KHYITTRINN	120

5

YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVPARGAHD PHAPDGKGGI 180
 LAHAFPGPSG IGGDAHFDEE EFWTHSGGT NLFLTAVHEI GHSGLGHSS DPKAVMFPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LFNPDNSEPA LCPNLSFDA VTTVGNKIFF 300
 FKDRFFWLKV SERPFTSVNL ISSLWPTLPS GIEAAEIEA RNQVFLFKDD KYWLISNLRP 360
 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
 NFGIGPKID AVFYSKNKYY YFFQGSNQFB YDFLLQRITK TLKSNSWFGC

10

Seq ID NO: 526 DNA sequence
 Nucleic Acid Accession #: NM_024423.1
 Coding sequence: 64..2590

15

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1 11 21 31 41 51
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 CGATGGCCG CCGCTGGGCC CCGCGGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCCCTG TGATCTTCAG TCGTGATGGT GAAGCGCTGA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
 TCTGCAGACG TCATCCGGTC AAGTGATCCT GATTTTCAGAG TTCTAAATGA TGGGTTCAGTG 300
 TACACAGCCA GGGCTGTGGC GCTGTCTGAT AAGAAAAGAT CATTACCAT ATGGCTTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
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 GAATCTGATG CAGCACAGAA CTATACTGTC TTCTACTCAA TAAGTGAAGC TGGAGTTGAT 600
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 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGGC 900
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 ATTGATGAAA TTTGAGGCT AATCAATACT TCCAAAATCC TGGATAGGGA GGTGAAACT 1680
 CCCAAAATG AGTTGTATTA TATTACAGTC CTGGCAATAG ACAAGATGA TAGATCATGT 1740
 ACTGGAACAC TTGCTGTGAA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA 1800
 GAATATGTAG TCATTTGCAA ACCAAAAATG GGGTATACCG ACATTTTATG TGTGTGCTCT 1860
 GATGAACCTG TCCATGGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC 1920
 AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCGCTCTTTC ATATCAGAAA 1980
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Seq ID NO: 527 Protein sequence
Protein Accession #: NP_077741.1

Seq ID NO: 528 DNA sequence
Nucleic Acid Accession #: NM_001941.2
Coding sequence: 64..2754

387

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5	TATGAAGCAT	TTGTAGAGGA	AAATGCATTG	AATGTGGAAA	TCTTACGAAT	ACCTATAGAA	1200
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10	GTTCAATGTA	GGGATCTGGA	TGAGGGGCGT	GAATGCACCT	CTGCAGCCCA	ATATGTGCGG	1500
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15	GAATATGTAG	TCATTGTCAA	ACCAAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
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	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGGG	2100
20	ACTTCAAGGA	TACAGGAGT	AATACCTGGA	AAATGGGCAA	TCTTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCCTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTCGG	TGCAACTAAA	2220
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	AGCCAAGGTT	TTTGTGGTAC	TATGGGATCA	GGAAATGAAA	ATGAGAGGCA	GGAAACCAAT	2400
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35	TCCTTTTCTT	TTTACCGGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAAAC	3060
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40	ACCAAAATCA	TTTGACTTTG	GAGGCAAAAT	GTGTTGAAGT	GGCCTATGAA	GTAGCAATTT	3300
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45	GTAAATTAAT	TAAACTTTTC	TGGTTCTGTT	GGGAAGGAAA	TAGGGAATCC	AATGGAACAG	3600
	TAGCTTTGCT	TTTCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTGCG	TGCAGCTGGG	GTTCCTGCTC	TTTGTGTAGC	AAGGGTCCAG	AGATGAGGTTG	3720
	TTTTTTTGGG	GGAGCTAATA	ACAAAAACAT	TTTAAAACTT	ACCTTTACTG	AAGTTAAATC	3780
	CTCTATTGCT	GTTCCTATTTC	TCTCTTATAG	TGACCAACAT	CTTTTAAAT	TAGATCCAAA	3840
50	TAACCATGTC	CTCTAGAGTT	TTAGAGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
	GCACCTGGGG	GAGATGTAAT	GTCTTAAAC	CTAAGGCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAGC	TACAAAATTT	CATTTTCTCT	CTCACTGCCC	TTCTTCTGAG	TGGCATTGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGGC	CCCTTCTTTT	CGGCTTCTG	CTAAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCCT	TAAAGTACTC	CAGGTTTTC	ACCATCTTTC	AGCGTGAAT	4140
55	AAATTTTAAAT	CAGTTTGCTT	TCTCCAGAGA	AAATTTTAAA	TAAATAGAGA	AATAGAAAT	4200
	TTGAATGTAT	AAAGAGAAAA	GATCAAGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCTTCAA	4320
	GGGCAAGGAG	AGGCCCAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTCTCTA	GGCTTGGCAC	TGCCCTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTGTA	4440
60	GTCCGGTGAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTGGGA	GTGAGAAATC	4500
	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
	GTGTGTCAGA	ACAAACAGGG	CATTCAATGG	AATGTGTGTA	TTCTTCTGTC	AGCCCTCCTT	4620
	CTGGGCACTA	AGAAGGCTTA	TGAATTAAT	GCCTATCTAA	AATCTGAT	TATTCCTACA	4680
	TTTTCTGTTT	TCTAATTTGA	CCCTAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
65	CCCCCCCCCT	TTTTTTTTTG	AGACGGAGTC	TGCTCTGAC	GCACAGGCTG	GAGTGCACTG	4800
	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGGTT	CATGCCATTC	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCAACAGG	CCCGGCTAAT	TTTTTGTATT	4920
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTGTTG	4980
70	ATCCGCTGTC	CTGGGCTTCC	CAGAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
	CTTGTTTCTC	GTTTAAAGTC	GTCTTCTTTT	AATGTAAATCA	TTTTGAACAT	GTGTGAAAGT	5100
	TGATCATAGC	AATTTGGATCA	ATCTTGAAT	ACTCAACCAA	AAGACAGTGC	AGAAGCCAGG	5160
	GGGAGAAAGA	ACTCAGGGCA	CAAAATATTG	GTCTGAGAAAT	GGAAATCTCT	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGCT	AACCAAGAGC	CAGTTTTATC	TAAAGGCTAC	TGAAACACCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
75	CTAGTCCGGA	TAAACTTTCT	CAAGAGGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
	TAACCATCTC	TTTGTCTTTT	GAACATGCTG	AAAACCACTT	GGTCTGCATG	TATGCCCGAA	5460
	TTTGTAAATC	TTTTCTCTCA	AATGAAATTT	TAATTTTAGG	GATTCAITTC	TATATTTTCA	5520
	CATATGTAGT	ATTATTAATTT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAT	GCTTTCAATT	TTCCCCAGT	GAATGATTTA	GAATTTTATA	5640
80	TGTAATATATA	CAGAATGTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAAATGCAGT	5700
	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAT	AAGCAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAAT	ATTAACCTGG	TTTCTGTTT	TGCTGTATT	5880
	TAGAGATTAA	ATAATTCTAA	GATGATCACT	TTGCAAAAT	ATGCTTATGG	CTGGCATGGA	5940
	AATAGAAATA	CTCAATTAATG	TCCTTGTGTT	ATTAATGGGG	AATATTTTGG	ACAATGTTTT	6000
85	ATTATCAAT	TGTGACATCT	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCATATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAAGATA	TTAGAGGGTG	GTTATAATTT	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180

5
10
15

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AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300
CAAGATGATC CAACCAATAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360
AGTGTGCTCC CTTACAAAAG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAAAT CCAGTAACTT CTATTGTAAC 6480
CATTAATTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGA ATAGTAAAT 6540
ACCGGATACA TTTCACTGT CTTTCAGTAT TGATTGGTT GAATATTGGG TCATAATGTT 6600
TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGCTACTTAC 6660
TTCTGTGTGA CTTTGAAGG GCTACTTATT TCCTCTCTTA GCTTCTCAT TAAAATCAAT 6720
GAACAATGCC AGCCTCATGG GGTGTTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT 6840
GTAGTTGGAT ATACTACCGA ACAAATATCTA ATCTCTTTTT AGGGAAATAA AGTTTGTGCA 6900
TATATATAAT CCGGAAACAT G

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Seq ID NO: 529 Protein sequence
Protein Accession #: NP_001932.1

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35

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1 11 21 31 41 51
MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
ADLIRSSDPD FRVLNDGSVY TARAVALSDK KRSPTIWLSD KRKQTKQEVV VLLEHQKKVS 120
KTRHTRFETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAQNYITVP YSISGRGVDK 180
EPLNLFYIER DTGNLFCRTP VDREEDVDFD LIAYASTADG YSADLPLPLP IRVEDENDNH 240
PVFTETIYNF EVLESSRPGT TVGVVCATDR DEPDIMHTRL KYSILQQTFR SPGLFSVHPS 300
TGVITTVSHY LDRBVVDKYS LMKVQDMDG QFFGLIGTST CIITVTSND NAPTFRQNAV 360
EAPVEENAFN VEILRIPIED KDLINTANWR VNFTILKQNE NGHFKISTDK ETNBSGLSVV 420
KPLNYEENQI RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAQNYITVP YSISGRGVDK 480
KENLAVGSKI NGYKAYDPEN RMNGNGLRYKK LHDPKGWITI DEISGSIITS KILDREVETP 540
KNELYNTIVL AIDKDRSCT GTLAVNIEDV NDNPEILQE YVVICPKMG YTDILAVDPD 600
EPVHGAPPYP SLPNTSPEIS RLWSLTKVND TAARLSVQKN AGFQBYTIPI TVKDRAGQAA 660
TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLTL VGVVFGATKG 720
KRPFEDLAQQ NLIISNTEAP GDDRVCASANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780
MMKGGNQTL ESCRAGHHHT LDSCRGGHTE VDNCRYTYSE WHSPTQPRLG EKLHRCNQNE 840
DRMPSQDYVL TYNVEGRGSP AGSVGCCSEK QEEDGLDPLN NLEPKFITLA BACTER

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Seq ID NO: 530 DNA sequence
Nucleic Acid Accession #: NM_016583.2
Coding sequence: 72..842

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1 11 21 31 41 51
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TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCAGAA 120
CCATGGCCCA GATTGGAGGC CTGCCCGTGC COCTGGACCA GACCCCTGCC TTGAATGTGA 180
ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
ATGGCCCTGC CTCTGGGGGC CTGTGGGSCA TTCTGGAAAA CCTTCOGCTC CTGGACATCC 300
TGAAGCCCTG AGGAGGTACT TCTGTGGGCC TCCTTGGGGG ACTGCTTGGG AAAGTGACGT 360
CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
AACTTGGCCT TGTGACAGGC CCTGATGGCC ACCGTCTCTA TGTACCATC CCTCTCGCA 480
TAAAGCTCCA AGTGAATAC CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
TTGGTGAATG CACCCATTCC CCTGGAAGCC TGCAAAATTC TCTGCTTGAT GGACTTGGCC 660
CCCTTCCCAT TCAAGGTCTT CTGGACAGCC TCACAGGGAT CTGGAATAAA GTCTGCTGCT 720
AGTTGGTTCA GGGCAACGTC TGCCCTCTGG TCATGAGGT TCTCAGAGGC TTGGACATCA 780
CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTGTG ATCAAGGTCT 840
AAGCCTTCCA GGAAGGGGCT GGCCCTCTGT GAGCTGCTTC CCAAGTGTCA CAGATGGCTG 900
GCCCATGTGC TGAAGATGA CACAGTTGCC TTCTCTCGA GGAACCTGCC CCTCTCTCT 960
TCCCAACAGG CGTGTGTAA ATCCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTGC 1020
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

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Seq ID NO: 531 Protein sequence
Protein Accession #: NP_057667.1

65
70

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1 11 21 31 41 51
MPQTGLLIVF YGLLAQTMAG FGGLPVPLDQ TLPLNVNPAI PLSPTGLAGS LTNALSNGLL 60
SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
VQSPDGHRLY VTIPGLIKLQ VNTPLVGASL LRLAVKLDIT ABILAVRDKQ ERIHLVLGDC 180
THSPGSLQIS LLDGLGLPLI QGLLDSLTGI LNKVLPVLVQ GNVCPVLNEV LRGLDITLVH 240
DIVNMLIHGL QFVIKV

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75
Seq ID NO: 532 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115..2223

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1 11 21 31 41 51
CTCAGGCGAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAAGCT 60
TCCTGGAACCT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
TCTCCCTCGG CCCCCTCCCA CAGATGTGTC ATCCCTGGCC AGAGGCTCCT GCTCAGAGCC 180
TCACTTCTAA CCTTCTGAA CCGCCACC ACTGCCAAGC TCACTATTGA ATCCAGCGCG 240
TTCAATGTG CAGAGGGGAA GAGAGTGCTT CTACTGTGCC ACAATCTGCC CCAGCATCTT 300
TTTGGCTACA TGTGGTACAA AGGTGAAAGA GTGGATGGCA ACOGTCAAAT TATAGGATAT 360
GTAATAGGAA CTCACCAAGC TACCCAGGG CCGCATACA GTGGTCGAGA GATAATATAC 420
CCCAATGCAT CCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCTA 480

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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCGG 540
 GAGCTGCCCA AGCCCTCCAT CTCAGCAAC AACTCCAAAC CGGTGGAGGA CAAGGATGCT 600
 GTGGCCCTCA CCTGTGAACC TGAGACTCAG GAAGCAACTG AACTGTGGTG GGTAAACAAAT 660
 CAGAGCCCTCC CGGTCACTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
 5 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAAT 780
 GCCAGGCGCA GTGATTCAGT CATCTGAAT GTCTCTATG GCCCGGATGC CCCCAACATT 840
 TCCCTCTTAA ACACATCTTA CAGATCAGGG GAAATCTGA AACTCTCTG CCACGCGACC 900
 TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTCACAGCA ATCCACCCAA 960
 10 GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT OCTATACGTG CCAAGCCCAT 1020
 AACTCAGACA CTGGCCCTCA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
 CCCAAACCTT TCATCACCAG CAACAACCTC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
 CTCGCCGTGA GTCCAGGCTG GCAGCTGTCC AATGACAACA GGACCTCAC TCTACTCAGT 1260
 15 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAAATC AGAACGAATT AAGTGTGAC 1320
 CACAGCGACC CAGTCATCTC GAATGTCTC TATGGCCAG AGGACCCAC CATTTCCTCC 1380
 TCATACACCT ATTACCTGTC AGGGGTGAAC CTCAGCTCTT OCTGCCATGC AGCTCTTAAC 1440
 CCACCTGTC AGTATCTCTG GCTGATTGAT GGGAACTCC AGCAACACAC ACAAGAGCTC 1500
 TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA OCTGCCAGGC CAATAACTCA 1560
 20 GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCAAG 1620
 CCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGTCTG GGCCTTCACC 1680
 TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
 GTCAGTCTGA GGTCTGAGCT GTCCAATGGC AACAGGACCC TCACCTTATT CAATGTCA 1800
 AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGTGTCG AAACCGCAGT 1860
 25 GACCCAGTCA CCTGTGATGT CCTCTATGGG CCGGACACCC CCATCAITTC CCCCCAGAC 1920
 TGTCTTATCC TTTGGGAGC GAACTCAAC CTCCTCTGCC ACTCGGCTC TAACCCATCC 1980
 CCGCAGTATT CTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTATC 2040
 GCGCAAAATA GCGCAATAA TAAACGGACC TATGCTCTGT TTGCTCTTAA CTGGCTACT 2100
 GCGCGCAATA ATTCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TCTCTCTGT 2160
 30 CTCTCAGCTG GGGCCATCTG CGGCATCATG ATTGGAGTGC TGGTGTGGGT TGCTCTGATA 2220
 TAGCAGCCCT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTGTGTTT GCTCTCTCT 2280
 TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTCTTTC ACCAAGGATA TTTACAGAAA 2340
 AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
 AAATACAAAA ATGAGCTGGG CTGTGTGGCG CGCACTGTGA GTCCAGTTA CTGGGAGGC 2460
 35 TGAGGCGAGA GAATGCTCTG AACCGGGAG GTGGAGATTG CAGTGAGCCC AGATGCGACC 2520
 ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAGAC 2580
 TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
 AACTTTAATG AACTAACTGA CAGCTTCATG AAACGTGCCA CCAAGATCAA GCAGAGAAAA 2700
 TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760
 40 TTCCAGATT TCCAGAAACT TTTTCTCTT TAAGCTATCC ACTCTTACAG CAATTTGATA 2820
 AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCTATG TGGTGCCTCC 2880
 AGACTTGGGA AACTATTCTA GAATATTAT ATTGTATGTT AATATAGTTA TTGCACAGT 2940
 TCAATAAAAA TCTGCTCTTT GTATACAGA AAAA

Seq ID NO: 533 Protein sequence
 Protein Accession #: NP_004354.1

1 11 21 31 41 51
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 50 MESPSAPHER WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVABGKE VILLVHNLPQ 60
 HLFYGSWYKG ERVDGNRQII GYVIGTQOAT PGPAYSGREI IYPNASLLIQ NIIQNDTGPFY 120
 TLHVIRSDLV NEEATGQFRV YPELPKPSIS SNNSKPFVEDK DAVAPTCEPE TQDATYLNWV 180
 NNQSLPVSPR LQLSNGNRTL TLPNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGPDAP 240
 TISPLNTSYR SGENLNLSCB AASNPPAQYS WPNVGTQQQS TQELFIPNIT VMNSGSYTCQ 300
 AHNSTGLANR TTVTTITVYA EPPKPPITSN NSNPVEDEDA VALTCEPEIQ NTTYLNWVNN 360
 55 QSLVSPRIQ LSNDRNLTL LSVTRNDVGP YECGIQNELS VDRSDPVLN VLYGPDPTI 420
 SPSTYYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQORTQ ELFISNITEK NSGLYTCQAN 480
 NSAGSHSRIT VKTITVSAEL PKPSISSMNS KPVEDKDAVA FTCEPEAQNT TYLWVWVQNS 540
 LPVSPRLQSL NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
 60 FDSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQOHTQVL PIKITPANN GTYACFVSNL 660
 ATGRNNSIVK SITVSASGTS PGLSAGATVG INIGVLVGVA LI

Seq ID NO: 534 DNA sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

1 11 21 31 41 51
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 65 AATCCGACA ATGCGGAAAG ACAACTCAAC TGTGTGTTGC TTCCAGGGCC TGCTGATTTT 60
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 70 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACACAGATG ACATCTATGG 180
 GGTGCTCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCGTGCTG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCTATC TGATGTTTAT 300
 AGTATATGCC TTTGAAGTGG CATCTGTGAT CACAGCAGCA ACACAAACGAG ACTTTTTCAC 360
 75 ACCCAACCTC TTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAACCAA 420
 TGATGACCCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GCGCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
 TGAGATAATG GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACCTCTC AACCTGGAGG CTGTGAAACT AGGGGTGCTT GGTTTTATC ACAATCAGGG 660
 80 CTGCTATGAA CTGATCTCTG GTCCAAATGAA CCGACACGCC TGGGGGGTTG CCGTGTGTTG 720
 ATTTGCCATT CTCTGTGGA CTTTGTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 535 Protein sequence
 Protein Accession #: NP_008883.1

1 11 21 31 41 51
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MAKDNSTVRC FQGLLIPGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
IGIFVGLCLF CLSVLGI VGI MKSSRKILLA YFILAFIVYA FEVASCITAA TQRDFPTPNL 120
FLKQMLERVQ NNSPPFNDQ WKQNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
DADYFWPRQC CVMNKLKPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAFPGFAI 240
LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 536 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120..473

1 11 21 31 41 51
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GCTGGAGCTG ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGAGC CTGTTCTAG 180
AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAATTAA AGGTCAAGAT AAAGTCAAAG 300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
TCCGGTGGC CATGTTGAAT CCCCTTAACC GCTGCTTGA AGATACTGAC TGCCAGGAA 420
TCAAGAAGTG CTGTGAAGGC TCTTGGGGA TGGCTGTATT CGTCCCCAG TGAAGGGAGC 480
CGGTCTTGC TGCACCTGTG CGTCCCCAG AGCTACAGGC CCATCTGGT CCTAAGTCCC 540
TGCTGCCCTT CCCCTTCCA CACTGTCCAT TCTTCTCCC ATTCAAGATG CCCACGGCTG 600
GAGCTGCCCT TCTCATCCAC TTTCACATAA A

Seq ID NO: 537 Protein sequence
Protein Accession #: NP_002629.1

1 11 21 31 41 51
| | | | |
MRASSFLIVV VFLLAGTLVL EAAVTGVPVK GQDTVKGRVP PNGQDPVKGQ VSVKGQDKVK 60
AQEPVKGPIVS TKPQSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCEGSCG MACFVPQ

Seq ID NO: 538 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71..2560

1 11 21 31 41 51
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AAAGGGCAA GAGCTGAGCG GAACACGGGC CGCCCGTGGC GGCAGCTGCT TCACCCCTCT 60
CTCTGACGCC ATGGGGCTCC CTGCTGGACC TCTGCGTCT CTCTCTCTTC TCCAGGTTTG 120
CTGGCTGACG TGGCGGCCCT CCGAGCCGTG CGGGCGGCTC TTCAGGGAGG CTGAAGTGAC 180
CTTGGAGGCG GGAGGCGCG AGCAGGAGCC CGGCCAGGCG CTGGGGAAGG TATTCATGGG 240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAAGCT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGTCTCAA TATCTGTCCC 420
TGAAATATGG AAGGTCCTCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCACGG GCGGGGGCA GACAGCCCC CTGAGGGTGT 540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTACAG AATGGTGCT CAGTGGAGGA 660
CCCCATGAAC ATCTCATCA TCGTGAACGA CCAGAATGAC CACAAGCCCA AGTTTATCCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTCTG TGAATCAGGT 780
GACAGCAAG GATGAGGATG ATGCCATCTA CACTACAAT GGGGTGGTTG CTTACTCCAT 840
CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTT ACCATTCAAC GGAGCACAGG 900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGCAATGG ATGGGGACGG CTCACCAACC ACGGCAGTGG CAGTAGTGGG 1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
GCCGTGAGAT GCACTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
TACCATCACC ACCCAACCTG AGAGCAACCA GGGCATCTCT ACAACAGGA AGGGTTTGGG 1260
TTTGTAGGCG AAAAACCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCCTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGTGCCAC GTGGAGGATG TGAATGAGGC 1380
ACCTGTGTTT TGTCCACCTT CCAAAAGTGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500
CATCTGAGA GAACCAAGCA GGTGGCTAGC CATGGAACCA GACAGTGGGC AGGTCAACGC 1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGTCTAAC 1680
ACTGATTGAT GTCAATGACC ATGGCCCAAT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGGCCACAG TGCTGAACAT CAAGGACAAG GACCTGTCTC CCCACCTTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAAGGTGAC ACAGTGTCTT TGTCCCTGAA GAAGTTCTGT AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCTT 2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGGT 2100
GAGAAGAAG GGAAGATCA AGGAGCCCTT CTAATCCCA GAAGATGACA CCGGTGACAA 2160
CGTCTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
GCTCCACGGA GGTCTGAGG CCAGGCCGGA GGTGTTCTC CGCATGACG TGGCAACAC 2280
CATCATCCCG ACACCATGAT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACCA GCCCCGCCCT ACACACCTT 2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACCGCGCG TCCCTGAGCT CCCTCACTTC 2460
CTCGCCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGGCTTCAA 2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG CGGCGCTGCC TGCAGGGCTG 2580
GGGACCAACG GTGAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TFCAGCTGAG 2640
GACTTGGAG CTGTGACAGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGTCTCAG AGGCCAAGTT TCCGAAGCC 2820
TCTTACCTGC CGTAAAAATG TCAACCTCTG GTCTGGGGCC TGGGCTGTCT GTGACTGACC 2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCTGTGTGCA ACTTAATTTT 2940

5
 TTTTITTAAT GCTATCTTCA AAAAGTTAGA GAAAGTCTCT CAAAAGTGCA GCCCAGAGCT 3000
 GCTGGGCCCCA CTGGCCGTCG TGCATTTCTG GTTTCAGAC CCCAATGCCT CCCATTCCGA 3060
 TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGCC CCTTATTTTT TATTTTCCCT 3120
 GTTGGGTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 539 Protein sequence
 Protein Accession #: NP_001784.2

10
 1 11 21 31 41 51
 MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGABQEPGQA LGKVPNGCPG 60
 QEPALFSTDN DDFTVRNGET VOERRSLKER NPLKIFPSKR ILRRHRRDWV VAPISVPENG 120
 KGFPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLILN KPLDREELAK 180
 15 YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKPTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDATYTYN GVVAYSIHSQ EPKDPFDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSGT TAVAVVEILD ANDNAPMFPD QKYEAHVPEV AVGEHVQLRT VTDLADPNP 360
 ANRATYILMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVH VEDVNEAPVE VPPSKVVEVQ EGIPTGEPVC VYTAEDPKE NQKISYRILR 480
 20 DPAGWLAMPD DSGQVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540
 VNDGFPVPEP RQITICNQSP VRQVLNITDK DLSPHSPFPQ AQLTDDSDIY WTAEVNNEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVYF YGEBGGGEED QDYDITQLHR 720
 25 GLEARPEVVL RNDVAPTIIP TMYRPRPAN PDEIGNPIE NLKAANTDPT APPYDTLLVF 780
 DYBSGSDAA SLSSLTSSAS DQDQDYDILN ENGSRPFKLA DMYGGGEDD

Seq ID NO: 540 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..672

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 1 11 21 31 41 51
 ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GGCGGCGGCC CCGGGGCGGG 60
 CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
 35 AAGGGCGGGG AGGGGGCGCC GCGGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGGG 180
 CTGCTCGCTG TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
 GCGAGACAAC GAGATCCAGA GCACTCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300
 TGTGATGTTT CTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAAATGG 360
 ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTT CACGTTTTTT CATGTTTGGC 420
 40 AAGCAGTGCT CGCTGCTTGG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
 CTCTCGAAGG AGCCCATGCC CTCTTTTAC CTCAGGTGTT GTAAAATTCG CTACTGCAAT 540
 TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600
 AGCTGTGGTG GCGTGTGGCT GGCCATCTCT CTGCTGCTGG CCTCCATTGC AGCCGGCCTC 660
 AGCCTGTCTT GA

Seq ID NO: 541 Protein sequence
 Protein Accession #: Eos sequence

50
 1 11 21 31 41 51
 MRLQRPRQAP AGGRRAPRGG RGSPPYRDPG RGARLRRPQ KGGEGAPRAD PPWAPLGTMA 60
 LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNVW CHVCERENTP BCQNFRRCCKW 120
 TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEPMPPFFY LKCKIRYCN 180
 55 LEGFPINSSV FKEYAGSMGE SCGGLNLAIL LLLASIAAGL SLS

Seq ID NO: 542 DNA sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

60
 1 11 21 31 41 51
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
 TGCGGGCCCC AAGCGGCGCG CGCTAGCGGC GCGGCGGGCC GAGGAGAAGG AAGAGGCGCG 120
 65 GGAGAAGATG CTGCGCCGCC AGAGCGCGGA CGCTCGGGCG CCGGCAGGCG AGGGCGAGGG 180
 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240
 TATCGGCTCG GGCATCTTCG TGAAGCCAC GGGCGTGTCT AAGGAGGCGG GCTCGCCGGG 300
 GCTGGCGCTG GTGGTGTGGG CCGCGTGGCG CGTCTTCTCC ATCGTGGCGG CGCTCTGCTA 360
 OCGGAGGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTACA TGCTGGAGGT 420
 70 CTACGCTCG CTGCGCCGCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCGGCGCTTC 480
 ATCGCAGTAC ATCGTGGGCC TGGTCTTCGC CACCTACCTG CTCAGCGCG TCTTCCCCAC 540
 CTGCGCGGTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGGGTGC TGCTGCTCAC 600
 GGCCTGTAAC TGCTACAGCG TGAAGGCCGC CACCCGCGTC CAGGATGCCT TTGCGCGCGC 660
 CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGGATG TGGGGAACAT 780
 75 TGTGCTGGCA TTATACAGCG GCGTCTTTGC CTATGGAGGA TGGAAATTA TGAATTTCTG 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCCTGCC 900
 CATCGTGAG CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACACCC TGTCACCGA 960
 GCAGATGCTG TGGTTCGAGG CGTGGCGCTG GAGACTCGGG AACTATCACC TGGGGTGCAT 1020
 GTCTCGGATC ATCCCGCTCT TCGTGGGCGT GTCCCTGCTC GGCTCCGTC ATGGGTCCCT 1080
 80 GTTCACATC TCCAGGCTCT TCTTGTGGG GTCCCGGAAA GGCCACCTGC CCTCCATCCT 1140
 CTCATGATC CACCCACAGC TCCTCACCCC CGTGGCGTCC CTGCTGTTC CTGCTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTTCCTCGTC ATCAACTTCT TCAGCTTCTT 1260
 CAACCTGGCT TGGTGGCGCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTQAG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
 85 CCTCTTCTG ATCGCGTCT CTCTCTGAA GACACCGGTG GAGTGTGGCA TCGGCTTCAC 1440
 CATCATCTC AGCGGGCTGC CGTCTACTT CTTCGGGGTC TGGTGGAAAA ACNAGCCCAA 1500
 GTGGCTCTC CAGGACATCT TCTCCAGCAC CGTCTGTGT CAGAAGCTCA TGCAGGTGTT 1560

CCCCCAGGAG ACATAGCCAG GAGGCGGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 543 Protein sequence

Protein Accession #: XP_035292.2

5
10
15
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11
21
31
41
51
MAGAGPKRRA LAAPAAEKEE EARETMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIGSGIFV TPTGVLEKAG SPGLALVVWA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
LEVYGSILPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FRTCPVPPEA AKLVACLCLV 180
LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
GNIVLALYSG LPAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSSSE VAVDFGNVHL GVMSHIIIPV VGLSCFGSVN GSLFTSSRLP FVGSREGHLP 360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFP SFFNWLCLAL AIIGMIWLRH 420
RKPELERPIK VNLALPVFPI LACLPLIAVS FWKTPVECGI GPTIILSGLP VYFFGVWVKN 480
KPKWLLQGIF STTVLCQKLM QVVPQET

Seq ID NO: 544 DNA sequence

Nucleic Acid Accession #: NM_005268.1

Coding sequence: 168..989

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25
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35
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45
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41
51
TAAAAAGCAA AAGAATTGCG GGCGCGCTCG ACACGGGCTT CCCCAGAAAC CTTCCTCCGCT 60
TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCCATTATGC CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGTCTCTGCT CTTCATCTTC CGGTGCTGG TGTACCTGGT GACGCGCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACCTCTGCT 360
TTGATGAGTT CTTCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTCT ACTGCTGCT GTCATGCAAG TGGCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAGGC CCGTGGGAGG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGACATAT GTCTGCAGCC TAGTGTTCAG GGCGAGCGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTGCTG GTCAAGTGCC 660
AOCGAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAAC 720
TTTTCACTCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCAAG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCAACCC CACGGTACCA CCTCTTCTCT CAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTCTGT GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCCGCCCC 960
GAGACCATGT GAAGAAACCC ATCTTGTGAG GGGCTGCCTG GACTGTGCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGTGGG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCATGCGGCC AGTTCCCTCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTTAGA ATGGAAATAG TGAGGGCCAA TGC

Seq ID NO: 545 Protein sequence

Protein Accession #: NP_005259.1

50
55
1
11
21
31
41
51
MNWSIFEGLL SGVNYKSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDHDKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLMALQ LILVTCPSLL VMHVAYREV QEKRHREAHG ENSGRLYLNP 120
GKKRGGWLMT YVCSLVFKAS VDIAFLYVPH SPYPRYLILP VVKCHADPCP NIVDCPISKP 180
SEKNITPLFM VATAATCILL NLVELIYLV S KRCHECLAAR KAQAMCTGSH PEGTSSCKQ 240
DDLSDGLDLP LGSDSHPLLL PDRPRDEHVK TIL

Seq ID NO: 546 DNA sequence

Nucleic Acid Accession #: NM_002391.1

Coding sequence: 26..457

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65
70
75
1
11
21
31
41
51
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCTCTCT 60
CGCCCTGCTG GCGCTCACTT CCGCGGTGCG CAAAAGGAAA GATAAGGTGA AGAAGGGGCG 120
CCCGGGGAGC GAGTGCCTGT AGTGGGCTGT GGGGCTGTGC ACCCCAGCA GCAAGGATTT 180
CGGCTGGGTG TTCCGCGAGG GCACCTGCGG GGCCAGACCC CAGGCGATCC GGTGCAAGGT 240
GCCCTGCAAC TGGAGAAGG AGTTTGAGC CGACTGCAAG TACAAGTTTG AGAAGTGGG 300
TGCGTGTGAT GGGGGCACAG GCACCAAGGT CCGCCAAGGC ACCCTGAAGA AGGCGGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGAAGTGAAG CCAAGCCTGG ATGCCAAGGA 480
GCCCTGGTGT TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCCA GAGCCGCTT TTGTCTCTCC CCACAATTC 720
ATTACTAAGA AACACATCAA ATAACTGAC TTTTTCCTCC CAATAAAGC TCTTCTTTT 780
TAATAT

Seq ID NO: 547 Protein sequence

Protein Accession #: NP_002382.1

80
85
1
11
21
31
41
51
MQHRGFLILT LLALLALISA VAKKDKVKK GSPGSECAEW ANGPCTPSSK DOGVGFREGT 60
CGAQTQIRIC RVPCNWKKEF GADCKYKFN WGACDGGTGT KVRQGTLEKA RYNAQCQETI 120
RVTKPCTPRT KAKAKAKKK GKD

Seq ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

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5 1 11 21 31 41 51
| | | | | |
ATGGATTGGG GGAGGCTGCA CACTTTCATC GGGGGGTGCA ACAAACTCTC CACCAGCATC 60
GGGAAGGTGT GGATTCACAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACOGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCTCG GTGTCCACA TCCGGCTGTG GGCCCTCCAG 240
10 CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAATAAGC ACAAGGTTTG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCGAA TCATCTTTGA AGCAGCCCTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
TACCACTGCG CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGCG 540
15 TTTATTCTTA GGCCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TCGCTCTGTG 600
ATTTGATGCG TGCTTAACTG GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
AGATCAAAGC AGACACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA
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Seq ID NO: 549 Protein sequence
Protein Accession #: NP_006774.1

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25 1 11 21 31 41 51
| | | | | |
MDWGLHTFI GGVNKHSTSI GKVMITVIFI FRVMILVVAQ QEVWGDDEQED FVCNTLQPGC 60
KNVCYDHFPP VSHRLWALQ LIPVSTPALL VAMHVAYYRH ETRKFRRGE KRNDPKDIED 120
IKKKVRIEG SLWYTTSSSI PFRIIFEAAP MYVPYFLYNG YHLPWVLKCG IDPCPNLVDC 180
30 FISRPTEKTV FTIPMISASV ICMLLNVAEL CYLLLLKVCPR RSKRAQTQKN HPNHALKESK 240
QNMENBLISD SGQNAITGFP S
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Seq ID NO: 550 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

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35 1 11 21 31 41 51
| | | | | |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCCTCTGC 60
TCACCCCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CTTGGCACTC CATGGCCATG GGGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACCTGTTC 240
CCACCCCGCA GGACCAACCT GAGATCGTTC TGACACAGAT GGAGAACAAAC AGCTGTGTTC 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAAGCA GGCCACGCTG CTCGATACCT ACTACGACAA TTCTCTGTTT CTCTGCCTAC 420
45 AGGACACCCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTCTGGTG 480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTTCA GCCCTGCCCC AGGCACCTAT 540
GGTACTTGTCT GAGACTTGAA CAGATGGAAG AGCGGTGCCG TTTCTAGCTC ACCTCCGCTC 600
CCAGGAAGAC CAGACTCCCA CCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCTC 720
50 TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCTCGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G
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Seq ID NO: 551 Protein sequence
Protein Accession #: NP_002562.1

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55 1 11 21 31 41 51
| | | | | |
MDIPQTKQDL ELPLKAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPPT EDNLEIVLHR 60
WENNSVEVKE VLGEKGTGNPK KFKINYTVAN EATLLDITDYD NFLPLCLQDT TPIQSMCMQ 120
YLARVLVEDD BIMQGFIRAF RPLPRHLWYL LDLKQMEEPK RF
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Seq ID NO: 552 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

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65 1 11 21 31 41 51
| | | | | |
ACTTGGCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
TGGCGGCTCT CTGCTGCTGT CCTCGCGTGG CGGGTGTGCC CGGAGAGGCT GAGCAGCCCT 120
CGCCTGAGCT GGTGGAGGTG GAAAGTGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGAGTAC GAGCAGCGGC 300
TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCTGACTCA AGTCACCCCC CAAGACGAGC 360
GCTACTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCTCAGG GTACCGCATC CAGCTCCGCG 420
75 TCTACAAAGC TCAGGAGGAG CCAAAATATC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGTACCCCC ATTCTCAAG 540
TCATCTGGTA CAAGAAATGG CGGCCTCTGA AGGAGGAGAA GAACCGGCTC CACATTCAGT 600
CGTCCAGAGC TGTGGAGTGG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
TGTTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCAGTGC 720
80 GGAACCACTT GAAGGAGTCC AGGGAAGTCA CGTCCCTGT TTTCTACCCG ACAGAAAAAG 780
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840
GTTTGGCTGA TGGCAACCCCT CCACCACTCT TCAACATCAG CAAGCAGAAC CCCAGCACCA 900
GGGAGGCAGA GGAAGAGACA ACCAAGGACA ACGGGTCCCT GGTGCTGGAG CCTGCCGSGA 960
AGGAACACAG TGGCGCTAT GAAATGTGAG CCTGGAACTT GGACACCATG ATATCGCTGC 1020
85 TGAGTGAACC ACAGGAACCT CTGGTGAAC ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080
CCCTCAGAGC ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
ACCTCAGGTT CCACTGGCTG AGAGAAGAGA CAGACCAAGT GCTGGAAGAG GGCCTCTGTC 1200
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	TTCAGTTGCA	TGACCTGAAA	CGGGAGGAG	GAGGCGGCTA	TGCTCGGTG	GCGTCTGTGC	1260
	CCAGCATACC	CGGCTGAAC	CGCACACAG	TGGTCAAGCT	GGCCATTTT	GGCCCCCTT	1320
	GGATGGCATT	CAAGGAGAGG	AAGGTGTGG	TGAAAGAGAA	TATGGTGTG	AATCTGTCTT	1380
5	GTGAAGCGTC	AGGGCACCCC	CGGCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCTGA	GCACCTCGAA	TGTCTCGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTTGAA	TGCACGGCTT	CCAAGGACCT	GGGCAAAAC	ACCAGCATCC	1560
	TCTTCTGGA	GCTGGTCAAT	TTAACCAACC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
	TCAGCACTTC	CACTGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
10	TGCGGAGCC	GGAGAGCCG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTG	ATCCTGGTCC	1740
	TGGCGGTGCT	GGGCGCTGTC	CTCTATTTC	TCTATAAGAA	GGGCAAGCTG	CGGTGCAGGC	1800
	GCTCAGGAA	CGAGAGATC	ACGCTGCCCC	CGTCTGTAA	GACCGAAGCT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAAGTCCCA	GAAGAGATGG	GCCTCCTGCA	GGGCAAGCAG	GGTGACAAGA	1920
	GGGCTCCGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
	CAGCTCCCTT	CCCTGCCCTG	ACCATTOCCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
15	CCTCCAAAG	GACTAGAGAG	AAGCCTCCTG	CTCCCTCCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
	GTCCACCACC	ATCTCTCCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
	CCGAGCGGGT	AGGAGAGTTT	CTTGCGAAGC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
20	AAATACAGCC	CTCCTGCCAG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
	CAAAAGGCTG	CTTCCACCAT	CCAGGTGCAC	CACTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GCCTGCTCAT	GTGGAAGTGC	GCTGTTTACA	CCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	CGAGTGTGTC	TGCCACCACC	CTCCTGCTCG	CCTCTTCAAA	GTCTCCTGTG	2520
	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAGA	TACGTGCCGG	2580
	GGCCAGGTGT	GGGTGCTCAG	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
25	TCACAAATC	AGGACGAGAC	CATCCTGGCT	AACACGGTGA	AACCTGTCT	CTACTAAAAA	2700
	TACAAAAAA	AATTAGCTAG	GCGTAGTGGT	TGGCACCTAT	AGTCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAG	AGAAATGGTAT	GAATCCAGGA	GGTGAGCTT	GCAGTGAGCT	GAGACCGTGC	2820
	CACTGCACTC	CAGCTGGGC	AACACAGCGA	GACTCGGTCT	CGAGGAAAAA	AAAAAGAAAG	2880
30	ACGCGTACCT	GGGTGAGGA	AGCTGGGCGC	TGTTTTGAG	TTGAGGTGAA	TTAGCTTCAA	2940
	TCCCGGTGTT	CACCTGCTCC	CATAGCCCTC	TGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
	GGGGAGCAGA	CAAGATAGAG	GTCTACACTG	TCCCTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAGGGG	CCCAATGAG	3120
	AGAATGGTAC	TAGGGATGAG	AAAAAGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGCTGT	3180
	CTGTGTGTAT	GCATCATAT	GTGTGTATAT	ATGTTTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
35	TTGTTTCCCT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCAGAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGG	CTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
	AGAGATCAGG	GCTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
40	CTACCTTACT	TTTCAGCAGC	AAAAAGTCCC	GTATGACGCA	GACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATCG	TTTCCGTCCA	CTT		

Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

45	1	11	21	31	41	51	
	GLPRLVCAFL	LAACCCCPRV	AGVPGAEQ	APELVEVEVG	STALLKQGLS	QSQGNLSHVD	60
	WFSVHKEKRT	LIFRVROGG	QSEPGVEBQR	LSLQDRGATL	ALTQVTPQDE	RIFLCQGRKP	120
50	RSQERYIQLR	VYKAPEEPNI	QVNPLGIPVN	SKEPEEVATC	VGRNGYPIPO	VIWYKNGRPL	180
	KEEKNRVHIQ	SSQTVSSGL	YTLQSIKLAQ	LKVEDKDAQF	YCELYNRLPS	GNNMKESREV	240
	TVPVFPYTER	VWLEVEPVGM	LKEGDRVEIR	CLADGNPPPH	PSISKQNPST	REABEBTND	300
	NGVLVLEPAR	KEHSGRYEQ	AWNLDTMISL	LSEPDLELVN	YVSDVRVSPA	APERQEGSSL	360
	TLTCEASSQ	DLEFQWLR	TDQVLERGPV	LQLHDLKREA	GGGYRCVASV	PSIPGLNRTQ	420
55	LVKLAIFFPP	WMAFKERKVV	VKENMVLALS	CEASGHPRPT	ISNNVNGTAS	EQDQDFQRLV	480
	STLNLVLTPE	LLETGVBECTA	SNDLGKNTSI	LFELELVNLT	LTFDSNNTTG	LSTSTASPH	540
	RANSTSTERK	LPEPESRGVV	IVAVIVCILV	LAVLGAVLYF	LYKKGKLP	RSQKEITLP	600
	PSRKTELVEE	VKSDKLPEEM	GLLQSSGDK	RAPGDQGEKY	IDLRH		

Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

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	GCTAGGCGCG	GCGGATCCCG	TCTCCCCCG	ATGTGAGCAG	TTTTCGAAA	CCCGCTCAGG	120
	CGAAGGCTGC	CCAGAGAGGT	GGAGTCGGTA	GCGGGCGCGG	GAACATGAGG	CAGTCTCTCC	180
	TATTCCTGAC	CAGCGTGGTT	CCTTTGCTGC	TGGCGCCGG	ACCTCCGGAT	GACCCGGGCT	240
70	TGGGCCCCCA	CCAGAGACTC	GAGAAGCTTG	ATTCTTTGCT	CTCAGACTAC	GATATTCTCT	300
	CTTTATCTAA	TATCCAGCAG	CATTCCGTAA	GAAGAAAGAGA	TCTACAGACT	TCAACACATG	360
	TAGAAACACT	ACTAAGCTTT	TCAGCTTTGA	AAAGGCATTT	TAAATTATAC	CTGACATCAA	420
	GTACTGAAAG	TTTTTCAAAA	AATTTCAAGG	TCGTGGTGGT	GGATGGTAAA	AACGAAAGCG	480
	AGTACACTGC	AAAATGGCAG	GACTTCTTCA	CTGGACAGCT	GGTTGGTGAG	CTGACTCTA	540
75	GGGTCTTAGC	CCACATAAGA	GATGATGATG	TTATAATCAG	AATCAACACA	GATGGGGCGG	600
	AATATAACAT	AGAGCCACTT	TGGAGATTGG	TTAATGATAC	CAAGACAAAA	AGAATGTTAG	660
	TTTATAAATC	TGAAGATATC	AAGAATGTTT	CACGTTTGCA	GTCTCCAAAA	GTGTGTGGTT	720
	ATTTAAAGT	GGATAATGAA	GAGTTGCTCC	CAAAAGGGTT	AGTAGACAGA	GAACCACTG	780
	AAGAGCTTGT	TCATCGAGTG	AAAAGAAGAG	CTGACCCAGA	TCCCATGAAG	AACAGTGTA	840
80	AATTATTGGT	GGTAGCAGAT	CATCGCTTCT	ACAGATACAT	GGGCAGAGGG	GAAGAGAGTA	900
	CAACTACAAA	TACTTAATA	GAGCTAATTG	ACAGAGTTGA	TGACATCTAT	CGGAACACTT	960
	CATGGGATAA	TGCGAGTTT	AAAGGCTATG	GAATACAGAT	AGAGCAGATT	CGCATCTCA	1020
	AGTCTCCACA	AGAGGTAAAG	CCTGGTGAAA	AGCACTACAA	CATGGCAAAA	AGTTACCCAA	1080
	ATGAAGAAAA	GGATGCTTGG	GATGTGAAGA	TGTTGCTAGA	GCAATTTAGC	TTTGATATAG	1140
85	CTGAGGAAGC	ATCTAAAGTT	TGCTTGGCAC	ACCTTTTCAC	ATACCAAGAT	TTTGATATGG	1200
	GAACCTCTTG	ATTAGCTTAT	GTGGCTCTC	CCAGAGCAAA	CAGCCATGGA	GGTGTGTTGC	1260
	CAAGGGCTTA	TTATAGCCCA	GTGGGAAGA	AAAATATCTA	TTTGAATAGT	GGTTTGAOGA	1320
	GCACAAAGAA	TTATGGTAAA	ACCATCTTAA	CAAGGAAGC	TGACCTGGTT	ACAATCATG	1380

	AATTGGGACA	TAATTTTGGA	GCAGAACATG	ATCCGGATGG	TCTAGCAGAA	TGTGCCCGGA	1440
	ATGAGGACCA	GGGAGGGAAA	TATGTCATGT	ATCCCATAGC	TGTGAGTGGC	GATCACCAGA	1500
	ACAAATAGAT	GTTTTCAAAC	TGCAGTAAAC	AATCAATCTA	TAAGACCAIT	GAAGTAAAG	1560
5	CCAGGAGTGT	TTTTCAAGAA	GCAGCAATA	AAGTTTGTGG	GAACCTGAGG	GTGGATGAAG	1620
	GAGAAGAGTG	TGATCCTGGC	ATCATGTATC	TGAACAACTG	CACCTGCTGC	AACAGCGACT	1680
	GCACGTTGAA	GGAAAGGTGTC	CAGTGCAGTG	ACAGGAACAG	TCCTTGCTGT	AAAAACTGTG	1740
	AGTTTGAAGC	TGCCAGGAAG	AAGTGCCAGG	AGGCGATTAA	TGCTACTTGC	AAAGGCGTGT	1800
	CCTACTGCAC	AGGTAATAGC	AGTGAGTGCC	CGCCTCCAGG	AAATGCTGAA	AATGACACTG	1860
10	TTTGGCTTGA	TCTTGGCAAG	TGTAAGGATG	GGAAATGCAT	CCCTTCTGTC	GAGAGGGGAA	1920
	AGCAGCTGGA	GTCCTGTGCA	TGTAATGAAA	CTGACAACTC	CTGCAAGGTG	TGCTGCAGGG	1980
	ACCTTCTGCG	CCGCTGTGTG	CCCTATGTGC	ATGCTGAACA	AAAGAACTTA	TTTTTGAGGA	2040
	AAGGAAAGCC	CTGTACAGTA	GGATTTTGTG	ACATGAATGG	CAATGTGAG	AAACGAGTAC	2100
	AGGATGTAA	TGAACGATT	TGGGATTTC	TTGACCACTG	GAGCATCAAT	ACCTTTGGAA	2160
	AGTTTTTAGC	AGACAACATC	GTTGGGTCTG	TCCTGGTTTT	CTCCTTGATA	TTTTGGATTC	2220
15	CTTTCAGCAT	TCTTGTCCAT	TGTGTGGATA	AGAAATTGGA	TAAACAGTAT	GAATCTCTGT	2280
	CTCTGTTTCA	CCCCAGTAAC	GTCGAAATGC	TGAGCAGCAT	GGATTTCTGA	TCGGTTGCGA	2340
	TTATCAAACC	CTTCTCTGCG	CCCCAGACTC	CAGGCGCGCT	CGACCTGACC	CCTGTGATCC	2400
	CTTGGGGGCC	AGCAGCTCCA	AAACTGGACC	ACCAGAGAA	GGACACCATC	CAGGAAGACC	2460
20	CCAGCACAGA	CTCCCATATG	GACGAGGATG	GGTTTGAGAA	GGACCCCTTC	CCAAATAGCA	2520
	GCACAGCTGC	CAAGTCATT	GAGGATCTCA	CGGACCATCC	GGTGGCCAGA	AGTGAAAAGG	2580
	CTGCTCTCTT	TAAACTGCAG	CGTCAGAAATC	GTTGTAACAG	CAAGAAACA	GAGTGCTAAT	2640
	TTAGTTCTCA	GCTCTTCTGA	CTTAAGTGTG	CAAAATATTT	TTATAGATT	GACCTACAAA	2700
	TCAATCACAG	CTTGATTTTT	GTGAAGACTG	GGAAAGTACT	TAGCAGATGC	TGGTCATGTG	2760
25	TTTGAACCTC	CTGCAAGTAA	ACAGTTCTTG	TGTGTTTGG	CCCTTCTCCT	TTTGAAAAGG	2820
	TAAGGTGAAA	GTGAATCTAC	TTATTTTGG	GCTTTCAGGT	TTTAGTTTTT	AAAAATCTT	2880
	TTGACCTGTG	GTGCAAAAGC	AGAAAAATACA	GCTGGATTGG	GTTATGAATA	TTTACGTTTT	2940
	TGTAATTTAA	TCTTTTATAT	TGATAACAGC	ACTGACTAGG	GAATGATCA	GTTTTTTTTT	3000
	ATACACTGTA	ATGAACCGCT	GAATATGAAG	CATTTGGCAT	TTATTTGTGA	GAAGAAGTGA	3060
30	ATAGTTTTTT	TTTTTTTTTT	TTTTTTTTTG	CTTCAACTAA	AAACAAAGGA	GATAAATTTA	3120
	GTATACATGT	TATCTAAAT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	TTTTATGTAG	3180
	CAGGGAATA	TATATCTTAA	ATTTAGAAAT	CATTTGGGTT	AATATGGCTC	TTTCAATATC	3240
	TAAGACTAAT	GCTCAGAAC	TAAACACTAC	CTTACAGTGA	GGGCTATACA	TGGTAGCCAG	3300
	TTGAATTTAT	GGAACTTACC	AACTGTTTAG	GGCCCTGATT	TGCTGGGCAG	TTTTCTGTGA	3360
35	TTTTATAAGT	ATCTTCAATG	ATCCCTGTTA	CTGATAGGGA	TACATGCTTT	AGAAAATTC	3420
	CTATTGGCTG	GGAGTGGTGG	CTCATGCGTG	TAATCCGAGC	ACTTGGAGAG	GCTGAGGTTG	3480
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Seq ID NO: 555 Protein sequence
Protein Accession #: NP_003174.2

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	QTSHTVETLL	TPSLKLRHFK	LYLTSSTERF	SQNFVQVVVD	GNSESYTAK	WQDFPTGHVV	120
45	GEPSRVLAH	IRDDVLIIR	NTDGAENIE	PLWRPVNDTE	DKRMLVYKSE	DIKNVSLQS	180
	PKVCGYLKVD	NEELLPKGLV	DREPPPELVH	RVKRRADPDP	MKNTCKLLVV	ADHRPFYRYM	240
	RGEESTITTY	LIELIDRVDD	YRNSTWDNA	GFKGYGQIE	QIRILKSPOR	VKPGKEHYNM	300
	AKSYPNEEKD	ANDVKMLLEQ	PSFDIAEEAS	KVCLAHLFTY	QDFDMGTGLL	AYVGSPPRNS	360
	HGGVCPKAYY	SPVFKQNIYL	NSGLTSTKNY	GKTLILTKEAD	LVTTHLGHNN	PGAREHDPGL	420
50	AECAPNEEDQ	GKYVMYPLAV	SGDHENNKMF	SNCSEKQSIYK	TIESKAQBCF	QERSNKVCGN	480
	SRVDEGEKED	PGIMYLANDT	CCNSDCTLKE	GVQCSDRNSP	CCRNQCFETA	QKKCQEAUNA	540
	TKGVSVCTYG	NSSBCEPPPGN	AENDTVCLDL	GKCKDGKCIIP	FCEREQQLS	CACNETDNSC	600
	KVCCRDLSGR	CVFVVDABEQ	NLFRLKKGKPC	TVGFCDMNGK	CEKRVQDVIE	RFWDFIDQLS	660
	INTFGKFLAD	NIVGSLVLFQ	LIFWIPPSIL	VHCVDKLLDK	QYESLSLFLP	SNVEMLSMD	720
55	SASVRIIKPF	PAPQTPGRLO	PAPVIPSAPA	APKLDHQHMD	TIQEDPSTDS	HMDDEGFEKD	780
	PPFNSSTAAK	SPEDLTDHPV	ARSEKAASF	LQRQNRVNSK	ETEC		

Seq ID NO: 556 DNA sequence
Nucleic Acid Accession #: NM_021832.1
Coding sequence: 164..2248

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65	CTAGGCGGGG	CGGATCCCGT	CCTCCCCCGA	TGTGAGCAGT	TTTCCGAAAC	CCCGTCAGGC	120
	GAAGGCTGCC	CAGAGAGGTG	GAGTCGGTAG	CGGGGCGGGG	AACATGAGGC	AGTCTCTCCT	180
	ATTCTGACC	AGCGTGGTTC	CTTTCGTGCT	GGCGCGCGGA	CCTCCGATG	ACCCGGGCTT	240
	CGGCCCCAC	CAGAGACTCG	AGAAGCTTGA	TTCTTTGCTC	TCAGACTAAG	ATATTCTCTC	300
	TTTATCTAAT	ATCCAGCAGC	ATTCGGTAAG	AAAAAGAGAT	CTACAGACTT	CAACACATGT	360
70	AGAAACACTA	CTAATCTTTT	CAGCTTTGAA	AAGGCATTTT	AAATTATACC	TGACATCAAG	420
	TACTGAACTG	TTTTTCAAAA	ATTTCAGGTT	CGTGGTGGTG	GATGTTAAAA	ACGAAAAGCG	480
	GTACACTGTA	AAATGGCAGG	ACTTCTTCAC	TGGACACGTG	GTTGGTGAGC	CTGACTCTAG	540
	GGTTCTAGCC	CACATAGAG	ATGATGATGT	TATAATCAGA	ATCAACACAG	ATGGGGCCGA	600
	ATATAACATA	GAGCCACTTT	GGAGATTGTT	TAATGATACC	AAAGACAAAA	GAATGTTAGT	660
75	TTATAAATCT	GAGGATATCA	AGAATGTTTC	ACGTTTGACG	TCTCCAAAAG	TGTGTGGTTA	720
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	AGAGCTTGTT	CATCGAGTGA	AAAGAAGAGC	TGACCCAGAT	CCCATGAAGA	ACACGTGTAA	840
	ATTATTGGTG	GTAGCAGATC	ATCGCTTCTA	CAGATACATG	GGCAGAGGGG	AAGAGAGTAC	900
	AACTACAAAT	TACTTAATAG	AGCTAATTGA	CAGAGTTGAT	GACATCTATC	GGAAACATTC	960
80	ATGGGATAAT	GCAGGTTTTA	AAGGCTATGG	AATACAGATA	GAGCAGATTC	GCAATCTCAA	1020
	GTCCTCCAAA	GAGGTAAAAC	CTGGTGAAAA	GCATACAAAC	ATGGCAAAAA	GTTACCCAAA	1080
	TGAAGAAAAG	GATGCTTGGG	ATGTGAAGAT	GTGTCTAGAG	CAATTTAGCT	TTGATATAGC	1140
	TGAGGAAGCA	TCTAAAGTTT	GCTTGGCACA	CCTTTTCACT	TACCAAGATT	TTGATATGGG	1200
	AACTCTTGGA	TTAGCTTATG	TTGGCTCTCC	CAGAGCAAAC	AGCCATGGAG	GTGTTTGTCC	1260
85	AAAGGCTTAT	TATAGCCCGC	TTGGGAAGAA	AAATATCTAT	TTGAATAGTG	GTTTGAGGAG	1320
	CACAAAGAAT	TATGGTAAAA	CCATCTTTAC	AAAGGAAGCT	GACCTGGTTA	CAACTCATGA	1380
	ATTGGGACAT	AAATTTGGAG	CAGAACATGA	TCGGATGGT	CTAGCAGAA	GTGCCCCGAA	1440

	TGAGGACCAG	GGAGGGAAAT	ATGTCATGTA	TCCCATAGCT	GTGAGTGGCG	ATCAGCAGAA	1500
	CAATAAGATG	TTTTCAAACT	GCAGTAAACA	ATCAATCTAT	AAGACCAATT	AAAGTAAGGC	1560
	CCAGGAGTGT	TTTCAAGAAC	GCAGCAATAA	AGTTTGTGGG	AACTCGAGGG	TGGATGAAGG	1620
	AGAAGAGTGT	GATCCTGGCA	TCATGTATCT	GAACAACGAC	ACCTGCTGCA	ACAGCGACTG	1680
5	CACGTTGAAG	GAAGGTGTCC	AGTGCACTGA	CAGGAACAGT	CCTTGCTGTA	AAAACCTGTC	1740
	GTITGAGACT	GCCGAGAAGA	AGTGCCAGGA	GGCGATTAAT	GCTACTTGCA	AAGGCGTGTC	1800
	CTACTGCACA	GGTAATAGCA	GTGAGTGCCC	GCCTCCAGGA	AATGCTGAAG	ATGACACTGT	1860
	TTGCTTGGAT	CTTGGCAAGT	GTAAGGATGG	GAATATGCATC	CCTTTCTGGG	AGAGGGGAACA	1920
10	GCAGCTGGAG	TCTGTGTCAT	GTAATGAAAC	TGACAACTCC	TGCAAGGTGT	GCTGCAGGGA	1980
	CCTTTCCGCG	CGCTGTGTGC	CCTATGTCGA	TGCTGAACAA	AAGAACCTAT	TTTTGAGGAA	2040
	AGGAAAGCCC	TGTACAGTAG	GATTTTGTGA	CATGAATGGC	AAATGTGAGA	AACGAGTACA	2100
	GGATGTAATT	GAAAGATTTC	GGGATTTTCAT	TGACCAAGCTG	AGCATCAATA	CTTTTGGAAG	2160
	GTITTTAGCA	GACAACATGG	TTGGGTCTGT	CCTGGTTTTC	TCCTTGATAT	TTTGGATTCC	2220
	TTTCAGCAIT	CTTGTCATIT	GTGTGTAAAG	TCGAAATGCT	GAGCAGCATG	GATTCTGCAT	2280
15	CGGTTGCGAT	TATCAAAACC	TTTCTGCGC	CCGAGACTCC	AGGCGCGCTG	CAGCCTGCCG	2340
	CTGTGATCCC	TTGCGGCCCA	GCAGCTCCAA	AACTGGACCA	CCAGAGAATG	GACACCATCC	2400
	AGGAAGAGCC	CAGCAGACAG	TCACATATGG	ACGAGGATGG	GTITGAGAAG	GACCCCTTCC	2460
	CAATAGCAG	CACAGCTGCC	AAGTCATTGG	AGGATCTCAC	GGACCATCCG	GTACCCAGAA	2520
	GTGAAAAGGC	TGCTCCTCTT	AAACTGCAGC	GTCAGAATCG	TGTTGACAGC	AAAGAAACAG	2580
20	AGTGCTAATT	TAGTCTCTAG	CTCTTCTGAC	TTAAGTGTGC	AAAATATTTT	TATAGATTGT	2640
	ACCTACAATC	AATCAGACGT	TATATTTTGT	GAAGACTGGG	AAGTGACTTA	GCAGATGCTG	2700
	GTCAATGTGT	TGAACCTTCT	GCAGGTAAAC	AGTTCTTGTC	TGGTTTGGCC	CTTCTCCTTT	2760
	TGAAAAGGTA	AGGTGAAGGT	GAATCTAGCT	TATTTTGAGG	CTTTCAGGTT	TTAGTTTITA	2820
	AAATATCTTT	TGACCTGTGG	TGCAAAAGCA	GAATAATACG	CTGGATTGGG	TTATGAGTAT	2880
25	TTACGTTTIT	TGAATTAAT	CTTTTATATT	GATAACAGGC	AACTGACTAGG	GAATGATCA	2940
	GTITTTTIT	ATACACTGTA	ATGAACCGCT	GAATATGAAG	CATTGTGCAT	TTATTTGTGA	3000
	GAAGAAGTGA	ATAGTTTIT	TTTTTTTTTT	TTTTTTTTTC	CTTCAACTAA	AAACAAAGGA	3060
	GATAAATTTA	GTATACATTG	TATCTAAATT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	3120
	TTTTATGTAG	CAGGGAAGAT	ATATATCTAA	ATTTAGAAAT	CATTGGGTTT	AATATGGCTC	3180
30	TTCTAATTC	TAGACTAAT	GCTCAGAAC	TAACCACTAC	CTTACAGTGA	GGGCTATACA	3240
	TGGTAGCCAG	TTGAATTTAT	GGAATCTACC	AACTGTTTAT	GGCCCTGATT	TGCTGGGCAG	3300
	TTTTTCTGTA	TTTTATAAGT	ATCTTCATGT	ATCCCTGTGA	CTGATAGGGA	TACATGTCTT	3360
	AGAAAATTCA	CTATTGGCTG	GGAGTGGTGG	CTCATGCGCT	TAATCCAGC	ACTTGGAGAG	3420
35	3421 GCTGAGGTTG CGCCACTACA CTCAGCCTG GGTGACAGAG TGAGATCTGC CTC						

Seq ID NO: 557 Protein sequence
Protein Accession #: NP_068604.1

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	GEPSRVLVAH	IRDDVVIIRI	NTDGAZYNI	PLWRPVNDTK	DKRMLVYKSE	DIKNVSRLQS	180
	PKVCGYLKVD	NEELLPKGLV	DREPPPELVH	RVKRRADPD	MKNTCKLLVV	ADHFRPYRYM	240
45	RGEESTITNY	LIELIDRVDD	LYRNTSWDNA	GFKGYGIQIE	QIRILKSPQS	VKPGKEHYNM	300
	AKSPVNEEKD	ANDWMLLEB	FSFDIAEAS	KVCLAHLFTY	QDFDMGTGL	AYVGSPPRNS	360
	HGGVCPKAYI	SPVCKKNIVL	NSGLTSTKNY	GKTLTKEAD	LVTTHELGHN	PGAREHDPGL	420
	AECAPNEDQG	GKIVMYPIAV	SGDHENKMP	SNCSTQSIYK	TIESKAQECF	QERSNKVCGN	480
	SRVDEGEED	PGIMYLNNDT	CCNSDCTLKE	GVQCSDRNSP	CCRNQCFETA	QKCKQEAINA	540
50	TCKGVSYCTG	NSSCEPPFPG	AEDDTVCLDL	GKCKDKGKIC	PCEREQQLS	CACNETDNC	600
	KVCCRDLSGR	CVFYDAEQR	NLFLRKGP	TVGFCDMNGK	CEKRVQDVIE	RFWDFIDQLS	660
	INTFGKPLAD	NIVGSVLVPS	LIPWIPPSIL	VHCV			

Seq ID NO: 558 DNA sequence
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Coding sequence: 20..2143

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	CCTGAGAACC	AATCTCACCG	ACAGGCAGCT	GGCAGAGGAA	TACCTGTACC	GCTATGTGTA	180
	CACCTCGGGT	GCAGAGATGC	GTGGAGAGTC	GAAATCTCTG	GGGCTGTGCG	TGCTGCTTCT	240
	CCAGAAGCAA	CTGTCCCTGC	CCGAGACCGG	TGAGCTGGAT	AGCGCCACGC	TGAAGGCCAT	300
65	CGGAACCCCA	CGGTGCGGGG	TCCAGACCTT	GGGCAGATTC	CAAACTTTTG	AGGGCGACCT	360
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	GGCGGTGATT	GACGACGCTT	TTGCCCGCGC	CTTCCGACTG	TGAGCGCGCG	TGACGCGGCT	480
	CACCTTCAC	CGCTGTGTACA	GCCGGGACGC	AGACATCGTC	ATCCAGTTTG	GTGTGCGGGA	540
	GCACGAGAC	GGGTATCCCT	TCGACGGGAA	GGACGGGCTC	CTGGCACACG	CCTTTCCTCC	600
70	TGGCCCGCGC	ATTCAAGGAG	ACGCCCATTT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660
	GGGCGTGTGT	GTTCACACTC	GGTTTGGAAG	CGCAGATGGC	GGGCGCTGCC	ACTTCCCTCT	720
	CATCTTCGAG	GGCGCTCTCT	ACTCTGCTGT	CACCAACGAC	GGTGTCTCCG	ACGCTTGTCC	780
	CTGGTGCAGT	ACCACGGCCA	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGCGA	840
	GAGACTCTAC	ACCGGGGACG	GCAATGTCTG	TGGGAAACCC	TGCCAGTTTC	CATTCTCTTT	900
75	CCAAAGGCCA	TCCTACTCCG	CCTGCACAC	GGACGGTCCG	TCCGACGGCT	ACCGCTGGTG	960
	CGCCACCCAC	GCCAACTACG	ACCGGGACAA	GCTCTTGGCG	TTCTGCGCGA	CCCGAGCTGA	1020
	CTCGACGGTG	ATGGGGGGCA	ACTCGGGGGG	GGAGCTGTGC	GTCTTCCCTT	TCATTTCTCT	1080
	GGGTAAAGGAG	TACTCTGACT	GTACCAAGCA	GGGCGCGCGA	GATGGGCGCG	TCTGGTGGCG	1140
	TACCACTCTG	AATTTTGACA	GGCAAGGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
80	TTTGTCTCTG	GTGGCGGCGC	ATGAGTTCCG	CCAAGCGCTG	GGCTTAGATC	ATTCTCTCAGT	1260
	GCGGAGGGCG	CTCATGTACC	CTATGTACCG	CTTCACTGAG	GGGCCCCCTT	TGCTAAGGGA	1320
	CGAGTGAAT	GGCATCGGCG	ACCTCTATGG	TOCTCGCCCT	GAACCTGAGC	CACGCGCTCC	1380
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	TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTTCAG	CTGGCCCCAC	1500
85	AGGTCCCCCC	CTCTGCGGCC	CTTCTAGCGC	CACACTGTGT	CCTTTGAGTC	GGTGGAGGGA	1560
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CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740
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GGTGTCTGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCGCAGCTGG CCCAGGTGAC 1860
CGGGGCCCTC CCGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG 1920
GTTGCACTGT AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
CCCCGGGTGC CCTTTGGACA CGCAGACGCT CTTCAGTAC CGAGAGAAAG CCTATTCTGT 2040
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GGGCTACGTG ACCTATGACA TCCTGCAATG CCCTGAGGAC TAGGGCTCCC GTCTGCTTTT 2160
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CAAACGTGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC 2280
TCACCTTGTG TTTTGTGTGG AGTGTCTCTA ATAACTTGG ATTCTCTAAC CTTT

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Seq ID NO: 559 Protein sequence
Protein Accession #: NP_004985.1

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1 11 21 31 41 51
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RGESKSLGPA LLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLRFPQTF EGDLLKWHHN 120
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FDGKDGLLAH AFPFGPGIQG DAHFDDELWL SLGKGVVVPY RFGNADGAAC HFFFIPEGRS 240
YSACTTGRS DLPLWCSSTA NYDTDDRFGP CPSERLYTRD GNADGKPCQF PFIFQGQSYS 300
ACTTDGRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
CTSEGRGDGR LMCATTNFD SDKKWGFPCD QGYSLFLVAA HEFHALGLD HSSVPEALMY 420
PMYRFTGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSE 480
PTAGTGPPTS AGPTGPPTAG PSTATTVPLS PVDADCNVNI FDLAEIGNQ LYLFRDGYKW 540
RPSSEGRSRP QDFPLIADKW PALPRKLDV FEEPLSKLFP FFSGRQVWVY TGASVLGPRR 600
LDKLGADGV AQVTGALRSR RGMMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMPFGVPLD 660
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Seq ID NO: 560 DNA sequence
Nucleic Acid Accession #: NM_000213.1
Coding sequence: 127..5385

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CGGCGCTGCA CACCCAGGCG GGAGCTGCTG CCGCGGGGCT GCCAGCGGGA GAGCATCGTG 360
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	GGCGGGAAGT	CCAGGTCTCT	CTACOGCACA	CAGGATGGCA	COGCGCAGGG	CAACCGGGAC	3240
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5	GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCTGCG	GGGCGCGCCA	GGTCCGCGGT	3360
	TTCCAGTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCACC	TGGGCCAGCC	CCACTCCACC	3420
	ACCATATCA	TCAGGGACCC	AGATGAACCT	GACCGGAGCT	TCAAGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCCCAACGG	OGACCTGGGC	CCCCCGCAGA	ACCCCAATGC	TAAGGCGCGT	3540
	GGGTCCAGGA	AGATCCATT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
10	GTAAGTACT	GGATTTCAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
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	GTGCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTCGTCT	CCTCCACGGT	GACCCAGCTG	3840
	AGCTGGGCTG	AGCCGCTGGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
15	CTGGTCAAG	ATGACAAACG	ACCTATTGGG	CCCATGAAGA	AAGTGTGGT	TGACAACCTT	3960
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	CAGCCCAAGA	GGCCCATGTC	CATCCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCAG	4140
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20	GGCAGCCAGA	GGCCAGCGT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
	TTTGCTTCC	CGGGCAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGTGCTC	4320
	TATGGCACCC	ACCTGAGCGC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380
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25	GACTACTCCA	CCCTCACCTC	GGTCTCTCTC	CACGACTCTC	GCCTGACTGC	TGGTGTGCCC	4500
	GACACGCCCA	CCCGCTGGT	GTTCTCTGCG	CTGGGGGCCA	CATCTCTCAG	AGTGAGCTGG	4560
	CAGGAGCCCG	GGTCCGAGCG	GCCTGTGACG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
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	GACCTCTCTC	CAAACCACTC	CTAGTGTTC	CGCTGGGGG	CCAGAGCCA	GGAAAGGCTG	4740
30	GGCCGAGAGC	GTGAGGGTGT	CATCACCAAT	GAATCCGAG	TGCACCCGCA	GAGCCCACTG	4800
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	TTCACTGCC	TGAGCCGACA	CTCGCTGACG	CTGAGCTGGG	AGCGGCCACG	GAGGCCCAAT	4920
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35	AACGTGCCCT	ACAAGTTCAA	GGTGACGGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGCGC	5100
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	GGCGGGCTCT	TCCAGCACCC	GCTGCAAAAG	GAGTACAGCA	GCATCAACAC	CACCCACACC	5220
	AGCGCCACCG	AGCCCTTCCT	AGTGGATGGG	CCGACCCCTG	GGGCCAGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TCAACCCGCA	TGTGACCAG	GAGTTGTGA	GCCGACACT	GACCAACGAG	5340
40	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCGCCCAT	GTCCAGCTAG	GGCTCTCTCC	GACTCCTCTC	CCGAGCGCTC	CTCAGCTACT	5460
	CCATCTCTGC	ACCCCTGGGG	GCCAGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
	TCCTGGGAGG	CATGAAGGGG	GCAAGGTCG	TCCTCTGTGG	GCCCAAACTT	ATTGTGTAAC	5580
45	AAAGAGCTGG	GAGCAGCACA	AGGACCCAGC	CTTTGTTCTG	CACCTAATAA	ATGTTTGTGC	5640
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Seq ID NO: 561 Protein sequence
Protein Accession #: NP_000204.1

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	PQTDMPREKL	KEPWPNSDPP	PSPKRVISLT	EDVDEPRNKL	QGERISGNLD	APEGGPDAIL	240
55	QTAVCTRDIG	WRPDSHLLV	PSTESAFHYE	ADGANVLAGI	MSRNDERCHL	DTTGTYYQYR	300
	TQDYPSPVPTL	VRLLAKHNI	PIFAVTNYSY	SYYEKLHTYF	PVSSLGVLQE	DSSNIVELLE	360
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	THVQQLPEDQ	KGNHLKPSF	SDGLKMDAGI	ICDVCTCELO	KEVRSARCSF	NGDPVCGQCV	480
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	PQCPTSGPL	CNDRGRCSMG	QCVCEPGWTG	PSCDCPLSNA	TCIDSNGGIC	NGRGHCBOGR	600
	CHCQQSLYT	DTICEINYSY	IHPGLCEDLR	SCVQCQAWGT	GEKKGRTECE	CNFKVKMVDK	660
	LKRAEEVVVR	CSFRDEDDDC	TYSYTMEDDG	APGPNSTVLV	HKQKDCPPGS	FWWLIPLLLL	720
	LLPLLALLLL	LCWKYCACCK	ACLALLPCCN	RGHMVGFKED	HYMLRENIMA	SDHLDTFMLR	780
65	SGNLKGRDVV	RWKVTNNMQR	PGPATHAASI	NPTLVPEYGL	SLRLARLCTE	NLLKPDTRFC	840
	AQLRQVEVEN	LNEVYRQISG	VHKLQQTQFR	QOPNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
	LTEKQVEQRA	FHDLKVAPGY	YTLTADQDAR	GMVEFQEGVE	LVDVRVPLFI	RPEDDDEKQL	960
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	KSQVSYRTQD	GTAQGNRDYI	PVEGELLFPQ	GEANKELQVK	LLELQEVDSL	LRGRQVRRFH	1080
70	VQLSNPKFGA	HLQPHSTTI	IIRDPELDR	SFTSQMLSSQ	PPPHGDLGAP	QNPNAKAAGS	1140
	RKIHFNWLPF	SGKPMGYRVK	YWIQDSESE	AHLLDSKVPS	VELTNLYPYC	DYEMKVCAYG	1200
	AQGGEPYSSL	VSCRTQHEVP	SEPGRLAFNV	VSSVTQLSW	AEPATNGEI	TAYEVCYGLV	1260
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75	FPGSTNSLHR	MTTTSAAAYG	THLSPEVPHR	VLSTSSLTTR	DYNSLTRSEH	SHSTTLPRDY	1440
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	LPGSAFTLST	PSAPGLVFT	ALSPDSLQLS	WERPRPNDG	IVGYLVCEM	AQGGGPATAP	1620
	RVDGSPESR	LTVPLSENV	PKFKVQART	TEGPGPEREG	ITITSEQDGG	PFPQLGSRAG	1680
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Seq ID NO: 562 DNA sequence
Nucleic Acid Accession #: NM_013332.1
Coding sequence: 1..63

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CAAGGCGCTT CCAGAGCCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420
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Protein Accession #: NP_037464.1

1 11 21 31 41 51
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Seq ID NO: 564 DNA sequence
Nucleic Acid Accession #: NM_023915.1
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CCCAAGCCTC AATCGTCCCC AAGTGTTCCT TGACAAGCAT CTTGCTTAC AGTGATCAC 240
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Seq ID NO: 565 Protein sequence
Protein Accession #: NP_076404

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FYANMYTSIV FLGLISIDRY LKVVKPPGDS RMYSTFTKV LSVCVWVIMA VLSLENIILT 180
NGQPTEDNHI DCSKLKSLPG VKMHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
ISQSSRRKRE NQSIIRVVAV FFTCFLFYHL CRIPFTPSHL DRLLDESAQK ILYYCKBITL 300
FLSACVCLID PIYFPMCRS PSRRLPKKSN ITRSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 566 DNA sequence
Nucleic Acid Accession #: NM_005365.1
Coding sequence: 1..948

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TCCTCTGACA GCAGAGGAGA GGAGGTGCTC GCTGCTGGGT CATCAAGTCC TCCCCAGAGT 180
CCTCAGGAGG GCGCTTCTCT CTCCATTTC GTCTACTACA CTTTATGGAG CCAATTGAT 240
GAGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGTCCGACCC AGCTCAGCTG 300
GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTGTGTTCA TTTCTGCTC 360

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CTTGGCCTCT	CGTGGGATAG	CATGCTGGGT	GATGGTCATA	GCAATGCCAA	GGCGCCCTC	600
CTGATCATTG	TCCTGGGTGT	GATCCTAACC	AAAGACAACT	GCGCCCTGTA	AGAGGTTATC	660
TGGGAAGCGT	TGAGTGTGAT	GGGGGTGTAT	GTGGAAGAGG	AGCACATGTT	CTACGGGGAG	720
CCGAGGAAGC	TGCTACCCCA	AGATTGGGTG	CAGGAAAAC	ACCTGGAGTA	CCGCGAGGTG	780
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AGCTATGAGA	AGGTCAATAA	TTATTGGGTC	ATGCTCAATG	CAAGAGAGCC	CATCTGCTAC	900
CCATCCCTTT	ATGAAGAGGT	TTTGGGAGAG	GAGCAAGAGG	GAGTCTGA		

Seq ID NO: 567 Protein sequence
Protein Accession #: NP_005356.1

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HKYRVKEPVT	KAEMLSEVIK	NYKRYFPVIF	GKASEFMQVI	PQTDVKEVDP	AGHSYILVTA	180
LGLSCDSMLG	DGHSMPKAAL	LIIVLGVILT	KDNCAPEEVI	WEALSVMGVY	VGKEHMFYGE	240
PRKLLTQDMV	QENLYEYRQV	PGSDPAHYEF	LWGSKAHAET	SYEKVINYL	MLNAREPICY	300
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Seq ID NO: 568 DNA sequence
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Coding sequence: 86..1126

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GATCTGGACT	CGAGGCTGGC	TGCTGCTGCT	GCTGCTTCGC	GGAGGAGCGC	AGGCCCTGGA	180
GTGCTACAGC	TGCGTGCGAG	AAGCAGATGA	CGGATGCTCC	CGAACAAGA	TGAAGACAGT	240
GAAGTGCGCG	CCGCGCGTGG	ACGCTGCGAC	CGAGGCCCGT	GGGGCGGTGG	AGACCATCCA	300
CGGACAAATC	TGCTGCGCAG	TGCSGGGTGG	CGGTTCCGGA	CTCCCCGGCA	AGAATGACCG	360
CGGCTGGAT	CTTCACGGGC	TTCTGGCGTT	CATCCAGCTG	CAGCAATGCG	CTCAGGATCG	420
CTGCAACGCC	AAGCTCAACC	TCACCTCGCG	GGCGCTCGAC	COGGCAGGTA	ATGAGAGTGC	480
ATACCGCGCC	AACCGCGTGG	AGTGCTACAG	CTGTGTGGGC	CTGAGCCGGG	AGGCGTGCCA	540
GGGTACATCG	CCGCGGCTCG	TGAGCTGCTA	CAACGCCAGC	GATCATGTCT	ACAAGGGCTG	600
CTTCGACGGC	AAGTCAACCT	TGACGGCAGC	TAATGTGACT	GTGTCTTTGC	CTGTCCGGGG	660
CTGTGTCCAG	GATGAATCTT	GCACTCGGGA	TGGAGTAACA	GGCCCAGGGT	TCAAGCTCAG	720
TGGCTCTCTG	TGCCAGGGGT	CCCGCTGTAA	CTCTGAOCTC	CGCAACAAGA	OCTACTTCTC	780
CCCTCGAATC	CCACCCCTTG	TCCGGCTGCC	CCCTCCAGAG	CCCAAGACTG	TGGCTCAAC	840
CACATCTGTC	ACCACTTCTA	CCTCGGCCCC	AGTGAGACCC	ACATCCACCA	CCAAACCCAT	900
GCCAGCGCCA	AGCAGTCAGA	CTCCGAGACA	GGGAGTAGAA	CACGAGGCCCT	CCCGGATGTA	960
GGAGCCCGAG	TTGACTGGAG	GCGCCGCTGG	CCACCAGGAC	CGCAGCAATT	CAGGGCAGTA	1020
TCCTGCAAAA	GGGGGCCGCC	AGCAGCCCCA	TAATAAAGGC	TGTGTGGCTC	CCACAGCTGG	1080
ATTGGCAGCC	CTTCTGTTGG	CCGTGGCTGC	TGGTGTCTTA	CTGTGAGCTT	CTCCACCTGG	1140
AAATTTCCCT	CTCACTTACT	TCTCTGSCCC	TGGGTACCCC	TCTTCTCATC	ACTTCTCTGT	1200
CCCAACCACT	GACTGGGCTG	GCCAGCCCCC	TGTTTTTCCA	ACATTCGCCA	GTATCCCCAG	1260
CTTCTGCTGC	GCTGTGTTGC	GGCTTTGGGA	AATAAAATAC	CGTGTATAT	ATTCTGGCAG	1320
GGGTGTTCTA	GCITTTTAGG	GACAGCTCCT	GTATCCTTCT	CATCCTTGTC	TCTCCGCTTG	1380
TCCTCTGTGG	ATGTTAGGAC	AGAGTGAGAG	AAGTCAGCTG	TCACGGGGAA	GGTGAGAGAG	1440
AGGATGCTAA	GCTTCTTACT	CATTTCTCC	TAGCCAGCCT	GGACTTTGGA	GCGTGGGGTG	1500
GGTGGGACAA	TGCTCTCCCA	CTCTAAGCAC	TGCCTCCOCT	ACTCCCCGCA	TCTTTGGGGA	1560
ATCGGTTCCC	CATATGTCTT	CCTTACTAGA	CTGTGAGCTC	CTCGAGGGCA	GGGACCGTGC	1620
CTTATGTCTG	TGTGTGATCA	GTTTCTGGCA	CATAAATGCC	TCAATAAAGA	TTTAATTACT	1680
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Seq ID NO: 569 Protein sequence
Protein Accession #: NP_055215

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SRALDPAGNE	SAYFPNGVBC	YSCVGLSREA	CQGTSPFVVS	CYNASDHVYK	GCDFGNVTLT	180
AANVTYSLFV	RGCVDQDEPT	RDGVTGPGPT	LSGSCQGSR	CNSDLRNKTY	FSPRIPLVLR	240
LPPPEPTTVA	STTSVTSTST	APVRPTSTTK	PMPAPTSQTP	RQGVHEASR	DEEPRLTGGA	300
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Seq ID NO: 570 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

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CACCTACTGT	CCCTCGGCTC	GTACGGGCGC	ATCCTGGGCC	TGCACCTGCT	CATTGAGAGC	180
CTTTTGTGCT	TCCTGGAGCA	CCGGCGCATG	CGACGTGCGG	GCCAGGCCCT	GAAGCTGCCC	240
TCCCCGGGCG	GGGGCTCGGT	GGCACTGTGC	ATTGCCCGGT	ACCAGGAGGA	CCCTGACTAC	300
TTGCGCAAGT	GCCTGGCTCT	GGCCAGCGCG	ATCTCCTTCC	CTGACCTCAA	GGTGTCTCAT	360
GTGGTGGATG	GCAACCGCCA	GGAGGAAGCC	TACATGTCTG	ACATCTTCCA	CGAGGTGCTG	420
GGCGGCACCG	AGCAGGCGCG	CTTCTTTGTG	TGCGCGAGCA	ACTTCCATGA	GGCAGGCGAG	480
GGTGAGACGG	AGGCCAGCCT	GCAGGAGGGC	ATGGACCGTG	TGCGGATGT	GGTGGGGGCC	540
AGCACCTTCT	CGTGATCAT	GCAGAGGTGG	GGAGGCAAGC	GCGAGGTCT	GTACACGGCC	600

5 TTCACGGCCC TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
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 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTCTGGAG 900
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 TACTTCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCCT CTGGATGACC 1140
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 TTCTACCGGG GCGGCATCTG GAACATTCTC CTCTTCTCTG TGACGGTGA GCTGGTGGG 1260
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 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGGCCA AGATCTTTGC CATTGTCTAC 1380
 15 ATCAACAAT CTGGCTGGGG CAOCCTCTGG CGAAAAACCA TTGTGGTGA CTTCTATTGG 1440
 CTCATTCTTG TGTCCATCTG GGTGGCAGTT CTCTGGGAG GGCTGGCCTA CACAGCTTAT 1500
 TGCCAGGACC TGTTTCAGTA GACAGAGCTA GCTTCTCTG TCTCTGGGG TATCTGTAT 1560
 GGCTGTCTCT GGTGGGCTT CCTCATGCTA TATCTGGCCA TCATCGCCC GCGATGTGGG 1620
 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

20 Seq ID NO: 571 Protein sequence
 Protein Accession #: NP_005320.1

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 LFLAFLEHRRM RRAGQALKLP SPRRGSVALC IAAVQEDPDY LRKCLRSAQR ISFPDLKVV 120
 VVDGNRQEDA YMLDIPHEVL GGTQAGFFV WRSNPFHEAGE GETEASLQEG MDRVRDVVRA 180
 STFSCLMQLM GSKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
 VGGDVQILAK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQGFLE 300
 30 DWYHQKFLGS KCSFGDDRLH TNRVLSLGRY TKYTARSKCL TETPTKYLWR LNQQTRWSKS 360
 YPREMLYNLS WPKHHLWMT YESVVTGFFP FFLIATVIQL PYRGRIWNIL LFLLLTVQLVG 420
 IIKATYACFL RGNAEWIFMS LYSLLVMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNFIG 480
 LIPVSIWVAV LLGLLAYTAY CQDLFSETEL APLVSGAILY GCYVWALLML YLAI IARRCG 540
 KKPEQYSLAP AEV

35 Seq ID NO: 572 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-7095

40 1 11 21 31 41 51
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 CGGCGAGGGG CCGCAGACGG TCTGGAAATG CGAATCTCAA AGCGTTTCTC CGCTTGCAAT 180
 45 CAGCTCCTCT GTGTTTGGCG CTTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTTGTTGAAG AGATTGGCTG GTCTATATCA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG 300
 AAATATCCAA CATGTAATAG CCCAAACAAA TCTCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGCTT GGGATAAAAC ATCATTGGAA 420
 50 AACACATCCA TTCATAACAC TGGGAAAAAC GTGGAAATTA ATCTCACTAA TGACTACCGT 480
 GTCAGCGGAG GAGTTTCAGA AATGGTGTIT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGAATTTCAA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAAAGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAAATTG 720
 55 GATTTCAAAG CGATTATTTG TGGAGTCGAA AGTGTTAGTC GTTTTGAGGA GCAGGCTGCT 780
 TTAGATCCAT TCATATCTGT GAACCTTCTG CCAAACTCAA CTGACAGTAA TTACATTAC 840
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTGG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTGTGTG AAGTTCTTAC AATGCAACAA 960
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 60 TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAGGGAAG AGATTATGA AGCAGTTTGT 1080
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 65 TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTGACAT GCCTACTGAT 1380
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 75 GCAACTCTCG CTATCCCATT CATCTCTGAG AACATATCCC AAGGATATAT ATTTTCTCTC 1980
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 TTTGCGCATC TGCATACAGT TTCTCAATC CTTCACAGG TTACTTCAGC TACCGAGAGT 2700
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	AGCCTTGCTC	AGTATCTGTA	TGTGCTGCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	TCITTTATAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTAGTG	CCATGATGCA	TGCAOGTTCT	TCAGGGGCTG	AACCTTCTTA	TGCGCTGTCT	2940
5	GATAATGAGG	GCTCCCAACA	CATCTTCAC	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACCTA	TCAGGGTTC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGCTTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACCT	GTTTCTGTAG	CTGAATTAC	ATATACAACA	3240
10	TCGTGTTTGG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
	ACTGAACTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
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	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCA	TTCAACCTAC	ACATACTGTC	3540
15	TCCTAAGCAT	TCGTGACAC	TTGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TCTGTATGTT	3720
	GACACCTTGC	TTAAACCTGT	TCTTCCAGCT	GTGCCAGTG	ATCCAAATAT	GGTTGAAACC	3780
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20	AGTGAACACA	TGCTGCACCT	TACATCTGTA	CCAGTTTTTG	ATGTGTGCGC	TACTTCTCAT	3900
	ATGCACCTCG	CTTCACTTCA	AGGTTTGACC	ATTTCTTATG	CAAGTGAGAA	ATATGAACCA	3960
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	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
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	GACACTAATG	AAAAGATGTC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCTC	4920
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	CAGATTCAAC	ACGATGGGAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	COGTTACACA	6060
	AGAAATATT	TGATCAAAAC	TGAGGAGCAA	TATGTCTTCA	TTTATGATAC	ACTGTTTGG	6120
	GCCATACCTA	TGAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTTATGCTTA	TGTTAATGCA	6180
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	GGAGAGGCA	CAGACTACAT	CAATGCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
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	AGAAATAATC	TGTTACTTAT	TGTAATAACT	GCCCTAGTGT	CTCATGGAC	CAAAATTTATA	7620
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85	GTTTAGTTTA	ATGAGTAGT	TCATTAGCTG	GTCTTACTCT	ACCAAGTTTT	TGACATTGTA	7740
	TTGTGTATCC	TAGTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAAAAAT	7800
	GAAATACCTT	CTTTTGAAGA	GAAGTTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTGTA	7860
	AATGTTTTTT	ATCCAAAGGA	TTGCAAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAAAATA	7920
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Seq ID NO: 573 Protein sequence:
Protein Accession #: Eos sequence

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10	ILPEVGTEEN	LDPKAIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEPNVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
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	LIGTEBIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GKYNKAKTN	480
15	RSPTRGSEPS	GKQDVFNLSL	NSTSQPVTLK	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSTGTAESL	NTVSIITYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETIITY	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSTDI	660
	TAQPPVGGGR	ESPLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAPT	SSRQQLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVPFL	VTPLLLDNQI	780
20	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPPLHSL	FVAGGDLILLE	PSLAQYSDVL	STTHAASETL	EPGSESGVLY	900
	KTLMPFSQVEP	PSSDAMMHAR	SGGPEPSYAL	SDNEGSOHIF	TVSYSSAIPV	HDSVGVITYQG	960
	SLFSGPSHIP	IPKSLITFT	ASLLQPTHAL	SGDGENSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVAEFTYT	TSVFGDDNKA	LSKSEIYGN	ETELQIPSPN	EMVYPSSEST	MPNMYDNVKN	1080
25	LNASLQETS	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	NNPSVQPTHT	VSQASGDTSL	1140
	KPVLANSANP	ASSDPASSE	LSPSTQLLFY	ETASPFSTEV	LLQSPFQASD	VDTLTKTVLP	1200
	AVPSDPIIVE	TPKVDKISST	MLHLIVNSGA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVVPISLYND	ELPQTANLEI	NQAPPKGRH	VFATPVLSID	1320
30	EPLNLTINKL	IHSDEILTST	KSSVTGKIVA	GIPTVASDTF	VSTDHSPVIG	NGHVAITAVS	1380
	PHRDGSVTST	KLLPFSKATS	ELSHSAKSDA	GLVGGGEDGD	TDDGDGDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVMNDSD	THENSIMQDN	NPISYSLSEN	SEEDNRVTSV	SSDSQTMGDR	1500
	SPGKSPSANG	LQKQNDGKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDEESG	SGQGTSDSLN	1560
	ENETSTDPSF	ADTNEKDADG	ILAAAGDSEIT	PGFPQSPSTSS	VTSENSEVPH	VSEAZASNSS	1620
35	HESRIGLAEG	LESEKKAIVP	LVIVSALTFI	CLVLVLGILI	YWRKCPQTAH	PYLEEDSTSPR	1680
	VISTPTPTIP	PISDDVGAIP	IKHPPKHVAD	LHASSGPTTE	PETLKEFYQE	VQSCVTDLGI	1740
	TADSSNHPDN	KHKNYRINI	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGLKSTAEAD	FWRMWERNV	EIVIMITNLV	EKGRRKCDQY	WPADGSEERY	NFLVTQKSVQ	1860
	VLAYYYTRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQMP	DMGVPEYSLP	VLTFRKAAAY	1920
40	AKRHAVGPVV	VSCSAGVGRT	GTIYIVLDSML	QIQIHBTGVN	IFGFLKHIRS	QRNYLVQTEB	1980
	QVVFVHDTLV	EALLSKETAP	LDSEIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIIQSDY	2040
	SAALKQCNRE	KNRTSSIIIP	ERSRVGISSL	SGEGTDYINA	SYMIGYQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WBNQAQLVVM	IPDQNMAD	EFVYWPNDKE	PINCSEFKVT	LMAEEHKCLS	2160
	NEEKLIQDP	ILEATQDDYV	LEVRHPQCPK	WPNFDSPISK	TFELISVIKE	EAANRDGPMI	2220
45	VHDEHGGVTA	GTFCALTTLM	HQLEKENSVD	YVQVARMINL	MRPGVPADIE	QYQFLYKVL	2280
	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESILV			

Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-4518

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55	CGCGAGGGGG	CGCGAGACCG	CTCGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
60	CAAGTAATAT	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTTGGA	420
	AACACATTCA	TTCATACAC	TGGGAAAAAC	GTGGAATAAT	ATCTCACTAA	TGACTACCGT	480
	GTACGCGGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
65	GGAAAGGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTT	720
	GATTTCAAAG	GATTATTGGA	TGGAGTGGAA	AGTGTAGTGC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCTGTCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTCTTTAC	AATGCAACAA	960
70	TCTGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAAAT	TTCAGAGACA	ACAGTACAGT	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTATGTA	ACAGCTTTGT	1080
	AGTTCAGAAC	CAGAAAAATG	TCAGGCTGAC	CCAGAGAATT	ATACCACTCT	TCTTGTTACA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCGA	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
75	GGTGCTATTC	TCAATAATTT	GCTACCCAA	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCCTAATG	GCTTATATG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAAAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCAACA	CACACTACAA	TGCGATAGGG	1560
80	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTATG	TTCCCAATAG	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCCT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACATG	TTCTTAGATC	TCCACATATG	1800
	AACITGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
85	AGTTTATTTG	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAAGAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100

	GTGTGCTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCC	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGCTTAATTA	CACTGAGATA	CGTGTGTATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTTCTG	CAGGCCCACT	GATGTACACG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
5	CATTATTCTA	CTTTGGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGTGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TGGAAATCCG	AGAAGAAGCG	AGTTATACCC	CTTGTGATCG	TGTGAGCCCT	GACTTTTATC	2520
	TGTCATGTGG	TTCTTGTGGG	TATTTCTATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
10	TTTTACTTAG	AGGACAGTAC	ATCCCTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTCGG	AGCAATTCCA	ATAAAGCACT	TTCCAAGACA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCCAGGA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
15	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
	TACAAACAGC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGAGAG	TGATATGGGA	ACATAATGTG	GAAGTATTAT	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAAGTG	TGATCAGTAC	TGGCTGCGCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACCTTCTGG	TCCTCAGAA	GAGTGTGCAA	GTGCTTGCCCT	ATTATCTGTG	GAGGAATTTT	3180
20	ACTCTAAGAA	ACACAAAAAT	AAAAAGGGC	TCCAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
	GTACACAGAC	GTACACTACAC	GCACTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	TGCTGGAGT	TGGAAGAAC	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTG	AACACGAAGG	AACGTGCAAC	ATATTGGGCT	TCTTAAAAACA	CATCCGTTCA	3480
25	CAAAGAAAT	ATTTGGTACA	AACGTAGGAG	CAATATGTCT	TCATTCTATG	TACACTGGTT	3540
	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGCT	ATATTCTATG	CTATGTTAAT	3600
	GCACTCTCTA	TTCTCTGACC	AGCAGGCAAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTGGCAT	TTCATCCCTG	3780
30	AGTGGAGAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
	GAATTCTATC	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCCT	GAGGATGATA	3900
	TGGGACCAT	ATGCCCAACT	GGTGGTTATG	ATTCTCTGAT	GCCAAAACAT	GGCAGAAGAT	3960
	GAATTTGTTT	ACTGGCCAA	TAAAGATGAG	CCTATAAAT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGCTG	AAGAACAACA	ATGCTATCT	AATGAGGAAA	AACCTATAAT	TCAGGACTTT	4080
35	ATCTTAGAAG	CTACACAGAA	TGATTATGTA	CTTGAAGTGA	GGCATTCTCA	GTGCTCTAAA	4140
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	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTCATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
40	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTGA	GCACAAGGCA	GGAGAGAAAT	4440
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	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTT	4560
	CTCTCTCTTA	AATTAGGCA	GAATAATCAGT	CTAGTTCTGT	TATCTGTGTA	TTTCCATCA	4620
	CCTGACAGTA	ACTTTTATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAAATGTG	4680
45	TGCTTTTTTG	CAAGACTTGT	AATTTACTTA	TTATGTTTGA	ACTAAAATGA	TTGAATTTTA	4740
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55	TCAAATGGTT	TTTATCCAA	GAATTGCAAA	AATAAATATA	AATATTGCCA	TTAAAAAAA	5340
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Seq ID NO: 575 Protein sequence:
Protein Accession #: Eos sequence

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65	FKASKITPHW	GKCNMSSDGS	ERSLEGQKFP	LEMQIYCFDA	DRPSSFEAV	KGKGLRLALS	180
	ILFEVGTEN	LDFAIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVPCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KPSRQVFPSSY	300
	TGKEEIHBAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKPAVLY	QQLDGEDQTK	360
70	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPPE	420
	LIGTEEIIKE	EEBEGDIEEG	AIVNPGRDSA	TNQRKKEPQ	ISTTTHYNRI	GTYNEAKTN	480
	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPFHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSTGAESL	NTVSTIEYKE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
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	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNABASNS	SHERIGLAE	GLESEKKAVI	780
	PLVIVSALPT	ICLVVLVGLL	IYWRKCFQTA	HFVLEDSTSP	RVISTPPTPI	FFISDDVGA	840
	PIKHFFPKHVA	DLHASSGFTE	EPETLKEFYQ	EVQSCVTVDLG	ITADSSNHPD	NKHQRYINI	900
	VAYDHSRVKL	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAB	DFWRMIWEHN	960
80	VEVIVMINTL	VEKGRKKDQ	YWPADGSEBY	GNFLVTQKSV	QVLAAYTVEN	FTLRNTKIKK	1020
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	TGTYIVLDSM	LQIQHEGTG	NIPGLKHIR	SQRNYLVQTE	EQYVFIHDTL	VEALLSKETE	1140
	VLDSDIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNLQQSD	YSAALKQCNR	EKNRTSSIIP	1200
	VERSRVGISS	LSGEGTDYIN	ASYIMGYYS	NEPIITQHPL	LHTIKDFWRM	IWDHNAQLVV	1260
85	MIPDQGNMAB	DEFVYWNPKD	EPINCESFKV	TLMABEKKCL	SNEEKLIIQD	FILEATQDDY	1320
	VLEVRFQCP	KWNPDSPIK	KTFELISVIK	EEAANRDGPM	IVRDEHGGVT	AGTFCALTTL	1380
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Seq ID NO: 576 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

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Seq ID NO: 577 Protein sequence:
Protein Accession #: EOS sequence

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Seq ID NO: 578 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

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Seq ID NO: 579 Protein sequence:
Protein Accession #: EOS sequence

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	VMIPOGQMA	EDFVYWPKNK	DEPINCESFK	VTLMAEHHC	LSNEEKLIQ	DFILEATQDD	1200
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Seq ID NO: 580 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4632

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Seq ID NO: 583 Protein sequence
 Protein Accession #: NP_002842.1

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 25 LNTTPAASS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSE LFRHLHTVSQ 840
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Seq ID NO: 584 DNA sequence
 Nucleic Acid Accession #: NM_005688.1
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Seq ID NO: 585 Protein sequence
 Protein Accession #: NP_005679.1

1 11 21 31 41 51
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 80 PVVAIIIGMIY NVIIILGPTGF LGSVAFILFY PAMMFASRLT AYFRKRCVAA TDERVQRMNE 360
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 85 KTSLSAILLG QMTLLBGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
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5 VPWSVYGVYI QAAGGFLAPL VIMALFMLNV GSTAFSTWNL SYWIKQSGN TTVTRGNETS 900
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 10 MLTIAHRLHT VLGSDDRMVL AQGVVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKVG

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 Coding sequence: 89..631

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Seq ID NO: 587 Protein sequence
 Protein Accession #: NP_001318.1

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 40 VLLKEPTVSG NLTIRLTAA DHRQLQLSIS SCLQLLSLLM WITQCFLPVP LAQPPSGQRR

Seq ID NO: 588 DNA sequence
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Seq ID NO: 589 Protein sequence
 Protein Accession #: Eos sequence

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Seq ID NO: 590 DNA sequence
 Nucleic Acid Accession #: NM_005562.1
 Coding sequence: 90..3671

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25	CAGAAAGTGA	AGCTTCTCTG	GGAAACACTA	ACATTCCTGC	CTCAGACCAC	TACGTGGGGC	2340
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	CTGTGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAAACAA	GTCCCTGGCC	CAGCAGTTGA	2580
30	CAAGGGAGCG	CATCTCAAGCG	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGTCTCCG	CTTCAGGAGG	TCAGTGATCA	GTCTTTTCAG	GTGGAAGGAG	2700
	CAAGAGGATG	CAACCAAAAA	GCGGATTTC	TCTCAACGCT	GGTAAACAGG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAAG	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAATGGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
35	AAGACAGAGC	ACAGAGAGCA	CTGAGTATGG	GCAATGCCAC	TTTTATGAAA	GTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAAGCTGAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GCGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGAGCG	CCTGGAAAATC	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
40	AAGCCATGAT	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
	GTGAGATGAG	GGAAAGTGA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGATGACAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAAGT	TGATACCAGA	GCCAAGAACG	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCTGCAAT	CTGATGGACC	3420
	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAAGCT	TCCCGAGCCA	3480
45	AGAACAGAGC	ACAGAGCCAA	CTGCGGCCCA	TGATGTCCAG	GCTGGAAGAG	AGGGCAAGTC	3540
	AGCAGAGGGG	CCACTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGAGTTCTG	GCTGATGTGA	3600
	AGAACTTGGA	GAACTTAGG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCAAT	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
50	TATGCTCAGG	TCAACTGACC	TGAOCCCAT	CCTGATCCCA	TGGCCAGGTT	GTGTCTTTAT	3840
	TGCACCATAC	TCCTTGCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAAGAAATG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGGCT	CATAATAGTG	GTAAGTGGAG	TCTTGGAAAT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATTTCTTGA	GTAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCAGGCC	4080
55	ATGAATTTCT	TCTAATGTG	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAAAT	4140
	ACTATTGGCT	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTTCT	CCTACTTACA	4200
	ACCCAGGGTG	TGAACATGTT	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCCC	ATTCAGAGCT	ATGGTGCTTG	CTGGTGCCCTG	CCACCTTCAA	4320
	GTCTGGAGC	TGGGCAATGAC	ATCCTTTCTT	TAAATGATGC	CATGGCAACT	TAGAGATTGC	4380
60	ATTTTATTA	AAGCATTTCC	TACCAGCAAA	GCAAAATGTT	GGAAAGTATT	TACTTTTTCG	4440
	GTTTCAAGAT	GATGAAAAAG	TGTGGCTTGG	GCATTGAAAG	AGGTAAAAAT	CTCTAGATTT	4500
	ATTAGTCTTA	ATTCAATCCT	ACTTTTTCGAA	CACCAAAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTTACT	4620
	CACACTTCAG	CTGGGTCACA	TCCATCCCTC	CATTTCATCT	TCCATCCATC	TTTCCATCCA	4680
65	TTACCTCCAT	CCATCTCTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
	GTGGGACAGT	GGTGACATAG	TCTCTGCCCC	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTTTA	AAAAATAAAT	TTAAACTTAC	AAACTTTGTT	TGTCACAGT	GGTGTATTAT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTG	CTCAACAGAA	CATATGTTGC	AAGACCCCTC	4920
	CATGGGGGCA	CTTGAGTTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTGTGCA	CATTTCCTTG	4980
70	CATTCCAGCT	GTCACTCTGT	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
	TAACACCAGT	GGGAATTGCT	GGAGGAACCA	GAGGCATCTC	CACCTGGCT	GGGAAGACTA	5100
	TGGTGTGCTC	TTGCTTCTGT	ATTTCCCTTG	ATTTTCTCTGA	AAGTGTTTTT	AAATAAAGAA	5160
	CAATTGTTAG	ATGCC					

75 Seq ID NO: 591 Protein sequence
Protein Accession #: NP_005553.1

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80	MPALMLGCCCL	CPFLLLPAAR	ATSRREVDCD	NGKSRQCFID	RELHRQTGNG	FRCLNNDNT	60
	DGIEHCEKCRN	GPYRHRERDR	CLPCNCSKQ	SLSARCDNSG	RCSCKPGVTG	ARCDRLPGF	120
	HMLTDAGCTQ	DQRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYYNLDDGN	180
	PEGCTQPCFY	GHSASCRSSA	EYSVKITST	PHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRLDPHY	FVPAKFLN	QQVSYGQSL	FDYRVDGGR	HPSAHDVILE	GAGLRITAPL	300
85	MPLGLTLPGL	LTKTYTFRLN	EHPSNNWSPQ	LSYFEYRLL	RNLTLRIRA	TYGBYSTGYI	360
	DNVTLISARP	VSGAPAPWVE	QCICFVGKYG	QFCQDCASGY	KRDSARLGPP	GTICPCNCQG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGPY	NDPFDPRCK	PCPCHNGPSC	SVMPETEYV	480

	CNNCPFGVVG	ARCELCADYG	PGDPFGEHGP	VRPCQPCQCN	NNVDPASAGN	CDRLTGRCLK	540
	CIENITAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCPMGS	EPVGCERSDGT	CVCKPGFGGP	600
	NCEHGFSCF	ACYNQVQIQM	DQFMQQLQRM	EALISKAGGG	DGVVPDTELE	GRMQQAQAL	660
5	QDILRDAQIS	EGASRSISLGLQ	LAKVRSQENS	YQSRILDLKM	TVKRVRLGS	QYQNRVRDTH	720
	RLITQMQLSL	AESASISLNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780
	ETEDYSKQAL	SLVRKALHEG	VGSGSGSPDG	AVVQGLVEKL	EKTKSLAQL	TREATQAEIE	840
	ADRSYQHSIR	LLDSVSRLLQ	VSDQSPQVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG	900
	NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEALSM	GNATFYEVES	ILKNLREFDL	960
10	QVNRKAEAE	EAMKRLSYIS	QKVSDASDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
	IEQBIGSLNL	EANVTADGAL	AMEKGLASLK	SEAREVEGEL	ERKELEFDTN	MDAVQMVITE	1080
	AQKVDTRAKN	AGVTIQDTLN	TLDGLLHMD	QPLSVDEEGL	VLLLEQKLSRA	KTQINSQLRP	1140
	MNSELEERAR	QQRGHLHLLE	TSIDGILADV	KNLENIRDNL	PPGCYNTQAL	EQQ	

Seq ID NO: 592 DNA sequence
Nucleic Acid Accession #: AF101051.1
Coding sequence: 221.856

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20	GAGCAACCTC	AGCTTCTAGT	ATCCAGACTC	CAGCGCCGCC	CGGGGCGCGG	ACCCCAACCC	60
	CGACCCAGAG	CTTCTCCAGC	GGGCGGCGAG	CGAGCAGGGC	TCCCGGCCCT	AACTTCCTCC	120
	CGGGGGCCCA	GCCACCTTCC	GGAGTCCGGG	TTGCCCACTC	GCAAACTCTC	CGCCTTCTGC	180
	ACCTGCCACC	CCTGAGCCAG	CGCGGGCGCC	CGAGGAGTGC	ATGGCCAAAG	CGGGGCTGCA	240
	GCTGTGGGCG	TTCATTCTCG	CCTTCTCTCG	ATGGATCGGC	GCCATCGTCA	GCACTGCCCT	300
25	GCCCCAGTGG	AGGATTACTT	CCTATGCGGG	CGACAACATC	GTGACCGCCC	AGGCCATGTA	360
	CGAGGGGCTG	TGGATGTCCT	GCGTGTGCGA	GAGCACCAGG	CAGATCCAGT	GCAAAAGCTT	420
	TGACTCTCTG	TGATATCTGA	GCAGCACATT	GCAAGCAACC	CGTGCCCTGA	TGGTGGTTGG	480
	CATCTCTCTG	GGAGTGATAG	CAATCTTGTG	GGCCACCGTT	GGCATGAAGT	GTATGAAGTG	540
	CTTGGAAGAC	GATGAGGTGC	AGAAGATGAG	GATGGCTGTC	ATTGGGGGTG	CGATATTCTT	600
30	TCTTGCAAGT	CTGGCTATT	TAGTTGCCAC	AGCATGGTAT	GGCAATAGAA	TGTTTCAAGA	660
	ATTCTATGAC	CCTATGACCC	CAGTCAATGC	CAGGTACGAA	TTTGGTCAAG	CTCTCTTAC	720
	TGGCTGGGCT	TGCTCTTCTC	TCTGCTTCTC	GGGAGGTGCC	CTACTTGTCT	GTTCCTGTCC	780
	CGGAAAAACA	ACCTCTTACC	CAACACCAAG	GCCCTATCCA	AAACCTGCAC	CTTCCAGCGG	840
	GAAAGACTAC	GTGTGACACA	GAGGCAAAAG	GAGAAAAACA	TGTTGAAACA	AACCGAAAAA	900
35	GGACATTGAG	ATACATCATC	TAAACATTAG	ACCTTAGAAT	TTTGGGTATT	GTAATCTGAA	960
	GTATGGTATT	ACAAAAACAA	CAAAACAAAC	AAAAACCCAT	GTGTTAAAT	ACTCAGTGCT	1020
	AAACATGGCT	TAACTCTTAT	TTATCTTCTT	TCCTCAATAT	AGGAGGGAAG	ATTTTACCAT	1080
	TGTATTACT	GCTTCCCAT	GAGTAATCAT	ACTCAATAGG	GGGAAGGGGT	GCTCTTAA	1140
40	TATATATAGA	TATGATATAT	TACATGTTTT	TCTATTAAAA	ATAGACAGTA	AAATACTATT	1200
	CTCATTTAGT	TGATACTAGC	ATACTTAAAA	TATCTCTAAA	ATAGGTAAAT	GTATTTAATT	1260
	CCATATTGAT	GAGATGTTT	ATTGGTATAT	TTTCTTTTTC	GTCTTATAT	ACATATGTAA	1320
	CAGTCAAAAT	TCATTTACTC	TTCTTCAAT	GCTTTGGGTG	CCTTTGCCAC	AAGACCTAGC	1380
	CTAATTTACC	AAGGATGAAT	TCTTTCAATT	CTTCATGCGT	GCCCTTTTCA	TATACTTATT	1440
45	TTATTTTAT	CCATAATCTT	ATAGCACTTG	CATCGTTATT	AAGCCCTTAT	TTGTTTGTG	1500
	TTTCAATGGT	CTCTATCTCC	TGAATCTAAC	ACATTTTATA	GCCTACATTT	TAGTTTCTAA	1560
	AGCCAAAGAG	AATTTATTAC	AAATCAGAAC	TTTGGAGGCA	AATCTTTCTG	CATGACCAAA	1620
	GTGATAAAGT	CTGTTTGACC	TTCCACACAC	ATCCCTGTAC	TCTGACCCAT	AGCACTCTTG	1680
	TTTGCTTTGA	AAATATTGTG	CCAATTGAGT	AGCTGCATGC	TGTTCCCCCA	GGTGTGTGTA	1740
50	CACAACTTGT	TTGATGGAAT	TTTAAAGCTA	CTTATTTCATA	GTTTTATATC	CCCCTAAACT	1800
	ACCTTTTGTG	TCCCATTTCC	TAAATTGTAT	TGTTTTCCTA	AGTGTAAATTA	TCATGCGTTT	1860
	TATATCTCTG	TAAATAGGTT	TGGTCTGTTT	GTCTGAACAA	AGTGTAGAC	TTTCTGGAGT	1920
	GATAACTCGG	TGACAAATAT	TCTCTCTGTA	GCTGTAAAGCA	AGTCACTTAA	TCTTTCTACC	1980
	TCTTTTCTCT	ATCTGCCAAA	TTGAGATAAT	GATACTTAAC	CAGTTAGAAG	AGGTAAGTGT	2040
55	AATATTAAAT	AGTTTATATT	ACTCTCATTC	TTTGAACATG	AACATAGCCT	ATGTAGTGTG	2100
	TTTATTGTCT	CAGCTGGGCT	AGACACTGAA	GAACTCACTG	AACAAAACCT	ACACAAGTAC	2160
	CTTCATGTGA	TTCACTGCTC	TCCTCTCTCT	ACCAGTCTAT	TTCCACTGAA	CAAAACCTAC	2220
	ACACATACCT	TCATGTGGTT	CAGTGCCTTC	CTCTCTCTAC	CAGTCTATTT	CCACTGAACA	2280
	AAACCTAAGC	ACATACCTTC	ATGTGGCTCA	GTGCTTCTCT	CTCTCTACCA	GTCTATTTC	2340
60	ATTCCTTCAG	CTGTGCTGGA	CATGTTTGTG	CTCTGTTCCT	TTTAAACAAC	TGCTCTTACT	2400
	TTTCCAGTCT	GTACAGAAAT	CTATTTCACT	TGAGCAAGAT	GATGTATGGA	AAGGGTGTG	2460
	GCACCTGGTG	CTGAGAGCCT	GGATTGAGT	CTTGTGCTA	TCAATCACCG	CTGTGTGTTG	2520
	AGCAAGGCTA	TGCGTGCTG	TAAGCTTATT	GCTTCATCTG	TAAGCGGTGG	TTTGTAAATC	2580
	CTGATCTTCC	CACCTCACAG	TGATGTTGTG	GGGATCCAGT	GAGATAGAAT	ACATGTAAAT	2640
	GTGGTTTGT	AAATTGAAAA	GTGCTATACT	AAGGGAAGAA	ATTGAGGAAT	TAACTGCATA	2700
65	CGTTTGGTGG	TGCTCTTTCA	AATGTTTGAA	AATAAAAAAA	TGTTAAGAAA	TGGGTTTCTT	2760
	GCCTTAACCA	GTCTCTCAAG	TGATGAGACA	GTGAAGTAAA	ATTGAGTGCA	CTAAACGAAT	2820
	AAGATTCTGA	GGAAGTCTTA	TCTTCTGCAG	TGAGTATGGC	CCAATGCTTT	CTGTGCTTAA	2880
	ACAGATGTAA	TGGGAAGAAA	TAAAAGCCTA	CGTGTGGTGA	AATCCACAG	CAAGGAGAT	2940
	TTTTGAATCA	TAATAACTCA	TAAAGTGCTA	TCTGTTCACT	GATGCCCTCA	CAGCTCTTGC	3000
70	TGTTAGCTGG	CAGCTGACGC	TGCTAGGATA	GTTAGTTTGG	AAATGGTACT	TCATAATAAA	3060
	CTACACAAGG	AAAGTCAGCC	ACCGTGTCTT	ATGAGGAATT	GGACCTAATA	AATTTTAGTG	3120
	TGCTTCCCAA	ACCTGAGAA	ATATGCTTTT	GGAAGTTAAA	ATTTAAATGG	CTTTTGCCAC	3180
	ATACATAGAT	CTTCATGATG	TGTGAGTGTA	ATTCCATGTG	GATATCAGTT	ACCAACAT	3240
	ACAAAAAAT	TTTATGCCCC	AAAATGACCA	ACGAAATGTT	TACAATAGAA	TTTATCCAA	3300
75	TTTGAATCTT	TTTATTTCTT	CTACCAACCC	TGGAACACAG	CCAATAGACA	TTTGGGGTT	3360
	TTATAATGGG	AAATTGTATA	AAGCATTAAT	CTTTTCAAT	AAATGTGTTT	TTAATTTAAA	3420
	AAAAGGAAAA	AAAAAAAAAA	AAA				

Seq ID NO: 593 Protein sequence
Protein Accession #: AAD16433.1

	1	11	21	31	41	51	
85	MANAGLQLLG	FILAPLGLWG	AIVSTALPQW	RIYSYAGDNI	VTAQAMYEGE	WMSCVSQSTG	60
	QIQCKVFDLS	LNLSSFLQAT	RALMVVGILL	GVIAIFVATV	GMKCMKCLEL	DEVQKMRMAV	120
	IGGAIFLLAG	LAILVATAWY	GNRIVQSFYD	PMTFVNARYE	PQDALPTGWA	AASLCLLGG	180
	LLCCSCPRKT	TSYTPRPYP	KPARSSGKDY	V			

Seq ID NO: 594 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

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	CCCCATTGG	CATCTAACAA	GGAATCTGCG	CCCCAGAGAG	TCCCGGACGC	CGCCGGTGGG	60
10	TGCCCGGCGC	GCCGGGCCAT	GCAGCGACGG	CCGCGCGGGA	GCTCCGAGCA	GCGGTAGGCG	120
	CCCCCTGTAA	AGCGGTTOGC	TATGCGGGGA	CCACTGTGAA	CCCTGCCGCC	TGCCCGAACA	180
	CTCTTCGCTC	CGGACCACT	CAGCCTCTGA	TAAGCTGGAC	TGGCAGCGCC	CGCAACAAGC	240
	ACCGAGGAGT	TAAGAGAGCC	GCAAGCGCAG	GGAAGGCCTC	CCCGCACGGG	TGGGGGAAAG	300
	CGGCGGTGTC	AGCGCGGGGA	CAGGCACCTG	GGCTGGCACT	GGCTGCTAGG	GATGTCTGCC	360
	TGGATAAGGT	GGCATGGACC	CGCCATGGCG	CGGCTCTGGG	GCTTCTGCTG	GCTGGTTGTG	420
15	GGCTTCTGGA	TGGCGCGCTT	CGCCTGTCCC	ACGTCTTGCA	AATGCAGTGC	CTCTGGATC	480
	TGGTGCAGCG	ACCCTTCTCC	TGGCATCGTG	GCAATTCGGA	GATTGGAGCC	TAAACAGTGA	540
	GATCCTGAGA	ACATCAACGA	AATTTTCATC	GCAAAACCAGA	AAAGGTTAGA	AATCATCAAC	600
	GAAGATGATG	TTGAAGCTTA	TGTGGGACTG	AGAAATCTGA	CAATTGTGGA	TTCTGGATTA	660
	AAATTGTGGG	CTCATAAAGC	ATTTCCTGAA	AACAGCAACC	TGCAGCACAT	CAATTTTACC	720
20	CGAAACAAAC	TGAGCAGTTT	GTCTAGGAAA	CATTTCGGTC	ACCTTGACTT	GTCTGAACCTG	780
	ATCCTGTGTT	GCAATCCATT	TACATGCTCC	TGTGACATTA	TGTGGATCAA	GACTCTCCAA	840
	GAGGCTAAAT	CCAGTCCAGA	CACCTCAGGAT	TTGTACTGCC	TGAATGAAAG	CAGCAAGAAAT	900
	ATTCCCCTGG	CAAACTGCA	GATACCCAAT	TGTGGTTTGC	CATCTGCAAA	TCTGGCCGCA	960
	CCTAACCTCA	CTGTGGAGGA	AGGAAAGTCT	ATCACATTAT	CCTGTAGTGT	GGCAGGTGAT	1020
25	CGGTTCTCTA	ATATGTATTG	GGATGTTGGT	AACCTGGTTT	CCAAACATAT	GAATGAAACA	1080
	AGCCACACAC	AGGGCTCCTT	AAGGATAACT	AACATTTTCT	CCGATGACAG	TGGGAAGCAG	1140
	ATCTCTTTGT	TGGCGGAAAG	TCTTGTAGGA	GAAGATCAAG	ATTCTGTCAA	CCTCACTGTG	1200
	CATTTTGCAC	CAACTATCAC	ATTTCCTGAA	TCTCCAACCT	CAGACCACCA	CTGTGTCATT	1260
30	CCATTCACTG	TGAAGGCAAA	CCCCAAACCA	GCGCTTCAGT	GGTTCTATAA	CGGGGCAATA	1320
	TTGAATGAGT	CCAAATACAT	CTGTACTAAA	ATACATGTTA	CCAATCACAC	GGAGTACCAC	1380
	GGCTGCCTCC	AGCTGGATAA	TCCCACTCAC	ATGAACAATG	GGGACTACAC	TCTAATAGCC	1440
	AAGAATGAGT	ATGGGAAGGA	TGAGAAACAG	ATTCTGCTC	ACTTCATGGG	CTGGCTTGGG	1500
	ATTGACGATG	GTGCAAAACC	AAATTATCCT	GATGTAATTT	ATGAAGATTA	TGGAATGCA	1560
35	GCGAATGACA	TGCGGGACAC	CAOGAACAGA	AGTAATGAAA	TCCCTTCCAC	AGACGCTCACT	1620
	GATAAAACCG	ITCGGGAACT	TCTCTCGGTC	TATGCTGTGG	TGGTGAATGC	GTCTGTGGTG	1680
	GGATTTTGCC	TTTTGGTAAT	GCTGTTTCTG	CTTAAGTTGG	CAAGACACTC	CAAGTTTGGC	1740
	ATGAAAGGCC	CAGCCTCCGT	TATCAGCAAT	GATGATGACT	CTGCCAGCCC	ACTCCATCAC	1800
	ATCTCCAATG	GGAGTAACAC	TCCATCTTCT	TGGAAGGTG	GCCCAGATGC	TGTCAATTAT	1860
40	GGATGACCA	AGATCCCTGT	CATTGAAAAT	CCCCAGTACT	TTGGCATCAC	CAACAGTCAG	1920
	CTCAAGCCAG	ACACATTTGT	TCAGCACATC	AAGCGACATA	ACATTGTCTT	GAAAAGGGAG	1980
	CTAGGCGAAG	GAGCCTTTGG	AAAAGTGTTC	CTAGCTGAAT	GCTATAACCT	CTGTCTCGAG	2040
	CAGGACAAGA	CTTGTGTGGG	AGTGAAGACC	CTGAAGGATG	CCAGTGACAA	TGCAAGCAAG	2100
	GACTTCCACC	GTGAGGCGGA	GCTCCTGACC	AACCTCCAGC	ATGAGCACAT	CTCAAGTTTC	2160
45	TATGGCGTCT	GCGTGGAGGG	CGACCCCTCT	ATCATGGTCT	TTGAGTACAT	GAAGCATGGG	2220
	GACCTCAACA	AGTTCCCTCAG	GGCACACGGC	CCTGATGCGG	TGCTGATGGC	TGAGGGCAAC	2280
	CGGCCACCGG	AACATGACGA	GTGCGAGATG	CTGCATATAG	CCGACGAGAT	CGCCGCGGGC	2340
	ATGGTCTACC	TGGGCTCCCA	GCACTTCTGT	CACCGGATTT	TGGCCACCAG	GAACTGCTGT	2400
	GTGCGGGAGA	ACTTGTCTGGT	GAAAATCGGG	GACTTTGGGA	TGTCCCGGGA	CGTGTACAGC	2460
50	ACTGACTACT	ACAGGGTCGG	TGGCCACACA	ATGCTGCCCA	TTGCTGTGAT	GCTCCAGAGC	2520
	AGCATCATGT	ACAGGAAATG	CACGACGGAA	AGCGACGTCT	GGAGCTGGGG	GGTGTGTGTT	2580
	TGGGAGATTT	TCACCTATGG	CAACAGCCCC	TGGTACCAGC	TGTCAACCAA	TGAGGTGATA	2640
	GAGTGTATCA	CTCAGGGCCG	AGTCTCTCAG	CGACCCCGCA	CGTGCCCCCA	GGAGGTGTAT	2700
	GAGCTGATGC	TGGGCTGTCT	GCAGCGAGAG	CCCCACATGA	GGAAGAACAT	CAAGGGCATC	2760
55	CATACCTCTC	TTCAAGAACT	GGCCAAAGCA	TCTCCGGTCT	ACCTGGACAT	TCTAGGCTAG	2820
	GGCCCTTTCT	CCGACACCGA	TCCTTCCCAA	CGTACTCCTC	AGACGGGCTG	AGAGGATGAA	2880
	CATCTTTTAA	CTGCCGCTGG	AGGCCACCAA	GCTGCTCTCC	TTCACTCTGA	CAGTATTAAAC	2940
	ATCAAAAGACT	CCGAGAGGCT	CTGAGGGGAA	CGAGTGTGTA	CTTCTTCTATC	CATAGACACA	3000
	GTATTGACTT	CTTTTGGGCA	TTATCTCTTT	CTCTCTTTCC	ATCTCCCTTG	GTGTTCTCTT	3060
60	TTTCTTTTCT	TAAATTTTCT	TTTTCTTCTT	TTTTTCTGCT	TTCCCTGCTT	CACGATTCTT	3120
	ACCCTTTCTT	TTGAATCAAT	CTGGCTTCTG	CATTACTATT	AACCTCTGAT	AGACAAAGGC	3180
	CTTAACAAC	GTAATTTGTT	ATATCAGCAG	ACATCCAGT	TTGCCACCA	CAACTAACAA	3240
	TGCCCTGTGT	TATTCCTGCT	TTTGATGTGG	ATGAAAAAAA	GGGAAAAACA	ATATTTCACT	3300
	TAAACTTTGT	CACCTCTGCT	GTACAGATAT	CGAGAGTTTC	TATGGATTCA	CTTCTATTTA	3360
65	TTTATTATTA	TACTGTCTCT	TATGTGTTTT	GGATGGCTTA	AGCCTGTGTA	TAAAAAGAA	3420
	AACCTGTGTT	CAATCTGTGA	AGCCTTTATC	TATGGGAGAT	TAAAAACCAG	GAGAAAGAAG	3480
	ATTTATTATG	AACCGCAATA	TGGGAGGAAC	AAAGACAACC	ACTGGGATCA	GCTGGTGTCA	3540
	GTCCCTACTT	AGGAAATACT	CAGCAACTGT	TAGCTGGGAA	GAATGTATTC	GGCACCTTCC	3600
70	CCTGAGGACC	TTTCTGAGGA	GTAAAAAGAC	TACTGGCCTC	TGTGCCATGG	ATGATTCTTT	3660
	TCCCATCACC	AGAAATGATA	GCGTGCAGTA	GAGAGCAAAAG	ATGGCTT		

Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

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	NSVDPENITE	IFIANQKRLK	IINEDDVEAY	VGLRLNLTVD	SGLKPFVAHKA	FLKNSNLQHI	120
	NFTRNKLTSL	SRKHFRHLDL	SELILVGNPF	TCSCDIMMIK	TLQRAKSSPD	TQDLYCLNES	180
80	SKNIPLANLQ	IPNCGLPAN	LAAPNLVTEE	GKSITLSCSV	AGDPVPNMWY	DVGNLVSKHM	240
	NETSHTQSSL	RITNISDDSD	GKQISCVLEN	LVGEDQDSVN	LTVHFAPTIT	FLSPTSDEH	300
	WCIPPTVKGN	PKPALQWFYN	GAILNESKYI	CTKIEVNTHT	EYEGCLQLDN	PTHMNGDYT	360
	LIAKNEYGKD	ERQISAFHMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSNIEPST	420
	DVTDKTRGHE	LSVYAVVVIA	SVVGPCLLVM	LFLLKLARHS	KFGMKGPASV	ISNDSDSASP	480
85	LREHISNGST	PSSSEGGPDA	VIIGMTKIPV	IENPQYPGIT	NSQLKPDFTV	QHKRHNIVL	540
	KRELGEAGNF	KVFLAEYCYNL	CPEQDKILVA	VRTLKDAASN	ARKDFHREAE	LLTNLQHEHI	600
	VKPYGVCEVG	DPLIMVFEYM	KRGDLNKLFLR	AHGPDVILMA	EGNPFTELTO	SQMLHIAQOI	660
	AAGMYVLASQ	HPVHRDLATR	NCLVGENLLV	KIGDFGMSRD	VYSTDYRVRG	GHTMLPIRMH	720

PPESIMYRKF TTSBDMVSLG VVLWEIFTYG KQPHYQLSNN EVIECTTQGR VLQRPRTCPQ 780
 EYIELMLGCV QREPMRNRNI KGIHTLLQNL AKASPVYLDI LG

Seq ID NO: 596 DNA sequence
 Nucleic Acid Accession #: AF410899
 Coding sequence: 483..2999

1 11 21 31 41 51
 10 GGGAGCAGGA GCCTGCTGG CTGCTTCTGCT CGCGCTCTAC GCGCTCAGTC CCCGGCGGTA 60
 GCAGGAGCCT GGAOCACAGC GCGGCGCGCG GCGTGAGGC GCGGAGCCC GGCCTCGAGG 120
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 CGCGCGGTGG GTGCGCGCGG CGCGGGGCCA TGCAGCGACG GCGCGCGCGG AGCTCCGAGC 240
 AGCGGTAGCG CCCCCCTGTA AAGCGGTTCT CTATGCGGGG ACCACTGTGA ACCCTGCGCG 300
 15 CTGCGGAAC ACTCTTCTGCT CCGGACCAGC TCAGCCTCTG ATAAGCTGGA CTCGGCAGCG 360
 CCGCAACAAG CACGAGGAGG TTAAGAGAGC CGCAAGCGCA GGAAGGCGCT CCCCGCAGCG 420
 GTGGGGAGAA GCGGCGGTG CAGCGCGGGG ACAGGCACCT GGGCTGGCAC TGGCTGCTAG 480
 GGATGTGCTC CTGGATAAAG TGGCATGGAC CCGCCATGGC GCGCTCTGGG GGCCTCTGCT 540
 20 GGCTGGTGT GGGCTTCTGG AGGGCGCGCT TCGCCTGTCC CAGTCTCTGC AAATGCACTG 600
 CCTCTGGAAT CTGCTGCGAG GACCTTCTC CTGGCATCGT GGCATTTCGG AGATTGGAGC 660
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 AAATCACTAA CGAAGATGAT GTTGAAGCTT ATGTGGGACT GAGAATCTG ACAATTGTGG 780
 ATTCTGGATT AAAATTGTGT GCTCATAAAG CATTTCTGAA AACACGCAAC CTGCAGCACA 840
 25 TCAATTTTAC CGAACAACAA CTGAGGAGTT TGTCTAGGAA ACATTTCCGT CACCTTGACT 900
 TGTCTGAAGT AGTCTGCTGT GGCAATCCAT TTACATGCTC CTGTGACATT ATGTGGATCA 960
 AGACTCTCCA AGAGGCTAAA TCCAGTCCAG ACACCTCAGG TTTGTACTGC CTGAATGAAA 1020
 GCAGCAGAAA TATTCCCTG GCAACCTGC AGATACCCAA TTGTGGTTTG CCATCTGCAA 1080
 ATCTGCGCGC ACCTAACCTC ACTGTGGAGG AAGGAAAGTC TATCACATTA TCCTGTAGTG 1140
 30 TGGCAGGTGA TCGGTTCTCT AATATGTATT GGGATGTGG TAACCTGGTT TCCAAACATA 1200
 TGAATGAAAC AAGCCACACA CAGGGCTCCT TAAGGATAAC TAACATTTCA TCGGATGACA 1260
 GTGGGAAGCA GATCTCTTGT GTGGCGGAAA ATCTTGTAGG AGAAGATCAA GATTCTGTCA 1320
 ACCTCACTGT GCATTTTGTG CCAACTATCA CATTTCTGGA ATCTCAACC TCAGACCAAC 1380
 ACTGGTGCAT TCCATTCCT GTGAAAGGCA ACCCCAAACC AGCGCTTCAG TGGTTCTATA 1440
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 35 CGAGGTACCA GGTCTGCTC CAGCTGGATA ATCCCACTCA CATGAACAAT GGGGACTACA 1560
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 GCTGCGCTGG AATTGACGAT GGTGCAAAAC CAAATTATCC TGATGTAATT TATGAAGATT 1680
 ATGGAAGTGC AGCGAATGAC ATCGGGGACA CCAAGAACAG AAGTAATGAA ATCCCTTCCA 1740
 CAGACGTACG TGATAAAACC GGTGCGGAAC ATCTCTCGGT CTATGCTGTG GTGGTGATTG 1800
 40 CGTCTGTGGT GGGATTTTGC CTTTGGTAA TGCTTTTCT GCTTAAAGTT GCAAGACACT 1860
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 GTGTTGCGCC AGCCTCGGTT ATCAGCAATG ATGATGACTC TGCCAGCCCA CTCATCACA 1980
 TCTCCAATGG GAGTAACACT CCATCTTCTT CGGAAGGTGG CCCAGATGCT GTCATTATTG 2040
 45 GAATGACCAA GATCCCTGTC ATTGAAAATC CCCAGTACTT TGSCATCACC AACAGTCAGC 2100
 TCAAGCCAGA GGTCTTGTG CAGCACATCA AGCGACATAA CATTGTCTG AAAAGGGAGC 2160
 TAGGCGAAGG AGCCTTTGGA AAGTGTTCCT TAGCTGAATG CTATAACCTC TGTCTGAGC 2220
 AGSACAAGAT CTGTGTGCGA GTGAAGACCC TGAAGGATGC CAGTGACAAT GCACGCAAGG 2280
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 50 ATGGCGTCTG CGTGAAGGCG GACCCCTCA TCATGGTCTT TGAGTACATG AAGCATGGGG 2400
 ACCTCAACAA GTTCTCAGG GCACACGCGC CTGATGCGGT GCTGATGGCT GAGGGCAACC 2460
 CGCCACGCGA ACTGACGCG TCGCAGATGC TGCATATAGC CCAGCAGATC GCGCGGGCA 2520
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 TCGGGAGAA CTGTCTGTTG AAAATCGGGG ACTTTGGGAT GTCCCGGAC GTGTACAGCA 2640
 55 CTGACTACTA CAGGTCGCT GGCACACAA TGCTGCCCAT TCGCTGGATG CCTCCAGAGA 2700
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 60 ATACCTCTCT TCAGAACTTG GCCAAGGCAT CTCGCGTCTA CTGAGCATT CTAGGCTAGG 3000
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 TCAAGACTC CGAAGAGCTC TOGAGGGAAG CAGTGTGTAT TTCTTCACTC ATAGACACAG 3180
 TATTGACTTC TTTTGGCAT TATCTTTTC TCTTTTCCA TCTCCTTGG TTGTTCTTT 3240
 65 TTCTTTTCTT AAATTTCTT TTCTTCTT TTCTTCTT TCCCTGCTTC ACGATTCTTA 3300
 CCTTTCTTCT TGAATCAATC TGGCTTCTGC ATTACTATTA ACTCTGCATA GACAAAGGCC 3360
 TTAACAAACG TAAATTGTGA TATCAGCAG CACTCCAGTT TGCCCAACC AACTAACAA 3420
 GCCTTGTGTG ATTCCTGCTT TTGATGTGGA TGAAAAAAG GAAAAACAA TATTTCACTT 3480
 70 AAACCTTTGC ACTTCTGCTG TACAGATATC GAGAGTTTCT ATGGAATCAC TTCTATTTAT 3540
 TTATTATTAT TACTGTCTT ATTGTTTTG GATGGCTTAA GCGTGTGTAT AAAAAAGAAA 3600
 ACTTGTGTTT AATCTGTGAA GCCTTTATCT ATGGGAGATT AAAACAGAG AGAAAGAAGA 3660
 TTTATTATGA ACCGCAATAT GGGAGGAACA AAGACAACCA CTGGGATCAG CTGGTGTGAG 3720
 TCCCTACTTA GAAATACTC AGCAACTGTT AGCTGGGAAG AATGTATTCG GCACCTTCCC 3780
 75 CTGAGGACCT TTCTGAGGAT TAAAAAGACT ACTGGCCTCT GTGCCATGGA TGATTCTTTT 3840
 CCCATCACA GAAATGATAG CGTGCACTAG AGAGCAAGA TGGCTTCCGT GAGACACAAG 3900
 ATGGCGCATA GTGTGCTCGG ACACAGTTT GTCTTGTAG GTTGTGATGA TAGCACTGGT 3960
 TTGTTTCTCA AGCGCTATCC ACAGAACCTT TGTCAACTTC AGTTGAAAAG AGGTGGATT 4020
 ATGTCCAGAG CTCATTTCCG GGTGAGGTGG GAAAGCC

Seq ID NO: 597 Protein sequence
 Protein Accession #: AAL67965.1

1 11 21 31 41 51
 85 MSSWIRWHPG AMARLWGFOW LVVGFWRAP ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRL EINEDDVEAY VGLRNLITVD SGLKPVAKKA PLKNSNLQHI 120
 NPTRNKLTSL SRKHPRHLDL SELILVGNPP TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSLTILSCSV AGDPVPNNYW DVGNLVSKEM 240

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NETSHTQSSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSRRH 300
WCIPFTVKGN PKPALQWFFYN GAILANESKYI CTKIHVTHET EYHGCLQLDN PTEMNNGDYT 360
LIAKNEYGKD EKQISAHFNG WPGIDDGANP NYFDVIYEDY GTAANDIGDT TNRSNEIPST 420
DVTDTKGRER LSVYAVVVIA SVVGFCLLVN LFLKLARHS KFGMDPSWF GFGKVKSRQG 480
VGPAVISND DDSASPLHHI SNGSNTSPSS EGGPDVAVIG MTKIPVIENT QYFGITNSQL 540
KPDTPVQHIK RHNIIVLKREL GBQAFGRVPL ABCYNLCPEQ DKILVAVKTL KDASDNARKD 600
FEREAELLTN LQESHIKCFY GVCVSGDFLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP 660
PTLSTQSQL HIAQOIAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720
DYIRVGGHTM LPIRMFPES IMYRKFTTES DVMSLGVVLV EIFTYKQPW YQLSNNEVIE 780
CITQGRVLQR PRTCPQEVYE LMLGCWQREP HMRKNIKGIH TLLQNLAKAS PVYLDILG

Seq ID NO: 598 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74..814

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AAAACCTTGA GGTGATTTCAT CTTCAGGCT CTCTTCCAT CAAGTCTCTC TCCTTAGCG 60
CTCTGGGTCC TTAATGGCAG CAGCCGCCGC TACCAAGATC CTCTGTGCTC TCCCGCTTCT 120
GCTCCTGCTG CCGGCTGGT CCGGGCTGG GCGAGCGAC CCTCACTCTC TTTCGTATGA 180
CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGGGGTTC AAGGCCAGGT 240
GGATGAAAAG ACTTTTCTTC ACTATGACTG TGGCAACAAG ACAGTCACAC CTGTCACTCC 300
CCTGGGAAG AACTAAATG TCACAACGGC CTGGAAGCA CAGAACCAG TACTGAGAGA 360
GGTGGTGAC ATACTTACAG AGCAACTGCG TGACATTCAG CTGAGAAATT ACACACCCAA 420
GGAAACCCCT ACCCTGCAGG CAGGATGTC TTGTGAGCAG AAAGCTGAAG GACACAGCAG 480
TGGATCTTGG CAGTTCACTG TCGATGGGCA GATCTTCTCT CTCTTGAAGT CAGAGAAGAG 540
AATGTGAGAC ACGTTTCATC CTGGAGCCAG AAAGATGAAA GAAAAGTGGG AGAATGACAA 600
GGTGTGGCC ATGTCTCTCC ATTACTTCTC AATGGGAGAC TGTATAGGAT GCGTTGAGGA 660
CTTCTTGATG GGCATGGACA GCACCCCTGA GCCAAGTGCA GGAGCACCAC TCGCATGTCT 720
CTCAGGCACA ACCCAACTCA GGGCCACAGC CACCACCTC ATCCTTTGCT GCTCTCTCAT 780
CATCTCCCC TGCTTCATCC TCCCTGGCAT CTGAGGAGAG TCCTTTAGAG TGACAGGTGA 840
AAGCTGATAC CAAAGGCTC CTGTGAGCAC GGTCTTGATC AAACCTCGCC TTCTGTCTGG 900
CCAGCTGCCC ACAGCTACG GTGTATGTCC AGTGGCCTCC AGCAGATCAT GATGACATCA 960
TGGACCAAT AGCTCATTC CAGCTTGAT TCCTTTTGCC AACAAATTTA CCAGCAGTTA 1020
TACCTAACAT ATTATGCAAT TTCTCTTGG TGCTACCTGA TGAATTTCT CCACTTAAAG 1080
TTCTGGCTGA CTAACACAGA TATATCATTT TCTTTCTCT CTTTTGTGT GGAATAATCA 1140
GTACTTCTT GAATGATGAT CTCCTTCTTG CAAATGATAT TGTCAATAA ATAATCACGT 1200
TAGACTTCAG ACCTCTGGG ATTCTTTCCG TGTCTGAAA GAGAATTTT AAATATTATA 1260
ATAAGAAAAA ATTTATATTA ATGATTGTTT CCTTTAGTAA TTTATTGTT TGTACTGATA 1320
TTTAAATAAA GAGTTCTATT TCCAAAAA AA

Seq ID NO: 599 Protein sequence
Protein Accession #: BAB61048.1

45
50

1 11 21 31 41 51
| | | | | |
MAAAATKIL LCLPLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGVDEKT 60
FLHYDCGNT VTPVSLGKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT 120
LQARMSCEQR AEGHSSGSMQ FSPDQIFLL FDSEKRMWT VHPGARMKE KWENDKVVAM 180
SFHYFSGMDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC 240
FILPGI

Seq ID NO: 600 DNA sequence
Nucleic Acid Accession #: NM_001898.1
Coding sequence: 57..482

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1 11 21 31 41 51
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GGCTCTCACC CTCTCTCCT GCAGCTCCAG CTTGTGTCTC TGCTCTGAG GAGACCATGG 60
CCCAGTATCT GAGTACCTG CTGCTCCTGC TGGCCACCT AGCTGTGGCC CTGGCCTGGA 120
GCCCAAGGA GGAGGATAGG ATAATCCCG GTGGCATCTA TAACGAGAC CTCAATGATG 180
AGTGGGTACA GCGTCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
ACTACTACAG ACGTCCGCTG CCGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
ATTACTTCTT CGAGGTAGAG GTGGGCGGCA CCATATGTAC CAAGTCCAG CCCAATTGG 360
ACACCTGTGC CTTCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTGAGA 420
TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCCAC TCCCACCCCT TGTAGTGCTC 540
CCACCCCTGG ACTGGTGGCC CCCACCTGC GGGAGGCTCT CCCATGTGCC TGCGCCAAGA 600
GACAGACAGA GAAGGCTGCA GGAGTCTTT GTTGCTCAGC AGGGGCTCT GCCTCCCTC 660
CTCTCTCTT GCTTCTAATA GCCCTGGTAC ATGGTACACA CCCCCCACC TCTGCAATT 720
AAACAGTAGC ATCGCC

Seq ID NO: 601 Protein sequence
Protein Accession #: NP_001889.1

75
80

1 11 21 31 41 51
| | | | | |
MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQALHP AISEYNKATK 60
DDYRRLPLRV LRARQQTGG VNYFFDVEVG RTICTKSQPN LDTCAPEQP ELQKKQLCSF 120
EIYEVFWENR RSLVKSRCQE S

Seq ID NO: 602 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299..961

85

1 11 21 31 41 51
| | | | | |

	CTCTGAGCTT	CTCTGAGCCT	TGTTTGCTCA	TCTGGAAAAA	GGGGATTAAA	CCATTTTACCT	60
	CATGGAGTTG	TGAAAGAATA	GCTGCAAAAGC	ACCTAACACA	TAGTAAGGTT	CCAGTGCAG	120
	CTACTTCTGC	TGGGTGTAGT	CTAGCTGTGT	AGGCCCTCTG	TTCTCACTT	GGAGAACTG	180
5	GGGTGGCAGG	CCGGTCCCCC	ACAAAAGATA	ACTCATCTCT	TAATTTGCAA	GCTGCCTCAA	240
	CAGGAGGGTG	GGGGAACAGC	TCAACAATGG	CTGATGGGGG	CTCCTGGTGT	TGATAGAGAT	300
	GGAACTTGGG	CTTGAGAGCC	TCTCCACGCT	GTCCCACTGC	CCCTGGCCTA	GGCGGCAGCC	360
	TGCCCTGTGG	CCCACTCTGG	CCGCTCTGGC	TCTGTGAGC	AGGCTGCGAG	AGGCCTCCCT	420
	GGGCTCGCGG	CCCCGACGCG	CTGCCCCCGG	CGAAGGCCCC	CCGCTGTCTC	TGGCGTCCCG	480
10	CGCGGGCCAC	CTGCGGGGGG	GACGACGGC	CCGCTGGTGC	AGTGGAGAG	CCGCGCGGCC	540
	GGCGCGCGAG	CCTTCTCGGC	CCGCGCCCCC	GGCGCTGCA	CCCCCATCTG	CTCTTCCCGG	600
	CGGGGGCCCG	GGGGCGCGGG	CTGGGGGCCG	GGGCAGCTCG	GCTCGGGCAG	CGGGGGCGCG	660
	GGGCTGTGCG	CTGCGCTCGC	AGCTGGTGGC	GGTGGCGCGG	CTCGGCTGGG	GCCACCGCTC	720
	CGACGAGCTG	GTGCGTTTCC	GCTTCTGCGG	CGGCTCCTGC	CGCGCGCGCG	GCTCTCCACA	780
15	CGACCTCAGC	CTGGCCAGCC	TACTGGGCGC	CGGGGCCCTG	CGACCGCCCC	CGGCTCCCGG	840
	GGCCGTGAGC	CAGCCCTGCT	GCGGACCCAC	GCGCTACGAA	GGGCTCTCCT	TCATGGACGT	900
	CACACGACCC	TGGAGAACCG	TGGACCGCCT	CTCCGCCACC	GCGTGGGGCT	GCGTGGGGCT	960
	AGGGCTCGTG	ATGAGGCTTT	GACAGCTGGA	CCCTTACCGG	TGGCTCTTCC	TGCGTGGGAG	1020
	CCTCCCGCAG	AGTCCCACTA	GCCAGCGGCC	TCAGCCAGGG	ACGAAGGCGT	CAAGCTGAG	1080
20	AGGCCCTTAC	CGGTGGGTGA	TGGATATCAT	CCCGAACAG	GTGAAGGGAC	AACTGACTAG	1140
	CAGCCCAACC	GCCCTACACC	TGCGGATCCC	AGCCTAAAG	ACACCAGAGA	CCTCAGCTAT	1200
	GGAGCCCTTC	GGACCCACTT	CTCACAGACT	CTGGCAGCTG	CCAGGCGCTG	AACTGGGGAC	1260
	CCCTCCTCTG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCG	CCCGCCAGCG	CCCTGTAGGG	1320
25	ACAGCATTTG	AAGGACACAT	ATTGCACTTG	CTTGGTTGAA	AGTGCTCTGT	CTGGAAGTGG	1380
	CCTGTACTCA	CTCATGGGAG	CTGGCCCC				

Seq ID NO: 603 Protein sequence

Protein Accession #: NP_003967.1

30	1	11	21	31	41	51	
	MELGLGLST	LSHCPWPRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	60
	PAGHLPGGRT	ARNWCSGRARR	PPQPSPRPAP	PPPAPPSALP	RGGRARAGG	PGSRARAAGA	120
	RGCLRLSQLV	PVRALGLGHR	SDELVRFRFC	SGSCRARRSP	HDLSLASLLG	AGALRPPPGS	180
35	RPVSQPCCRP	TRYEAVSFMD	VNSTWRTVDR	LSATACGCLG			

Seq ID NO: 604 DNA sequence

Nucleic Acid Accession #: NM_057091.1

Coding sequence: 783..1445

40	1	11	21	31	41	51	
	ACTGGCCGCT	GAGAGAAGAA	TGGGGTGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
	GGACCCCCAA	ATCTGCACGT	ACCAGCAGTC	AGCCGCCCCA	CGCAGGGACC	GGCTTACCCC	120
	TGGCTCCCGG	CCCTCACTCA	CTTCTCTCCG	CCCTCGGGCC	GGCTCCGAG	CTCTCTACTT	180
45	CGCGTGTCTA	CAAACTCAAC	TCCCGGTTTC	CGTGCCTCTC	CACCGCTCGA	GTTCTCTACT	240
	CTCCATATCC	GAGGGGCCCC	TCCAGCATC	TACCCCTCTC	CCAACTCCG	GGGACCTAGC	300
	CAAGCTAGGG	GGGACTGGAT	CCGACGGGTG	GAGCAGCCAG	GTGAGCCCG	AAAGGTGGGG	360
	CGGGGCAGGG	GCGTCCGAG	CCCCACCCCG	GGATCTGGTG	ACGCTGGGGC	TGGAATTGGA	420
	CACCGACAGG	CTGGGGGGCG	GGGCAGGAGG	CTGCTGAGGG	ATGGAGTTGG	GCCCGGCCCG	480
50	CAGACAAGGC	CGGGGGGCTC	CGCCAGCAGC	AGGTCCCTCG	GGCCCGAGCC	CTCGCTGCCA	540
	CCCGGGCTCG	GAGCCCCACA	CCGAGGGGTG	CAGACTGGCT	GCCAAGGCCA	CACCTTTGGC	600
	TAAAAGAGGC	ACTGCCAGGT	GTACAGTCTC	GGCATGCGC	TGTTTGAGCT	TGGGGGGAGA	660
	GCCAGCACT	GGTCCCGCGA	AAGGTGCCTA	GAAGAACAAG	GTGCAGGACC	CCGTGCTGCC	720
	TCAACAGGAG	GGTGGGGGAA	CAGCTCAACA	ATGGCTGATG	GGCGCTCCTG	GTGTGTATAG	780
55	AGATGGAAT	GGGCTTGGGA	GGCCTCTCCA	CGCTGTCCCA	CTGCCCTGG	CTAGGGGGGC	840
	AGCCTGCGCT	GTGGCCCACT	CTGGCCGCTC	TGGCTCTGCT	GAGCAGCGTC	GCAGAGGCGT	900
	CCCTGGGCTC	CGCGCCCGCG	AGCCCTGCCC	CCCGCGAAGG	CCCCCGGCTC	GTCTGGGCGT	960
	CCCGCGCGCG	CCACTCTGCG	GGGGGACGCA	CGGCCCGCTG	GTGCACTGGA	AGAGCCCGGC	1020
60	GGCGCGCGCG	CGACCTTCT	CGGCCCGCGC	CCCGCGCGCG	TGCACCCCA	TCTGCTCTTC	1080
	CGCGCGGGGG	CGCGCGGGGG	CGGGCTGGGG	GCCCGGGCAG	CGCGCTCGG	GCAGCGGGGG	1140
	CGCGGGGCTG	CGCGCTCGCG	TGCGAGCTGG	TGCGGCTGGG	CGCGCTCGCG	CTGGGCCACC	1200
	GCTCGGACGA	GCTGGTGGCT	TTCCGCTTCT	GCAGCGGCTC	CTGCCCGCGC	GCGCGCTCTC	1260
	CACACGACCT	CAGCTTGGCG	AGCCTACTGG	GCGCGGGGGC	CCTGCGACCG	CCCGCGGGCT	1320
	CCCGCGCGCT	CAGCCAGCCC	TGCTGCGGAC	CCACGCGCTA	CGAAGCGGTC	TCCTTCATGG	1380
65	AGCTCAACAG	CACCTGGAGA	ACCCTGGACC	GCCTCTCCGC	CACCGGCTGC	GGCTGCTGGG	1440
	GCTGAGGGCT	CGCTCCAGGG	CTTTGCAGAC	TGGACCCCTA	CGGTGGGCTC	TTCTGCGCTG	1500
	GGACCCCTCC	GCAGAGTCCC	ACTAGCCAGC	GGCCTCAGCC	AGGAGCGAAG	GCCTCAAAGC	1560
	TGAGAGGCGC	CTACCGGTGG	GTGATGGATA	TCATCCCGGA	ACAGGTGAAG	GGACAACTGA	1620
	CTAGCAGCCC	CAGAGCCCTC	ACCCTGGGGA	TCCAGCCCTA	AAAGACACCA	GAGACCTCAG	1680
70	CTATGGAGCC	CTTGGACCC	ACTTCTCACA	GACTCTGGCA	CTGGCCAGGC	CTGAACTCTG	1740
	GGACCCCTCC	TCTGATGAAC	ACTACAGTGG	CTGAGGCATC	AGCCCGCGCC	CAGGCCCTGT	1800
	AGGGACAGCA	TTTGAAGGAC	ACATATTGCA	GTTGCTTGTT	TGAAAGTGCC	TGTGCTGGAA	1860
	CTGGCCTGTA	CTCACTCATG	GGAGCTGGCC	CC			

Seq ID NO: 605 Protein sequence
Protein Accession #: NP_003967.1

80	1	11	21	31	41	51	
	MELGLGLST	LSHCPWPRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	60
	PAGHLPGGRT	ARNWCSGRARR	PPQPSPRPAP	PPPAPPSALP	RGGRARAGG	PGSRARAAGA	120
	RGCLRLSQLV	PVRALGLGHR	SDELVRFRFC	SGSCRARRSP	HDLSLASLLG	AGALRPPPGS	180
	RPVSQPCCRP	TRYEAVSFMD	VNSTWRTVDR	LSATACGCLG			

Seq ID NO: 606 DNA sequence
Nucleic Acid Accession #: NM_057160.1

Coding sequence: 1..714

1 11 21 31 41 51
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ATGCGCGGCC TGATCTCAGC CGAGGACAG CCCCTCCTTG AGTCTCTTCC TCCCCAAGCC 60
CACCTGGGTG CCCCTCTTCT CCCTGAGGCT CCACCTTGCT TCTCCGCGCA GCCTGCCCTG 120
TGGCCACACC TGGCGCTCTT GGCCTCTGCT AGCAGGCTCG CAGAGGCCTC CCGGGCTTCC 180
GGGCCCCGCA GCCCTGCCCC CGCGAAGGC CCCCCGCTG TCTGGGCTTC CCGCGCGGCG 240
CACTGCGCG GGGAGCGCAC GGCCTGCTGG TGAGTGGAA GAGCCCGCG GCGCGCGCG 300
10 | | | | |
CAGCCTTCTC GGCCTGCGCC CCGCGCGCT GCACCCCAT CTGCTCTTCC CCGCGCGGCG 360
CGCGCGCGCG GGCCTGGGGG CCGCGGCGAG CGCGCTCGGG CAGCGGGGCG GCGGGGCTGC 420
CGCTGCGCTT GCGAGCTGGT GCGGCTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
CTGGTGGCTT TCGAGCTTCT CAGCGGCTCC TGGCGCGCG CGCGCTCTCC ACACGACCTC 540
AGCTGGGCGA GCTTACTGGG GCGCGGGGCC CTGCGACCGC CCGCGGGCTC CCGCGCGGTC 600
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AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGCTT CCTTCATGGA CTTCAACAGC 660
ACCTGGAGAA CCGTGGACCG CCTCTCGGCC ACCGCTGGCG GCTGCGTGGG CTGAGGGCTC 720
GCTCCAGGGG TTTGAGAGCT GGAACCTTAC CGGTGGCTCT TCTGCGCTGG GACCTCCCG 780
CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGAAGGAAG CCTCAAAGCT GAGAGGCCCC 840
TACCGGTGGG TGATGGATAT CATCCCGAA CAGGTGAAG GACAACGAC TAGCAGCCCC 900
20 | | | | |
AGAGCCCTCA CCGTGGCGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
TTGGAACCCA CTCTCAGAC ACTCTGGCAC TGGCCAGGCC TGAACCTGG GACCCCTCTT 1020
CTGATGAACA CTACAGTGGC TGAGGCATCA GCGCCCGGCC AGGCCCTGTA GGCACAGCAT 1080
TTGAAGGACA CATATTGAG TTGCTTGGTT GAAAGTGCTT GTGCTGGAAC TGGCCTGTAC 1140
25 | | | | |
TCACTCATGG GAGCTGGCCC C

Seq ID NO: 607 Protein sequence

Protein Accession #: NP_476501.1

1 11 21 31 41 51
30 | | | | |
MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
APRSPAPRGG PPPVLASPAQ HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
RAARAGGPGS RARAAGARGC RLRSQLVFVR ALGLGHRSD LVRFRFCSGS CRRARSPEDL 180
35 | | | | |
SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TAOGCLG

Seq ID NO: 608 DNA sequence

Nucleic Acid Accession #: NM_057090.1

Coding sequence: 29..715

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CGCTCCAGGG CTTTGCAGAC TGGACCTTAA CCGGTGGCTC TTCTGCGCTG GGCACCTCCC 780
55 | | | | |
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Seq ID NO: 609 Protein sequence

Protein Accession #: NP_476431.1

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Seq ID NO: 610 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1746

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85 | | | | |
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25	GGATTTCOGA	TTCTATACCC	TGGGCTTCTT	TOGAGAGGGC	TCTTCTTCCA	AATCTCTCCC	2040
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30	TGAGTTCTCT	CTCAAAAGAA	GACTTCAAA	CATTTAACCT	GTTCCTTAAG	AGCCGCTCAAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TGATGCCGCT	CAGTTCTCTG	2400
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	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAACTGCA	AACTTTCTCT	2520
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35	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGG	TCCCTGTGTT	2640
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	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCTCTGGC	TTTTCCAGAA	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGAA	GCCAGGACGG	2880
40	TCCCCCCACA	GTCAGCTGTG	GCAAGGCCCC	CGTGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
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	AGAGACCTTG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGTCAG	CCACACCCCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
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	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCAGATC	AGCTGGCAGC	3300
	TGAACCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTATGG	3360
	GTCTGGGGGC	TCCCTGGAGC	TCTCTCTGG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
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50	CTGCTATACA	GATATTCACA	TGGGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGCTCTT	3540
	CTCTGGACAA	CTGGCCAGT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTACAGCTGAC	TCCACGGGGA	TCTGGAATC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCGCTCTC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
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55	CCCGATCGGC	TCTTATTAGC	TCCCGCTTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
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70	GGGCTGGAAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAGTTTT	4680
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	TGGGCTGTAT	GTATATTGTT	CTTCTCTT	AGAAATTAGA	GATACAAAG	TTCTACTTAG	5220
	AACCTTTTCA	GGACACAAT	TCCACAACCT	TTGAGATGCT	GATGTAGAGC	TATTTGGGAA	5280
80	GAACCTCCAA	ACTCAGGAAT	TTTGACAGAG	GCAGACAGCT	AGAGATAACT	CGGACCCAG	5340
	AGTTGGTCTG	CAGATGTTAG	ATGTATCCTA	GCTTTTAGCC	ATAAACCACT	CAAAGATTCA	5400
	GCCCCAGAT	CCACAGTCA	GAACCTGAAT	TGCGTTGTTG	GGAGGCCAGC	AGTGGCCTTG	5460
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	CTCCTCTCCG	CCAGGTTTTC	TCTTCTCTT	AAGGAGAGAT	TGTTCTCACC	AACCCGCTGC	5580
85	CTTCACTGCT	CCTTCAAGC	TAGATCATGT	TTGCTTGTCT	TAGAGAAATTA	CTGCAAAATCA	5640
	GCCCCAGTGC	TTGGGATGTC	ATTTACAGAT	TTCTAGGCC	TCAGGTTTTT	GTAGAGTGTG	5700
	AGCCCTGGTG	GGCAGGTTG	GGGGTCTGT	CTTCTGCTG	ATGCTGCTG	TAATCCATT	5760

GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 611 Protein sequence
Protein Accession #: BAB84587.1

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10
15
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10	POGLDSLESL	LLSSNQILQI	QPAHFSQCSN	LKELQIAGNH	LEYIPDGAFD	180
GKNSLTHISP	RVPQHLGNLQ	VLRLYENRLT	DIPMGTFDGL	VNLQELALQQ	NQIGLLSPGL	240
FHNHNLRL	YLSNNHISQL	PPSIFMQLPQ	LNRLTLFGNS	LKELSLGIFG	PMPNLRRLWL	300
YDNHISLPLD	NVFSNLRLQ	VLILSRNQIS	FISPGAFNGL	TELRELSLHT	NALQDLGDNV	360
FRMLANLQNI	SLQNNRLRQL	PGNIFANVNG	LMAIQLNQNO	LENLPLGIFD	HLGKLCLELRL	420
15	YDNPNRCDSD	ILPLRNWLLL	NQPRLGTDTV	PVCFSPANVR	GQSLIIINVN	480
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Seq ID NO: 612 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

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25	TCGTGGATGG	GAGCTGGGAG	TCAGTGTGG	AGAAGAAACA	ACAAAAGCCA	180
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30	TCTCTAGCCC	TCAGCACCCC	TGCGGTAGGA	GTGCGGCTCT	TACCACTTGG	300
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Seq ID NO: 613 Protein sequence
Protein Accession #: XP_098151

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40	LFLKAYCAQ	ILPKHWIWL	SLALSTPAVG	VPPLPTCDGV	QRELLPCMVF	120
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Seq ID NO: 614 DNA sequence
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Coding sequence: 77..1372

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55	TCACCTTTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	360	
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60	AAAGCCCTCC	TCTCTTCCAG	AAGAATTAAA	ATTTCACTGT	GGCCAAAAGA	600	
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85	ACCTGTGACC	AGCACTGTCT	CAGTTTCACT	TTCCATAGAA	TGTCCCTTTC	2160	
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Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

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HCEIDRSKTK YEGNGHFYRG KASTDTMGRF CLPWN SATVL QOTYHAHRSD ALQLGLGKHEN 120
YCRNPDNRNR FWCVYVQVLK PLVQECMVHD CADGKPKSSP PEELKPKQCG KTLRPRFKII 180
10 GGEFTTIENQ FWFAAIYRRH RGGSVTYVOG GSLISPCWVI SATHCPIIDY KKEYDIYVYLG 240
RSRLNMTQGG EMKFEVENLI LHKDYSADTL AHNDIALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGFGK ENSTDVLYPE QLKMTVVKLI SHRECCQPHY YGSEVTTKML 360
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Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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25 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCGCGCCCTC CGGCTCCTG GAACGGAGCC 240
CTCTGCGCGG TGCTCTCTGG GACCTCGCG ATCTTAATAT TTGCCAGTGA TGCCCTGCAA 300
AATGTGACAT TACATGTTCC CTCCAACTA GATGCGGAGA AACTTGTGG TAGAGTTAAC 360
CTGAAGAGAT GCTTTACAGC TGCAAACTA ATTCATTCAA GTGATCCTGA CTTCCAAATT 420
TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTTCTAT TGTCTCTGGA GAAGAGAAGT 480
30 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540
GAGCATCAAA CAAAGGTCTT AAAGAAAAGA CATACTAAAG AAAAGTCTT AAGGCGCGCC 600
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CTTTTCTTTC AACAGGTTCA ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720
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35 AACTTGTATT GTACTGTCCT TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
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GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
GACACGATCG ACACACGCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCACCC 1080
40 CTATTTTCTA TGCCATCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
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GGTCTACAGA CAACCTCAAT TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
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45 ACCATTTTAA AGGCAATGA AAATGGCAAT TTTAAAATTG TAACAGATGC CAAACCAAT 1440
GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
CAAATTGGTG TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
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50 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAAGTG GAACAACAAG CAATGGATAT 1680
AAAGCATATG ACCGCAATGA AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTAT 1740
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CGTCTTCTCT ATCAGAATGA TCCTCCATT GGTCTCATATG TAGTACCTAT AACAGTGAGA 2160
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60 AAGTGGGCGA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGAT CCGTGTTAAG 2340
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65 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGGAGG ACACCGAGCC 2580
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70 GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 2880
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75 TCTATCCAAG GAGGTCTACA GAGAAATTA AGTCTGCCCT ATTTGTACA TTTGGGTATA 3180
ATGACAACAG CCAATTTATA GTGCAATAAA ATGTAATTA TTCAAGTCTT TATTATAGAC 3240
TATTTGAAGC ACAACCTAAT GGAATTTGT AGAGACCTTG CTTTAACATT ATCTCCAGTT 3300
AATTAAGTGT TCATGTGGTG CTGGAAACT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360
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TTCTAGCCA GGCATTGACT ATTACAATTT CATT
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Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

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85      1      11      21      31      41      51
MEARPSGSM NGALCRLLLL TLAILIFASD ACKNVTILHP SKLDAEKLVG RVNLKECFPTA 60
ANLIHSSDPD FOILEDGSSV TINTILLSSE KRSFTILLSN TENQEKKIIF VFLEHQTKVL 120
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	KKRHTKEKVL	RRAKRRWAPI	PCSMLENSLG	PPPLFLQVQV	SDTAQNYTIY	YSIRGPGVDQ	180
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	PIFTEETTYF	TIFENCRCVGT	TVGQVCATDK	DEPDTHMTRL	KYSIIQGVPP	SPTLFSMEPT	300
5	TGVTITTSQ	LDRELIDKQ	LKIKVQDMDG	QYPLQTTST	CIINLIDVND	HLPTFTTSY	360
	VTSVEENTVD	VEILRVTVED	KDLVNTAMWR	ANYTILKQNE	NGNFKIVTDA	KTNEGLVCVV	420
	KPLNYEEKQQ	MILQIGVNE	APFSREASPR	SAMSTATVTV	NVEDQDGGPE	CNPIQTVRM	480
	KENAEVGTTS	NGYKAYDPET	RSSSGIRYKK	LTDPTGWVTI	DENTGSIKVP	RSLDREAEIT	540
	KNGLYNITVL	ASDQGGRTCT	GTLGIILODV	NDSNPFIPKK	TVIICKPTMS	SABIVAVDPD	600
10	EPHGGPFFD	SLESTSEVQ	RMWRLKAIND	TAARLSYQND	PPFGSYVVP	TVRDLGMSS	660
	VTSLDVTLCD	CYTENDCTHR	VDPRIGGGGV	QLGKMAILAI	LLGLALLPCI	LFTLVCGASG	720
	TSRQPKVIPD	DLAQNLIVS	NTEAPGDDKV	YSANGPTTQT	VGASAQGVCG	TVSGGIKNGG	780
	QETIEMVKG	HQTSSECRGA	GHHHTLDSR	GGHTEVDNCR	YTYSEMHSFT	QPRLGEKVYL	840
	CNQDENHKA	QDYVLTYNE	GRGSVAGSVG	CCSERQEDG	LEFLDNLEPK	FRTLAEACMK	900
15	R						

Seq ID NO: 618 DNA sequence

Nucleic Acid Accession #: NM_004949.1

Coding sequence: 202..2745

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	GCTCCGCGCG	CGGCGCTCG	CCCCGCGAGC	CCTCCTACCC	CGGCCCGAGC	CTCGGCCCGC	180
25	GACCTCGCCC	GAGCCTCTC	CATGGAGGCA	GCCCGCCCTC	CGGCTCCTG	GAAACGAGCC	240
	CTCTGCGCGC	TGCTCTGCT	GACCTCGCG	ATCTTAATAT	TGCGCAGTGA	TGCGTGCATA	300
	AATGTGACAT	TACATGTTCC	CTCCAAACTA	GATGCCGAGA	AACCTGTGTTG	TAGAGTTAAC	360
	CTGAAGAGAT	GCTTTACAGC	TGCAAACTCTA	ATTCAITCAA	GTGATCCTGA	CTTCCAAATT	420
	TTGGAGGATG	GTTCACTCTA	TACAACAAAT	ACTATTCTAT	TGTCTCTGGA	GAAGAGAAGT	480
30	TTTACCATAT	TACTTTCCAA	CACTGAGAAC	CAAGAAAAGA	AGAAAATATT	TGTCTTTTGT	540
	GAGCATCAAA	CAGAAGTCTC	AAAGAAAAGA	CATACTAAAG	AAAAAGTTCT	AAGGCGCGCC	600
	AAGAGAGAT	GGGCTCCAAT	TCCTTGTTCG	ATGCTAGAAA	ACTCCTTGGG	TCCCTTTCCA	660
	CTTTTCTTTC	AACAGGTTCA	ATCTGACACG	GCCCAAACT	ATACCATATA	CTATTCCATA	720
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35	AACCTGTATT	GTACTCCTCC	TGTAGATCGT	GAGCAGTATG	AATCTTTTGA	GATAATTGCC	840
	TTTGCAACAA	CTCCAGATGG	GTATACTCCA	GAACCTCCAC	TGCCCCAAT	AATCAAAATA	900
	GAGGATGAAA	ATGATAACTA	CCCAATTTTT	ACAGAAGAAA	CTTATACTTT	TACATTTTTT	960
	GAAAATTGCA	GAGTGGGCAC	TACTGTGGGA	CAAGTGTGTG	CTACTGACAA	AGATGAGCCT	1020
40	GACACGATGC	ACACACGCTC	GAACTACTCC	ATCATTGGGC	AGGTGCCACC	ATCACCACCC	1080
	CTATTTTCTA	TGCATCCAA	TACAGGCGTG	ATCACCACAA	CATCATCTCA	GCTAGACAGA	1140
	GAGTTAATGT	ACAATGACCA	GTTGAAAATA	AAAGTACAAG	ACATGGATGG	TCAGTATTTT	1200
	GGTCTACAGA	CAACTCAAC	TGTATCATTT	AACATTGATG	ATGTAATAGA	CCACTTGCCA	1260
	ACATTTACTC	GTACTTCTTA	TGTGACATCA	GTGGAAGAAA	ATACAGTTGA	TGTGAAAATC	1320
	TTACGAGTTA	CTGTGTAGGA	TAAGGACTTA	GTGAATACTG	CTAACTGGAG	AGCTAATTAT	1380
45	ACCATTTTAA	AGGCAATGA	AAATGGCAAT	TTTAAATTTG	TAACAGATGC	CAAAACCAAT	1440
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50	CCAATACAGA	CTGTTCCGAT	GAAAGAAAAT	GCAGAAGTGG	GAACAACAAG	CAATGGATAT	1680
	AAAGCATATG	ACCCAGAAAC	AAGAAGTAGC	AGTGGCATAA	GGTATAAGAA	ATTAACTGAT	1740
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	GATAGAGAGG	CAGAGACCAT	CAAAAATGGC	ATATATAATA	TTACAGTCTT	TGCATCAGAC	1860
	CAAGGAGGGA	GAACATGTAT	GGGGACACTG	GGCATTATAC	TTCAAGACGT	GAATGATAAC	1920
	AGCCCATTTA	TACCTAAAAA	GACAGTGATC	ATCTGCAAA	CCACCATGTC	ATCTGCGGAG	1980
55	ATTGTTGCGG	TGATCTCTGA	TGAGCCTATC	CATGGCCAC	CCTTTGACTT	TAGTCTGGAG	2040
	AGTTCTACTT	CAGAAGTACA	GAGAATGTGG	AGACTGAAAG	CAATTAAATGA	TACAGCAGCA	2100
	CGTCTTTCTC	ATCAGAAATGA	TCCTCCATTT	GGCTCATATG	TAGTACCTAT	AACAGTGAGA	2160
	GATAGACTTG	GCATGTCTAG	TGTCACTTCA	TGGATGTTA	CACTGTGTGA	CTGCATTACC	2220
	GAAAATGACT	GCACACATCG	TGTAGATCCA	AGGATTGGCG	GTGGAGGAGT	ACAACCTTGA	2280
60	AAGTGGGCCA	TCCTTGCAAT	ATTGTTGGGC	ATAGCATTGC	TCTTTTGCAT	CCTGTTTACG	2340
	CTGGTCTGTG	GGGCTCTCGG	GACGTCTAAA	CAACCAAAAG	TAATTCTCTGA	TGATTTAGCC	2400
	CAGCAGAAC	TAATTGTATC	AAACACAGAA	GCTCCTGGAG	ATGACAAAGT	GTATTCTGCG	2460
	AATGGCTTCA	CAACCCAAAC	TGTGGGCGCT	TCTGCTCAGG	GAGTTTGTGG	CACCGTGGGA	2520
	TCAGGAATCA	AAAACGAGG	TCAGGAGACC	ATCGAAATGG	TGAAGGAGG	ACACCAAGCC	2580
65	TCGGAATCCT	GCOCGGGGGC	TGGCCACCAT	CACACCCTGG	ACTCCTGCG	GGGAGGACAC	2640
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	CTTGGTGAAG	AATCCATTAG	AGGACACACT	CTGATTAATA	ATTAACAAT	GAAAGAAAGT	2760
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70	AGATGGGCTT	GAATTTTGG	ATAATTTGGA	GCCCAATTT	AGGACACTAG	CAGAAGCATG	2940
	CATGAAGAGA	TGAGTGTGTT	CTAATAAGTC	TCTGAAAGCC	AGTGGCTTTA	TGACTTTTAA	3000
	AAAAAATTAC	AAACCAAGAA	TTTTTTAAAG	CAGAAGATGC	TATTTGTGGG	GTTTCTCTC	3060
	TCATTATTTG	GATGGAATCT	CTTTGGTCAA	ATGCACATTT	ACAGAGAGAC	ACTATAAACA	3120
	AGTACACAAA	TTTTTCAATT	TTTACATATT	TTTAAATTAC	TTATCTTCTA	TCCAAGGAGG	3180
75	TCTACAGAGA	AATTAAGTC	TGCCTTATTT	GTTACATTTG	GGTATAATGA	CAACAGCCAA	3240
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	CCTAATGGAA	AATTGTAGAG	ACCTTGCTTT	AACATTATCT	CCAGTTAAAT	AAGTGTTCAT	3360
	GTGGTGTCTG	GAAACTGTGT	TTTTCTGAA	CATCTAAAGT	GTGTAGACTG	CATTCTTGCT	3420
80	ATTATTTTAT	TCTGTAAATG	TGACCTTTTC	ACTGTGCAAA	GGGAGATTTC	TAGCCAGGCA	3480
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Seq ID NO: 619 Protein sequence

Protein Accession #: NP_004940.1

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 KKRHTKEKVL RRAKRRNAPI PCSMLENSLG PFPLPQQVQ SDTAQNYITY YSIRGPGVDQ 180
 EPRNLVYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPELPLPLI IKIEDENDNY 240
 PIFTEETVTF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIQGVFP SPTLFMSHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQMDMG QYFGLQTTST CINIIDDVND HLPFTFRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKQNE NGNFKIVTDA KTNQGVLCVV 420
 KPLNVEEKQQ MILQIGVUNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYK LIDTPTGWTI DENTGSIKVP RSLDREAETI 540
 KNGIYNIIVL ASDQGGRTCT GTLGIILQDV NDNSPFIKPK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPPPDF SLSSSTSEVQ RMWRLKAIND TAARLSYQND PPFQSVVVPV TVRDLRGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLGKWLAI LIGIALLFCI LFTLVCGASG 720
 TSKQPKVIPD DLAAQNLIVS NTEAPGDDKV YSANGPTTQT VGASAQGVCG TVGSGIKNGG 780
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Seq ID NO: 620 DNA sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 46..718

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 CGAGGGCTGG GGGCGGAGG AGCGGCTCCC TACTCTCCGG GCTTTGGGAG AGGGTGGCTC 300
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 CGTCTCCAG CGGGAGCGCG GCCCTGCGG AAGCGCGGGA CTGGGCGATC GCCTTTAATT 720
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Seq ID NO: 621 Protein sequence
 Protein Accession #: NP_115934.1

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 VTGSAEGWGP EEPLPYRAF GEGASARPR CRNGGTCVLG SPCVCPAHFT GRYCEHDQRR 120
 SECGALEHGA WTLRACHLCR CIPGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
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Seq ID NO: 622 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..390

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 CAGTGTGTTT ACAATGAGCG CATCGTGTCC CTGAGCGAGA CCGGCAATG TGGTCCCCCC 240
 TGCACCTTCT GGCCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300
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Seq ID NO: 623 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 QCCYNDIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLVQGV NSQCHSSPIS 120
 SKCERGRIC

Seq ID NO: 624 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 51..1085

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 ATGTGCGAGA GGGGAAGGAG GTTCTTTTAC TCGCCACCAA OCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACTCA ACAGCTACC CCAAGGCGCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
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 TGCCCAAGCC TCCTATCTCC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
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 GCCTCCCGGT CAGTCCCAAG CTGCAGCTGT CCAATGGCAA CATGACCCCT ACTCTACTCA 660

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CCTCAAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCCTCTA 840
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Seq ID NO: 625 Protein sequence
Protein Accession #: AAA59907.1

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45

1 11 21 31 41 51
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TLQVKSIDL VNEEATGQPHV YPELKPSPIS SNNSNPVEDK DAVAPTCEPE VQNTTYLWV 180
NGQSLPVSPR LQLSNGNMTL TLLSVKRNDA GSYECIONP ASANRSDPVT LNVLYGPDVP 240
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Seq ID NO: 626 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

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ATGTGSCAGA GGGGAAGGAG GTTCTTCTAC TCGCCACCAA CCGCCCCAG AATCGTATTG 240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
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CCTTCAACCTG TGAACCTGAG GTTCAGAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
GCTTCCCGGT CAGTCCAGG CTGCAGCTGT CCAATGGCAA CATGAOCCTC ACTCTACTCA 660
GCCTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
ACCGCAGTGA CCCAGTCAACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCOC 780
CCTCAAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCCTCTA 840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
TCCCTCTAGC TGTGGCCACC GTGGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
TATAGCAGCC CTGGTGATTT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCCT 1140
GAATCTCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAATTT TAAAGGGAAA 1260
ACCTTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAAC TAGAGA CAGTCAAACT 1320
GCAAAACCATG GTGAGAAATT GAOGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
AACAAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCTT TGCTTATGCC 1440
TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
GGGTAACTTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAAAAG 1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CGGTGTGTTC 1620
AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTTCTAGACT CACCTGTCTT CACTCCCTGT 1680
TTTAAATCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
GGAGGAGTCT GTGAGTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAAATG CTACACTCAT 1860
CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
CTCTTGATAT TACCCCTCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
CTCTAAAGC TTTAAATGTC TGCAATGCAG CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160

5 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AGATAGATC CAATTAAAAA AAATTAAAAA CAATTAAAAA AAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
TGTTTCTCTG TTCCAATTGG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTGTAGAGT TGGTGTCTGT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
TAGCTCTATA ACT

10 Seq ID NO: 627 Protein sequence
Protein Accession #: AAA59908.1

1 11 21 31 41 51
MDSFSDVKT RLLIMIRLLP PFNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV 60
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

20 Seq ID NO: 628 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 2370..2501

1 11 21 31 41 51
GGAGCTCAAG CTCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
CCTCAGCCCC TCCTGTCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
TTCTAACCTT CTGGAACCCA CCCCACTCTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCCAACA CCTGCCCCAG AATCGTATTG 240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
TAGGAATCTA ACAGGTACCC CCAGGGCCCC CATACAGTGG TCGAGAGACA ATATACCCCA 360
ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
TCATAAAGTC AGATCTTTGG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
TGCCCAAGCC CTCCATCTCC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
CCTTCACTGT TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
GCCTCCCGGT CAGTCCCGAG CTGCAGCTGT CCAATGGCAA CATGACCTCT ACTCTACTCA 660
GGGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
ACCGCAGTGA ACCGACTCAC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
CCTCAAGGCG CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCACGCTCTA 840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGAAGTT CCAGCAATCC ACACAAGAGC 900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCTGT 1020
TCCTCTCAGC TGTGGCCACC GTGCGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
TATAGCAGCC CTGGTGATTT TTGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
GAATTCTTCT AGTCTCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260
ACCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320
GCAAAACATG GTGAGAAATT GAOGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
AACCAAGACTC CTGATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
TGCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560
AGATCTCTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTAAACACAG CGTGTGTTC 1620
AAATGTACAG TGTCTCTTTT CAGAGTTGGA CTCTAGACT CACCTGTCTT CACTCCCTGT 1680
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
CTGACTCAT TTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
CTCTGGTAT TACCTCTCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
CTCTAAAGC TTTAAATGTC TGCAATGAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
GGCTGGAATT ACAAATGTC GAGAAATGTG TCATCAGGAG AACATCATAA CCAATGAAGS 2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
TCTCACTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AGATAGATC CAATTAAAAA AAATTAAAAA AAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
TGTTTCTCTG TTCCAATTGG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTGTAGAGT TGGTGTCTGT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
TAGCTCTATA ACT

Seq ID NO: 629 Protein sequence
Protein Accession #: AAA59909.1

1 11 21 31 41 51
MLTNVPIFV LFPSCNLTKP TVLVLYCPGG AITVLVEMCC PNS

75 Seq ID NO: 630 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

1 11 21 31 41 51
GCGGCGGGCG CAGACAGCGG CGGGGCGAGG ACCTGCACTA TGGCTGGGGG CTGCTGCGC 60
CGGTTGCTCG GGTCTCTCTG GCTGGGGCTC TGGCTGGCGT TGGCTGGCTC CGTGGCCGGG 120
GAGCAAGCGC CAGGCAACGC CCCCTGCTCC CGGGGAGCTC CTGGAGCGG GGAAGTGGAC 180
AAGTGCATGG ACTGCGCGTC TTGAGGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
GCTGCAGCAC CTCTGCCCCC CTTCGGGCTG CTTTGGGCCA TCTTGGGGG CGCTCTGAGC 300
CTGACCTTGG TGCTGGGGCT GCTTCTGGGC TTTTGGTCTT GAGAGCATG CGCAGGAGA 360
GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGCGAGAGG GCTGCCACGC TGTGGGCGTC 420

5 ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTTCATCCA 480
 TTCTAGAGCC AGTCTCTGCG TCCAGAGCCG GCGGGGAGCC AAGCTCCTCC AACCACAAGG 540
 GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
 AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
 ACAAACACGC TGACACTGAC TAAGGAACCTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
 CCTTCTTAGT GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
 TCACTCAGAT GTCTCGAAT TCCACCACGG GGGTCAACCT GGGGGGTTAG GGACCTATT 840
 TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCACACT 900
 10 CCAAGACGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT 960
 AATAAAAGAA TCITTAACCT TAAAAAATAA AAAAAAAA

Seq ID NO: 631 Protein sequence
Protein Accession #: NP_057723.1

15 1 11 21 31 41 51
 MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SNSADLDKCM DCASCRARPH 60
 SDFCLGCAA PPAPFRLLWP ILGALSLTF VLGLLSGLV WRRCRREKFP TPIETGTGE 120
 GCPAVALIQ

Seq ID NO: 632 DNA sequence
Nucleic Acid Accession #: NM_003816.1
Coding sequence: 79..2538

25 1 11 21 31 41 51
 CGGCAGGGTT GGAAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGGCTTTTC CCTCGGGGAC CCTTCGTGTC 120
 30 CCGTGGTGGC TGTTGCTTGG CCTGGTGGGC CCACTCCTCG GTGCGGCGCG GCCAGGCTTT 180
 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTGGAGATT AACTAGAGAA 240
 AGAAGAGAAG CCGCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAGAGCATA TTATTCACTT GGAAGGGAAC AAAGACCTTT TGCGTGAAGA TTTTGTGGTT 360
 TATACTTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420
 35 CATTATCGGG GCTATGTGGA GGGAGTTTAT AATTTCATCCA TTGCTCTTAG CGACTGTTTT 480
 GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC 540
 AGCTCTCATT TTGAGCACAT CATTATOGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG 720
 40 GAGCTGTCCA TTGTCGTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAAG AGATGATTCT CCTGGCAATC TACTTGGATA GTATGTATAT TATGTTAAAT 840
 ATTGCAATGT TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGTGCTG GTGATGTGCT GGGGAACCTC GTGCAGTGGC GGGAAAGATT TCTTATCACA 960
 CGTCCGAGAC ATGACAGTGC ACAGCTAGTT CTAAGAAAG GTTTTGTGTG AACTGCAGGA 1020
 45 ATGGCATTGT TGGGAACAGT GTGTTCAAGG AGCCACGCG GCGGGATTAA TGTGTTTGA 1080
 CAAATCACTG TGGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAATCTTGA 1140
 ATGAATCAGC ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTA 1200
 GGAGCATCG GTTCCAGAAA CTTTAGCAGT TGCAGTGCA AGGACTTTGA GAAGTTAACT 1260
 TTAATAAAG GAGGAAACTG CCTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320
 50 CCGCTCTGTG GTAATAAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380
 GAATGTGAAT TGGACCTCTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCATATG GTGACTGTTG TAAAGACTGT CCGTTCCTTC CAGGAGGTAC TTTATGCCGA 1500
 GGAAAAACA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTGAG 1560
 CCAGATGTTT TTATTCCAG TGGATATCCT TGCCAGAATA ACAAAGCCTA TTGTACAAC 1620
 55 GGCATGTGCC AGTATTATGA TGCTCAATGT CAACTCATCT TTGGCTCAA AGCCAGGCT 1680
 GCCCCAAAG CTGTGTTTCT TGAAGTGAAT TCTAAAGGTG ACAGATTGG CAATTGTGGT 1740
 TTCTCTGGCA ATGAATACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAATG TACAAGAGAT ACCTGTATT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 60 AGTCAGAGCA CCAAATGTTG GGGTGTGGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1980
 GGGATGGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAAGA TCTGTAGAAA CTTCAGATGT 2040
 GTAGATGCTT CTGTCTGAA TTATGACTGT GATGTTTCTA AAAAGTGTCA TGGACATGGG 2100
 GTATGTAATA GCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCCC AAATTGTGAG 2160
 ACTAAGAGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAT GAATCTGCA 2220
 65 TTGAGGGAAG GACTCTCTGT CTCTCTCTC CTAATTGTTT CCGCTTATTGT CTGTGCTATT 2280
 TTTATCTTCA TCAAGAGGGA TCACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACAA 2340
 ACATATGAGT TACATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTCTCT 2400
 CGACATGTTT CTCCAGTGAC ACCTCCAGCA GAAGTTCCTA TATATGCAA CAGATTGCA 2460
 GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCTAT CAAGGCCACC TCCACCACAA 2520
 70 CCGAAAGTAT CATCTCAGGG AAACCTTAAT CCTGCCGTC CTGCTCCTGC ACCTCCTTTA 2580
 TATAGTTCCC TCACTTGATT TTTTAACTT TCTTTTGTCA AATGTCTTCA GGGAACTGAG 2640
 CTAATACITT TTTTCTTCT TGATGTTTC TTGAAAGGCC TTTCTGTTGC AACTATGAAT 2700
 GAAACAAAA CACCACAAA CAGACTTCAC TAACACAGAA AAACAGAAAC TGAGTGTGAG 2760
 AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGAAT TACAATAACA TTTCGGTTTC 2820
 75 CATCAITGAA TAAGTCTTAT TCAGTCATCG GTGAGGTTAA TGCACATAAT ATGGATTITT 2880
 TGAACATGTT ATTGCACTGA TTCTCAAAT AACTGTATTG GTGTAAGATT TTGTCTATT 2940
 AGTGTTTAAG TGTATTCTG AATTTCTAC CTTAGTTATC ATTAAGTAG TTCTCATTTG 3000
 AACATGTGAT AATCTAATAC CTGTGAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3060
 TTTTTCATCA TGCACGAAT AATAATCAT ATACTCTAGA ATCTTGTCTG TCACTCACTA 3120
 80 CATGAATAG CAATATTGTT CTTCAAAGA ATGCACAGA ACCACAATA AGATGTCATA 3180
 TTAATTTGAA AGTACAAAAT ATACTAAAAG AGTGTGTGTG TATTACGCA GTTACTGCT 3240
 TCCATTTTTA TGACCTTTCA ACTATAGGTA ATAACTCTTA GAGAAATTA TTTAATATTA 3300
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTGTT CACAATAGCA CTATTTTAAA 3360
 TAAATTATAA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAATAT GTTGATTCT 3420
 85 GGCATAATAA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3480
 CTTGAGAAAT TCAATAGCAC TTTAAAATCT GAACCTTCAA AGCTTGTCTT TAAATCATTT 3540
 AGAATGTTTA CATTTCTAAC GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3600
 CATAGAAAT AGGCTGAGGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAAG 3660
 TTACTGTGAT ATCTATGAGT TATCATCTTA GCTGTGTTAA AAATGAATTT TTACTATGGC

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAAT TTTTCATAAC CTTTCATAAT 3720
 AAAGTTTAAT AATAGGTTTA TTAACGAAAT TTCATTAGTT TTTTAAAGT GTTTTGGTT 3780
 TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAAAACTT GAAATCTCA 3840
 AAAAAAAAA AAAAAAAAA AAAAA

5

Seq ID NO: 633 Protein sequence
 Protein Accession #: NP_003807.1

10 1 11 21 31 41 51
 | | | | | |
 MGSARFPSPG TLRVRMLLL GLVGPVLGAA RPPGQQTSHL SSYEIITPWR LTRERREAPR 60
 FYSKQVSYVI QABGKEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNECHYRGVY 120
 EGVHNSIAL SDCFLRLGLL HLENASYGIE PLQNSSHFEE IYRMDVYK EPLKCGVSNK 180
 DIEKETAKDE EEEPPSMTQL LRRRAVLPO TRYVELPIVV DKERYDMQGR NQTAVREEMI 240
 15 LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 AQLVLKKGFG GTAGMAFVGT VCSRSAGGI NVFQGITVET PASIVAHLEL HNLGMNHDG 360
 RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTILNKGKN CLLNIPKPE AYSAPOGKNK 420
 LVDAGREBCD GTPKECELOP CCEGSTCKLK SPAECAYGDC CKDCRPLPGG TLCRGKTSEC 480
 DVPEYCNSSG QFCQPDVFIQ NGYPCQNNKA YCYNGMCQYY DAQQQVIFGS KAKAAPKDCP 540
 20 IEVNSKGDNP GNCQPSGNEY KKCATGNALC GKLCENVQE IPVFGIVPAI IQTPSRGTCK 600
 WGVDFQLGSD VPDPMVNBG TKCGAGKICR NFQCVDAVL NYDCOVQKCC HGHGVCSNENK 660
 NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
 DQLWRSYFRK XRSQTVESDG KNQANPSRQP GSVPRHVSFV TPPREVPIYA NRPVPTTYAA 780
 KQPQKFPSPR PPKQPKVSSQ GNLIAPAPAP APFLYSSLT

25

Seq ID NO: 634 DNA sequence
 Nucleic Acid Accession #: NM_002091.1
 Coding sequence: 56..503

30 1 11 21 31 41 51
 | | | | | |
 AGTCTCTGCT CTTCCAGCC TCTCCGGCG GCTCCAAGG CTTCCCGTCG GGAACATGCG 60
 CGGCAGTGAG CTCGCCGCTG TCCTGCTGGC GCTGGTCTTC TGCTAGCGC CCGGGGGCG 120
 AGCGGTCCCG CTGCGTGGGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
 35 CCACTGGGGG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
 TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
 GAATTTGCTG GATCTCATAG AAGCAAAGGA GAACAGAAAC CACCAAGCCAC CTCACCCAA 360
 GGCTTGGGCG AACTCAGCAGC CTTCTGGGGA TTCAGAGGAT AGCAGCAACT TCAAAGATGT 420
 AGGTTCACAA GGCAGAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
 40 CCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACACAAACCC 540
 TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAGAGAT TCCTTGTGCA 600
 AAATATTGTA CTATCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTC CAAGCAGCAT 660
 CTTCTGGTTT AAACCTGTGT GCTGTGAACA ATTTGCGAAA AGAGTCTTCC AATTAATGCT 720
 TTTTATATC TAGCTACTCT GTTGGTTAGA TTCAAGGCC CGAGCTGTTA CCATTACAA 780
 TAAAAGCTTA AACACAT

45

Seq ID NO: 635 Protein sequence
 Protein Accession #: NP_002082.1

50 1 11 21 31 41 51
 | | | | | |
 MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTKMYPR GNHNAVGHLM GKSTGESS 60
 VBERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPQP PKALGNQQPS WDSDDSNFK 120
 DVGSKGKVR LSAPGQREG RNPQLNQQ

55

Seq ID NO: 636 DNA sequence
 Nucleic Acid Accession #: NM_016522.1
 Coding sequence: 265..1299

60 1 11 21 31 41 51
 | | | | | |
 GCGGAAGCAG CGAGGAGGGA GCCCCCTTTG GCCGTCTCTC GTGGAACCGG TTTTCCGAGG 60
 CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGGCG 120
 TTTTCTCTCT CCGCGCGCTC CCGGTCCGCG CGGGTTCAAC GCTCAGTCCC CGCGCTCGCT 180
 65 CCGCACCCCA CCCACTTCTT GTGCTCGCCC GGGGGGGGTG TGCCGTGCGG CTGCGGAGT 240
 TCGGGGAAGT TGTGGCTGTC GAGAAATGGG GTCTGTGGGT ACCTGTCTCT GCCCTGGAAG 300
 TGCCCTGCTG TCGTGTCTCT CAGGCTGCTG TTCCTGTATC CCACAGGAGT GCCCGTGCSC 360
 AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACTGTA CGGTCCGCGA GGGGAGAGGC 420
 70 GCCACCTCTA GGTGCACTAT TGACAAACCG GTCAACCGGG TGGCTGGCT AAACCGCAGC 480
 ACCATCTCTT ATGCTGGGAA TGACAAAGTG TGCTGGATC CTGCGTGGT CTTCTGAGC 540
 AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACTGG ATGTGTATGA CGAGGGCCCT 600
 TACACCTGCT CGGTGCAGAC AGACAAACC CCAAGACCT CTAGGGTCCA CCTCATTTGT 660
 CAAGTATCTC CCAAAATTGT AGAGATTCTC TCAGATATCT CCATTAAATG AGGGAACAAT 720
 ATTAGCTCA CCGTCACTAGC AACTGGTAGA CCAGAGCTTA CGGTACTTGT GAGACACATC 780
 75 TCTCCCAAAG CGGTGGCTTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
 CGGGAACAGT CAGGGGACTA CGAGTGCAGT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA 900
 CGGAGAGTAA AGGTACCGT GAACATATCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960
 GTCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGTG ACAGAGATGA CAAAGACTG ATTTGAAGAA AGAAAGGGGT GAAAGTGGAA 1080
 80 AACAGACTT TCTCTCAA AACTCATCTT TCAATGTCT CTGAAATGA CTATGGGAAC 1140
 TACACTTGGG TGGCTCCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CCAGGCGCGG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
 TCGCTCTCT TGGTCTTGA CCGCTTCTC AAATTTTGT GTGAGTGCCA CTTCCCAACC 1320
 CGGGAAGGCG TGGCGCCACC ACCACCAACA ACACACAGC AATGGCAACA CCGACAGCAA 1380
 85 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATTGGAG AGAAATTGTA 1440
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAATTG 1500
 CCTTGCAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560

COOGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CAOGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTCAAATC AGTCCATAGA GACGAACAGA ATGAGACCTT COGGCCCAAG CGTGGCGCTT 1740
 COGGCCCAAG CGTGGCGCTG CGGCACTTT GTTAGACTGT GCCACCACGG CGTGTGTGT 1800
 5 GAAACGTGAA ATAAAAAGAG CAAAAA AAAA

Seq ID NO: 637 Protein sequence
 Protein Accession #: NP_057606.1

10 1 11 21 31 41 51
 MGVCGYLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTRVAMLN RSTILYAGND KWCLDPRVVL LSNITQYYSI EIQNVVDVDE GPYTCSVQTD 120
 15 NHPKTSRVHL IVQVSPKIVE ISSDISINBG NNISLTCTAT GRPEPTVTWR HISPKAVGFV 180
 SEDEYLEIQG ITRBQSGDYE CSASNDVAAP VVRVKVTN YPPYISEAKG TGVVPGQKGT 240
 LQCSASAVPS AEPQWKDDK RLIEGKGVK VENRPLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FPGVAVSEVS NGTSRRAGCV WLLPLLVLHL LLKF

20 Seq ID NO: 638 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

25 1 11 21 31 41 51
 GATTTGCTCT GCCAGCAGCT GTGGGTGCGG CGCTGACAC CGAGTCTCTAG CTAGGGGCTC 60
 ACAGAATAGC CGCTCCCTCC CTCCCCTTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGGCGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCAGTCGCA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCAGATT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAAAGAAT 300
 30 GGAAATCTTC TCAGGCCCTT CCACTAACCC TGAAGAAAGAT ATATTGTGG TGCGGGAAAA 360
 TGGGACGAGC TGCTCATGCG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TAAGTAGATC TGATCAGAGA ACAGGCCGAT ATCGCAATGA CCGGGGGAGC 480
 TGAGGTGAAG GSCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGAGCTGA 600
 35 GGGAGCTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCACTT 660
 CAAAGACGCA GTCACTGTGG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCTTGGT 720
 CACCCCGCTT GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCTCTAG 780
 TGATCCGAGC AAGACGCTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTGACAT 840
 40 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACG AGGGGGAGAC TTTTGGGGCT CATCTTGGGC CTGCTCATCA TGGTAACACT 960
 CGGATTTTAC CAGTCCACG ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
 ATCCAGTAT AAGCAGTAGC GTAGAGGCC GTTAGGCAGG CACCCCTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTCCATC TTGTACACGA GATACACAA 1140
 45 CATAGCTACA ATCAAAACAG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
 ATGCTGGGGA GGAGGGGAGG AGGCTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380
 TTGAAAACAT GCTTCTTTGA GGAGGAAACC CCTTAGGTT CAGAAGAATA TGGGTGCTT 1440
 50 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500
 TCATGCTCCC TTGAGCAAGA CCCCAGAAAG TGATTATGCT TTCTGGCTGG CATTCTGCT 1560
 GTTTAGTATG TGCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAATAT GCAGAGTTGT TTGAGCTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGAGCTTG AAGATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AACACACTA 1740
 55 TTCTCTGGC

Seq ID NO: 639 Protein sequence
 Protein Accession #: NP_036393.1

60 1 11 21 31 41 51
 MDLQGRGVPS IDRLRVLLML PHTMAQIMAE QEVENLSGLS TNPEKDIPVV RENGTTCLMA 60
 EFAAKFIPVY DVWASNYVDL ITBQADIALT RGAEVKGRGQ HSQSELQVFW VDRAYALKML 120
 FVKESHNMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSEHLS ALVTPAGKSY 180
 65 EQQAQQTISL ASSDPQRTVT MILSAVHIQF FDIISDFVPS EERKCPVDER BQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM

Seq ID NO: 640 DNA sequence
 Nucleic Acid Accession #: NM_002993.1
 Coding sequence: 64..408

70 1 11 21 31 41 51
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 75 GCGCTGCTCG CGCTGCTGCT CCGCTGAGC CCGCGGGGCG CCCTCGCCAG CGCTGGTCTT 180
 GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTATTAC GCGTTACGCT GAGAGTAAC 240
 CCCAAACGCA TTGGTAAACT GCAGGTGTTC CCGCGAGGCC GCGAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCGTGAAGAA GGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTCTTA 360
 80 AAGAAAGTCA TCCAGAAAT TTTGGACAGT GGAACCAAGA AAAACTGAGT AACAAAAAAG 420
 ACCATGCATC ATAAATATGC CAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
 CAGTAAAGAT AAGAAGGAAG GGTGTGTTTT TTTCCATTTT CTACATGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAGGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
 85 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCITGG 660
 CAATTGAACA TATTGTGAGC AAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATT CTATCATACA TTCCTTAAAG TCTTACGAA AAGGCTGTG 780
 ATTTCTATAG GAAATAATGT TTTATTAGTG TGCTGTGAG GAGGTATCC TGTGTGTCTT 840
 ACTCACTCTT CTCATAAAT AGGAATATT TTAGTCTGT TTTCTTGGG AATATGTTAC 900

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TCITTTACCC AGGATGCTAT TTAAGTTGTA CTGTATTAGA AACTGGGGTG TGTCATACCG 960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAAGG 1020
CTAATATATT CTCTTCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
CATGATTAC TCATTAAACT TTGATTITGT ATGCTATTIT TTCACTATAG GATGACTATA 1140
ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTC 1200
TGATTGCTAA TTTACATAGA AATGATTCT CTGGTTTTT TAAATAAAG CAAATTAAC 1260
AATGATCTGT GCTCTGCAA GTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT 1320
CAITTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
TTTAAAGGTT TTGAACATT TTGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAIT 1500
TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA

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Seq ID NO: 641 Protein sequence

Protein Accession #: NP_002984.1

1 11 21 31 41 51
MSLPSSRAAR VPGPSGLCA LLALLLLLT PGLASAGPV SAVLTELRC TLRVTLRVNP 60
RTIGKLQVFP AGPQCKVEV VASLKNKQV CLDPEAPFLK KVIQKILDSG NKKM

Seq ID NO: 642 DNA sequence

Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

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TCTGCGCGCG GCGCGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCGG CCCTTGGCTG 180
AGACTGGGCG TCCTCGCGCG TTCCGGGGGT CAGTGCCCGG AGGTGAGGCG CGGGGGGGCG 240
TGCAAGAGCT GCGCGGGGCG CTGGGCGATC TGCTGGAGGC CGAACGTCAG GAGCGGGGCG 300
GGCGCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGGCT CCTGGCGCAG CTGCTGCGCG 360
TCTGGGGGCG CCCCCGCAAC TCTGATCCGG CTCTGGGCTT GGACGACGAC CCGGACGCGC 420
CTGCAGCGCA GCTCTGCTCG GCTCTGTCTC GCGCGCGGCT TGACCTGTCC GCCCTAGCAG 480
CCGAGCTTGT CCGCGCGGCG GTCCCGCGCG CGGCGCTCGG ACCCGGCGCC CGGCTCTACG 540
ACGAGCGGCG CGCGGGCGCG GATGCTGAGG AGGCGAGCGA CGAGACACCC GACGTGGACC 600
CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGGCGG AAGCGCGGAC TCGAGGGGGG 660
TGGCAGCCCC GCGCGGCTCT CGCGGTGCGG CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
CTGAGGGCGT GCTGGGGGCG CTGCTGGGTG TGAAACGCTT AGAGACCCCG GCGCGCCAGG 780
TGCGTGCAGC CGCGCTCTTG CCAACCTGAG CACTGCCCGG ATCCCGTGCA CCTGGGAC 840
CAGAAGTGCC CCGCCATCC CGCCACAGG ACTTCTCCCC GCGAGCAGT CCAGAGCAAC 900
TTACCCCGCG CAGCCAGCCC TCTCACCGGA GGATCCCTAC CCGCTGGCCC ACAATAACAT 960
GATCTGAGC

Seq ID NO: 643 Protein sequence

Protein Accession #: NP_037403.1

1 11 21 31 41 51
MAGSPLLWGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
RSVPRGEAAG AVQELARALA HLLEAERQER ARAEAQEAED QARVLAQLL RVWGAPRNSD 120
PALGLDDDPD APAQLARAL LRRLDPAAL AAQLVPAPVP AAALRPRPPV YDDGPAQFPA 180
EAGDETPDV DPFLRLYLQ RILAGSADSE GVAAPRRLRR AADHDVGSSE PPEGVLGALL 240
RVKRLTPAP QVPARLLFP

Seq ID NO: 644 DNA sequence

Nucleic Acid Accession #: NM_002214

Coding sequence: 681..2990

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CTGCCGACTT GTCTTTGCCC GCTGCTCGC AGACGGGGCT GCAAGAGTGC AACTAATGGT 120
GTTGGCCTCC CTGCCCACTT GTGGAAGCAA CTGCGCTGAT TGATGGGCCA CAGACTTTTT 180
TCCCTCGAC CTGCGCGGCG TACCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT 240
TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTGG 300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCCTTTCTT 360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGCAG GCGGGGCCCT 420
TGGCGTCCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCGGTGCC GAGCGGGGAG 480
GGCGTAGGG GCGCTGAGAT GCGGAGCGGT GCGCGGGCCC GCTTACCTGC ACCGCTTGCT 540
CGAGCGCGCG GGTCCGCTCT GCTAGGCTTG CGGAAAAGCT CTTAGCGACA CTGCGCGCGG 600
GGCCCGGAGG TCGCCCGGGA GCGCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGGCG 660
GGGGCGGGCT GTTTTGCAIT ATGTGCGGCT CGGCGCTGGC TTTTITTACC GCTGCATTGT 720
TCTGCTGCA AAACGACCGG CGAGGTCCCG CCTCGTCTCT CTGGGCGAGC TGGGTGTTTT 780
CACTGTCTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840
CCTGTGCCAG GTGCTTGGG CTGGGTCCAG AATGTGGATG GTGTGTCAA GAGGATTICA 900
TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAGGCTT 960
GCTCAGTTGA TTCAATAGAA TACCATCTG TGCAATGTTT AATACCCACT GAAATGAATA 1020
TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCGGAAGCTA 1080
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ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCGTGGGA AACGATTAT 1200
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AAACGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
ACAATTAGA CTGCATGCCCT CCCCATGGAT ACATCCATGT GCTGTCTTGG ACAGAGAACA 1380
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AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560

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GCAAAITGGC AGGCATATG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACCAAGTCT 1620
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CAGGCATGGA AGGATGACGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAAACG 1980
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TCAATTCAAA GGGCCAAAGT TGCAAGTGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
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TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACAAC GCATTATGT GACCAAACTT 2700
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TTAAACACTT AATGGGAAAC TGGAAATGTT AATAATGTCT CCTAAAGATT ATAATTTTAA 3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTGTG ACACCTGAAAC 3120
GAAGACTGAC AAGTATCTCT ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
AAAATGTGTC TTAATCTGTT TTGAGACTAG TGTGTTGTA GCACCTTACT GTAATATATA 3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
TACCTGTTAT CCCTAGCTTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360
CACTACAGGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAAATA ATCTGGCAAG 3420
TATATTCTAA GGTGTGCCAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
ATGAATAAAT GATTCGTGTT TCACCTCTTC AAGAGGTGAA CAGATACAA CTTAATCTTA 3540
AAAGATTATT GCTTTTAAAA GTGTGTAGTT TTAGCATGAT GTGTTTATGG TTTGCTTATT 3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTCT 3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
TACTGCCATA AAAAATAAT AATACATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780
GAATGTTAA

Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

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1 11 21 31 41 51
MCGSALAFPT AAFVCLQND RGPASFLMAA WVFLVLGLG QGEDNRCASS NAASCARCLA 60
LGPEOCWCVQ EDPISGGSR ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
GEVSIQLRPG AEANFRLKVH PLKKYPVDLY YLVDVSASMH NNIIEKLSVG NDLSRKMAPP 180
SRDFRLGPGS YVDKTVSPYI SIHPIRIHQ CSDYNLDOMP PHGYIHVLSL TENITEPEKA 240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300
VPNDGMCHLK NNVYVSTTM EHPSLGQLSE KLIDNNINVI FAVQGRQFHW YKDLLPLLP 360
TIAGEIESKA ANLNLNVVEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPGMEGRK 420
NVTSDNDELV NVTVTMKKCD VTGGKYNVLI KPIGFNETAK IHIEHNCSCQ CEDNRGPKFK 480
CVDETFLDK CFQCDENKCH FDEQDFSSBS CKSHKQDQVC SGRGVCVCGK CSCHKIKLGK 540
VYGYKCEKDD FSCPYHHGML CAGHGECEAG RCQCPGSGWB DRQCPGSAAS QHCVNSKQV 600
CSGRGTCVCG RCBCCTDPRS GRPCEHCPTC YTACKENMWC MQCLPHNLNS QAILDQCKTS 660
CALMEQOHVY DQTSCECFSS SYLRIFFIIF IVTFILGLLK VLIIRQVILQ WNSNKRKSSS 720
DYRVSAKSKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

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1 11 21 31 41 51
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ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC 180
AACCAGAGGG ACTGGTTGAG TTTGTTGCTC AAACAGAGAG AAAACAGTGT TCCGCTAAGT 240
GATGCTCTTT TAAATAAATT GATTGGTGGT TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300
GATAAATATG GCCAAATGGA GAGTTTGTCT AGAATTCAGT TGAGATTTCG TGAATTAATA 360
GCTATTCAAG AGCCAGATGA TGCAAGTGAC TACTTTCAAA TGGCCAGAGC AAACAGCAAG 420
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AAGAATTTAT CAGCATCTAC GGTATTAAC TCCCAAGAAAT CATTTTCCGG TTCACTTGGG 660
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	GATTACATGA	GCTGTTTTAG	AACTCCAGTT	GTAAGAATG	ACTTTCCACC	TGCTTGTCAG	1440
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	ACTCCACTTC	AAAATTTACA	GGTTTTAGCA	TCTTCTTCAG	CAAATGAATG	CATTTCGGTT	1560
5	AAAGGAAGAA	TTTATTCAT	TTTAAAGCAG	ATAGGAAGTG	GAGGTTCAAG	CAAGGTATTT	1620
	CAGGTGTTAA	ATGAAAAGAA	ACAGATATAT	GCTATAAAAT	ATGTGAACCT	AGAAGAAGCA	1680
	GATAAACCAA	CTCTTGATAG	TTACCGGAAC	GAATAGCTT	ATTGAATAA	ACTACAACAA	1740
	CACAGTGATA	AGATCATCCG	ACTTTATGAT	TATGAAATCA	CGGACCACTA	CATCTACATG	1800
	GTAATGGAGT	GTGGAAATAT	TGATCTTAAT	AGTGGGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
	CCATGGGAAC	GCAAGAGTTA	CTGGAAAAAT	ATGTTAGAGG	CAGTTCAAC	AATCCATCAA	1920
10	CATGGCATTG	TTACAGTGTA	TCTTAAACCA	GCTAACTTTC	TGATAGTTGA	TGGAATGCTA	1980
	AAGCTAATTG	ATTTTGGGAT	TGCAAAACCA	ATGCAACCA	ATACAAACAG	TGTTGTTAAA	2040
	GATTCTCAGG	TTGGCAGAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGTCTTCC	2100
	TCCAGAGAGA	ATGGGAAATC	TAAAGTCAAG	ATAAGCCCCA	AAAGTGATGT	TTGTCTCTTA	2160
	GGATGTATTT	TGTACTATAT	GACTTACGGG	AAAAACCAT	TTACGACAGT	AATTAATCAG	2220
15	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTCC	CGATAITCCA	2280
	GAGAAAGATG	TTCAAGATGT	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
	TCCATTCTCTG	AGCTCCTGGC	TCATCCCTAT	GTTCAAATTC	AAACTCATCC	AGTTAAACCA	2400
	ATGGCCAAGG	GAACCACTGA	AGAAATGAAA	TATGTTCTGG	GCCAACTTGT	TGGTCTGAAT	2460
20	TCTCCTAACT	CCATTTTGAA	AGCTGCTAAA	ACTTTATATG	AACACTATAG	TGGTGGTGAA	2520
	AGTCATAAAT	CTTCATCTTC	CAAGACTTTT	GAAAAAATAA	GGGGAAAAAA	ATGA	

Seq ID NO: 647 Protein sequence
Protein Accession #: NP_003309.1

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	MESEDLSEGR	LTIDSIMNKV	RDINKKFKNS	DLTDELSLNK	ISADTTDMSG	TVNQIMMMAN	60
	NPEDWLSLLL	KLEKNSVPLS	DALLNKLIGR	YSQAIEALPP	DRYQWNEFPA	RIQVRPAELK	120
	AIQEPDARD	YFQMARANCK	KPAFVHISPA	QFELSQGNVK	KSKQLLQKAV	ERGAVPLEML	180
30	EIALRNLIQ	KKQLLSEEEK	NKLSASTVL	AQESFSGSLG	HLQNRNNSCD	SRGQTTKARF	240
	LYGNNMPPQD	ASIGYRNSLR	QTNKTKQSCP	FGRVFVNLN	SPDCDVKTDD	SVVPCPMKRQ	300
	TSRSECRDLV	VPGSKPSGMD	SCELRNLKSV	QNSHFKEPLV	SDEKSSSELII	TDSITLKNKT	360
	ESSLLAKLEE	TKEYQEPFVP	BSNQKQWQSK	RKSECIQNP	AASSNHWQIP	ELARKVNTBQ	420
	KHTTFBQFVP	SVSKQSPPTS	TSKWDFPKSI	CKTPSSNTLD	DYMSCPRTVP	VKNDFPPACQ	480
35	LSTPYQGPAC	FQOQHQIILA	TPLQNLQVLA	SSSANECISV	KGRYISILKQ	IGSGGSSSKVF	540
	QVLNEKKQIY	AIKYVNLLEE	DNQTLDSYRN	ELAVLNKLOQ	HSDKIIRLYD	YEITDQVIYM	600
	VMEGCRIDL	SWLKKKSID	PWERKSYWKN	MLEAVHTIQH	HGIVHSDLPK	ANFLIVDGLM	660
	KLIDFGIANQ	MQPDTSVSVK	DSQVGTVNYM	PPEAIKDMSS	SRENGKSKSK	ISPKSDVWSL	720
	GCLLYMYTIG	KTPFQIQIDQ	ISKLHAIIDP	NHEIEFPDIP	ERDLQDVLC	CLKRDPRQRI	780
40	SIPELLAHFY	VQIQTHPVNQ	MAKGTTEEMK	VVLGQLVGLN	SPNSILKAAK	TLVEHYSGGE	840
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Seq ID NO: 648 DNA sequence
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Coding sequence: 241..1902

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	CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGCGCGCTT	AGCTGCTACG	180
	GGGTCCGGCC	GCGCCCTTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
	ATGCTCTGCG	CTGCTGCTGC	TGCGTCTCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
	GGGAACGGGG	CCAGTGCAAG	GCATCAGCGG	TGTTTAGCAT	CGGCACGCTA	GCCTGGGGTC	360
55	TGTCACTATG	GAATCAAACT	GGCCTGCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
	TGTGAAGCTA	CATGCGAAC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
	AGATGCTTTC	CAGGATACAC	CGGGAARACC	TGCAGTCAAG	ATGTGAATGA	GTGTGAATG	540
	AAACCCCGGC	TAGCCCAACA	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
	CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
60	ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
	TCAGGACTCC	GCTTGCCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCCTCT	780
	GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGGGAAG	CTACTACTGC	840
	AAATGTCACT	TTGGTTTCTG	ACTGCAATAT	ATCAGTGGAG	GATATGACTG	TATAGATATA	900
	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
65	GGGTCTCTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
	ATCCTGAAA	ATTCTGTGAA	GGAAGTCTCT	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
	AAGAAGTTGC	TGTCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAATTTAA	AAATGTTACC	1140
	CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
	ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAATGAAGAA	1260
70	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
	AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCCTGATT	1380
	CTGGTCCAAA	GGAAAGCGCT	AACTTCCAAA	CTGGAACATA	AAGATTAAAA	TATCTCGGTT	1440
	GACTGCGAGT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
	TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGSCA	1560
75	GTCACAAAGA	AAGACATTGG	CGGATTGAAA	CTTCTCTTAC	CTGACCTGCA	ACCCCAAAGC	1620
	AACTTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCCCGAGACA	AACTCGGGAA	ACTTCGAGTG	1680
	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCAGAGTGA	GGATGAAAAG	1740
	TGGAAGACAG	GGAATAATCA	GTTGTATCAA	GGAACGTGAT	CTACCAAAGG	CATCATTTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
80	TCAGGCTTAT	GTCCGATTGG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
	TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCAAT	1980
	TTAGAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCCT	2040
	TCTTGTATAA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCAGTGTATC	TTCTCAGTCA	2100
	TTTCTGAATC	TTTCCCAATT	ATATTATAAA	ATATGGAAT	GTCACTTTAT	CTCCCTCTCT	2160
85	CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACT	TTCTAGAAAA	2220
	TAGAAAAAAA	AGCACAGAGA	AATGTTTAAC	TGTTTGACTC	TTATGATACT	TCTTGGAAAC	2280
	TATGACATCA	AAGATAGACT	TTTGCCCTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340

TGTATATTTA AATTCCTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

5

1	11	21	31	41	51	
MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	VGWRNRSKGV	60
CEATCEPGCK	PGCEVGNPKC	RCPPGYTGKT	CSQDVNECGM	KPRPCQHRV	NTHGSYKCF	120
LSGMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPQCLCPS	SGLRLAFNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYVC	KCHIGFELQY	ISGRYDCIDI	NECTMDSETC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
PEPTRTPFPK	VNLQPFNYEE	IVSRGGNSHG	GKKGNEEKMK	EGLEDEKRES	KALKNDIEER	360
SLRGDVFFPK	VNEAGEFGLI	LVQRKALTSK	LEHKDLNISV	DCSPNHGICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPALA	GHKKIDIGRLK	LLLPDLQPQS	NFCLLPDYRL	AGDKVKGKLRV	480
FVKNNSNNALA	WKTTSSEDEK	WTKGIQLLYQ	GTDATKSIIF	EAERGKKGKT	EIAVDGVLIV	540
SGLCPSDLSL	VDD					

20

Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

25

1	11	21	31	41	51	
GCAGCTCCAG	TCCCGGAOCG	AACCCCGGAG	CCGTCTCAGG	TCCCTGGGGG	GAAACGGTGGG	60
TTAGACGGGG	ACGGGAAGGG	ACAGCGGCCCT	TCCAGCGCCC	CCCGAGTAAT	TGACCCAGGA	120
CTCATTTTCA	GGAAGCCTGT	AAAATGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
ATCAGGAATT	TGAGGAAAAAT	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
CTCCTAAGAG	GGCAGACGCT	CTTCACCTGT	GAAACCAATTA	CTGTTCOCAG	ATGTATGAAA	360
ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
GCGGTGGAAA	TGGAGCATTT	TCCTCCTCTC	GCAAAATCTGG	AATGTTCAACC	AAACATTGAA	480
ACTTCTCTCT	GCAAGCATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GGTTCACCTT	540
TGTGCTAAAC	TGTGTGAGAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACTTTGGGG	600
ATCCGATGGC	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTCTCT	660
GTAACTTTTG	ATCCACACAC	AGAAATTTCT	GGTCTCTAGA	AGAAAACAGA	ACAAGTCCAA	720
AGAGACATTG	GATTTTGGTG	TCCAAGGCAT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
TTTCTGGGAA	TGACACAGTG	TGCGCCTCCA	TGCCCCAACA	TGTATTTTAA	AAGTGATGAG	840
CTAGAGTTTG	CAAAAAGTTT	TATTGGAACA	GTTTCAATAT	TTTGTCTTTG	TGCAACTCTG	900
TTCACTATCC	TTACTTTTTT	AATTGATGTT	AGAAGATTCA	GATACCCAGA	GAGACCAATT	960
ATATATTATT	CTGTCTGTGA	CAGCAATTGA	TCTCTTATGT	ACTTCAITGG	ATTTTGTGCT	1020
GGCGATAGCA	CAGCCTGCAG	TAAGGCAGAT	GAGAAGCTAG	AACCTTGGTGA	CACGTGTGTC	1080
CTAGGCTCTC	AAATAAAGGC	TTGCACCGTT	TTGTTCATGC	TTTTGTATTT	TTTCACAATG	1140
GCTGGCAATG	TGTGGTGGGT	GATTCTTACC	ATTACTTGGT	TCTTAGCTGC	AGGAAGAGAA	1200
TGGAGTTTGT	AAGGCATCGA	GCAAAAAGCA	GTGTGGTTTC	ATGCTGTTGC	ATGGGGGAACA	1260
CCAGGTTTCC	TGACTGTTAT	GCCTCTTGCT	CTGAAACAAAG	TTGAAGGAGA	CAACATTAGT	1320
GGAGTTTGTCT	TTGTGGCCCT	TTATGACCTG	GATGCTTCTC	GCTACTTTGT	ACTCTTGCCA	1380
CTGTGCTTTT	GTGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTTAAAT	1440
CATGTTGCAAC	AAGTCATACA	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAAATTTATG	1500
ATTGCAATTG	GAGTCTTCAG	CGGCTTGAT	CTTGTGCCAT	TAGTGACACT	TCTCGGATGT	1560
TACGTCTATG	AGCAAGTGAA	CAGGATTACC	TGGGAGATAA	CTTGGGTCTC	TGATCAITGT	1620
CGTCAGTACC	ATATCCCATG	TCCTTATCAG	GCAAAAGCAA	AAGCTCGACC	AGAATTGGCT	1680
TTATTTATGA	TAAATACCTT	GATGACATTA	ATTGTTGGCA	TCTCTGCTGT	CTTCTGGGTT	1740
GGAAAGCAAA	AGAGATGCAC	AGAATGGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
CCAATCAGTG	AAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCACAAT	1860
TCTAAAGTTA	AACACAAAAA	GAAGCACTAT	AAACCAAGTT	CACACAAGCT	GAAGGTCAIT	1920
TTCAAATCCA	TGGGAACCGA	CACAGGAGCT	ACAGCAAATC	ATGGCACTTC	TGCAGTAGCA	1980
ATTACTAGCC	ATGATTAACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAAC	CTCACCAGAA	2040
ACATCAATGA	GAGAGGTGAA	AGCGGACGGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
TGTGGTGAAC	CTGCGCTGCC	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTGCGC	2160
GGGAAGGGCC	AGCGACGCGA	TGTATCTGAA	AGTGGGCGGA	GTGAAGGAAG	GATTAGTCCA	2220
AAGAGTGATA	TTACTGACAC	TGGCCTGGCA	CAGAGCAACA	ATTTCAGAGT	CCCCAGTTCT	2280
TCAGAACCAG	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTACCCAGT	TTCAGGAGTG	2340
AGAAAAGAGC	AGGGAGGTGG	TTGTCAATTCA	GATACCTTGA	GAACAATTTT	TCTCGTTACT	2400
CAGAAGCAAA	TTTGTGTTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
TACGTTCTTC	TTTGTGCACTT	AAAGTTGCAT	TGCCTACTGT	TATACTGGAA	AAAAATAGAGT	2520
TCAAGAATAA	TTAGACTCAT	TTACACAAA	GGTTAATGAC	AACAATATAC	CTGAAAACAG	2580
AAATGTGACG	GTTAATAATA	TTTTTTTAAT	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCCTT	2760
GTATCTTTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACITTT	TTGAAATCCT	2820
ATTCAAGTAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTACACTGA	2880
ATTTCTAAGA	AAATGTGAAA	ATAGTCTTCT	TTTATACTGT	AAAAAAGAT	ATACCAAAAA	2940
GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTTATTG	ATACCTTACC	ATCTAAAAATG	3000
TGTGATTTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTATGTA	ACTGAAATAA	3060
GGTGCTTACT	CAAAAGAGTG	CCACTATTGA	TTGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
ATATTTAAAA	AAAATGTGTC	TAAAGGGTTA	GTAGACAAAA	TGTTAGTCTT	TTGTATATTA	3180
GGCCAGATGC	AAATGACTTC	CCTTTTTTAA	TGTTTTCATG	CCACCCATTG	ATTGTATTAT	3240
AACCACTTAC	AGTTGCTTAT	ATTTTTTGT	TTAACTTTTG	TTTCTTAAAC	TTTAGAATAT	3300
TACATTTTGT	ATTATACAGT	ACCTTTCTCA	GACATTTTGT	AG		

Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

85

1	11	21	31	41	51

MEMFTPLLTCT IFLPLLRGHS LFTCEPITVP RCMKMYNMT FFPNLMGHYD QSIAAEMEH 60
 FLPLANLECS PNIEFTFLCA FVPTCIEQIH VVPPCRKLCE KVSJDCCKLI DTFGIRNPEE 120
 LECORLQYCD ETVPVTFDPH TEPLGPQKKT BQVQRDIPW CPHRLKTSBG QGYKFLGIDQ 180
 CAPCPNMFV KSDLEFVKS FIGTVSIFCL CATLFTFLTP LIDVRRFRYP ERPIIYYSVC 240
 5 YSIVSLMYPF GFLGLDSTAC NKADKLELG DTVVLGQSNK ACTVLFMLLY PFTMAGTVWN 300
 VILITITWFLA AGRKWSCEAI BQKAVWFHAV ANGTGPGFLT VMLLALNKVEG DNISGVCFVG 360
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLHVVRQVI QHDGRNQEL KCFMIRIGVF 420
 SGLVLVPLVT LLGCYVYEV NRITWEITWV SDHCQRQYHIP CPYQAKAKAR PELALPMIKY 480
 10 LMTLIVGISF VFWVGSKTC TEWAGPFKRN RKRDPISER RVLQESCEPF LKHNSKVXKH 540
 KHKYKPSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQSTLLEIQ TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNLQ VPSSSEPSL KGSTSLLVHP VSGVRKEBQG GCHSDT

Seq ID NO: 652 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

1 11 21 31 41 51
 20 TTGGGGGGCG GAAGCGGCCA CAACCCGGCG ATCGAAAAGA TTCTTAGGAA CGCGGTACCA 60
 GCGCGGTCTC TCAGGACAGC AGGCCCTCTG CCTTCTGTG GCGCGCGCTC AGCGGTGCCC 120
 TCGGCCCTC AGGTCTCTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAATC TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GCGCTTGCAA 240
 25 AGGTCAAATC TGCGTCCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 AAAACACACT AGGGAGTGAT TTGCCCGGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360
 TGAGACATCA GCATATATGT CAACCTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTCTCTGA GTACTGCCCT GGAGGAGAGC TGTITGACTA TATAATTTC CAGGATGCGC 480
 TGTGAGAAGA GSAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600
 30 ATAAATTAAG GCTGATTGAC TTGCTCTCT GTGCAAAACC CAAGGTAAC AAGGATTACC 660
 ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAT 720
 CATATCTGG ATCAGAGGCA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780
 GTGGATTCTT ACCATTGATG GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 35 GAAATATGTA TGTTCCTCAAG TGGCTCTCT CCGATAGCAT TCTGCTTCTT CAACAAATGC 900
 TGCAAGTGGA CCCAAAGAAA CGGATTCTTA TGAATAATCT ATTGAACCAT CCTGGATCA 960
 TGCAAGATTA CAATATCTCT GTTGAAGTGG AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020
 ATGATTGGCT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAAAAC ATGGAGGATT 1080
 TAATTTCACT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA 1140
 40 AGGCTCGGGG AAAACACAGT CGTTTAAGGC TTTCTTCTT CTCTGTGGA CAAGCCAGTG 1200
 CTACCCCACT CACAGACATC AAGTCAAATA ATTGGAGTCT GGAAGATGTG ACOGCAAGTG 1260
 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGCTAC TCCCGAACA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAG 1440
 45 AATCTAAATC ATTAACCTCA CCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAG 1440
 AAAATGTATA TACTCTTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCTGAGC 1500
 CAAAGACTCC AGTTAATAAG AACCAAGCATA AGAGAGAAAT ACTCACTACG CCAATGCTT 1560
 AACTACACCC CTCAAAGCT AGAAACCACT GCCTGAAAGA AACTCCAATT AAAATACAG 1620
 TAAATTCAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCTGAG AGCGGTGCCC 1680
 GCTCAGTGGA ATTGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG 1740
 50 CCAAGTGTG TTGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAAGA 1800
 GCAAAAGGAA GGGTCTGCGC AGAGACGGGC CCAGAAGACT AAAGCTTAC TATAATGTGA 1860
 CTACAACTAG ATTAGTGAAT CCAGATCAAC TGTGTAATGA AATAATGTCT ATTCTTCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAAGGCTT ATACACTGAA GTGTCAAAAC CAGTCAGATT 1980
 TTGGGAAAGT GACAATGCAA TTTGAATTAG AAGTGTGCGA GCTTCAAAAA CCGATGTGG 2040
 TGGGTATCAG GAGGACGGG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGAAG 2100
 55 ACATCTATC TAGCTCAAG GTATAATTGA TGGATTCTCT CATCTGCGC GATGAGTGTG 2160
 GGTGTGATAC AGCTACATA AAGACTGTTA TGATCGCTT GATTTTAAG TTCATTGGA 2220
 CTACCAACTT GTTCTTAAG AGCTATCTTA AGACCAATAT CTCTTTGTT TTAACAAAA 2280
 GATATTATT TGTGATAGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGCTTTT 2340
 60 TAATCATGTG GTTTGTATA TTAATAATTG TTGACTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAAT TCTTTCTGAA ATAAAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 653 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 65 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 LKNLRHQHIC QLYHVLESTAN KIPMVLEYCF GGELFDYIIS QDRLESEETR VVFRQIVSAV 120
 70 AYVHSQGYAH RDLKPENLLF DEYHKLKID FGLCAKPKGN KDYHLQTCG SLAYAAPELI 180
 QKSYLGSSEA DVWSMGLILY VLMCGFLPFD DDNVMAlyKK IMRGKYDVPK WLSPPSILL 240
 QQMLQVDPKK RISMKNLNLR PWIMQDYNYP VEQSKNPF I HLDGDCVTEL SVHRNRNQT 300
 MEDLISLMQY DHLTATYLL LAKKARGKPV RLRLSSFSFG QASATPPTDI KSNMWSLEDV 360
 75 TASDRNYVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL 420
 KNKENVYTPK SAVKNEEYFM FPEKTPVKN NQHKREILT PNRYYTPSKA RNQCLKETPI 480
 KIPVNSTGTD KMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVPSL ERGLDRVITV 540
 LTRSKRKGSA RDGPRRLKLI YNVTITRLVN PDQLLNEIMS ILPKKHVDFV QKGYTLKCOY 600
 QSDFGKVTMQ FELEVQQLK PDVVGIRQR LKGDAMVYKR LVEDILSSCK V

Seq ID NO: 654 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
 85 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AACCGCGACC AAGGAAAAC CACTACCATG AGAATTGCAG TGATTGCTT TTGCTCCTTA 120

	GGCATCACCT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAGCAG	180
	CTTTACAAAC	AAATACCCAGA	TGCTGTGGCC	ACATGGCTAA	ACCCTGACCC	ATCTCAGAAG	240
	CAGAATCTCC	TAGCCCCACA	GACCTTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCACATG	300
5	GATGATATGG	ATGATGAAGA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
	AACGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
	TCTGATGAAT	CTGATGAAC	GGTCACTGAT	TTTCCCACGG	ACCTGCCAGC	AACCGAAGTT	480
	TTCACTCCAG	TTGTCCCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTTAT	540
	GGACTGAGGT	CAAAATCTAA	GAAGTTTTCG	AGACCTGACA	TCCAGTACCC	TGATGCTACA	600
10	GACGAGGACA	TCACCTCACA	CATGGAAGC	GAGGAGTTGA	ATGGTGCTAT	CAAGGCCATC	660
	CCCGTTGCC	AGGACCTGAA	CGCGCCTTCT	GATTGGGACA	GCCGTGGGAA	GGACAGTTAT	720
	GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
	TATAAGCGGA	AAGCCAATGA	TGAGAGCAAT	GAGCATTCCG	ATGTGATTGA	TAGTCAGGAA	840
	CTTTCCAAAG	TCAGCCGTGA	ATTCCACAGC	CATGAATTTT	ACAGCCATGA	AGATATGCTG	900
	GTGTGATAGC	CCAAAAGTAA	GGAAGAAGAT	AAACACCTGA	AATTCGTAT	TTCTCATGAA	960
15	TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAGGAGAAAA	AATACAAATT	CTCATTTCG	1020
	ATTTAGTCAA	AAGAAAAAAT	GCTTTATAGC	AAAATGAAAG	AGAACATGAA	ATGCTTCTTT	1080
	CTCAGTTTAT	TGGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	GTGTTTGATA	1140
	ATTAGTTTAG	TTTGTGGCTT	CATGGAACCT	CCCTGTAAAC	TAAAGCTTC	AGGGTTATGT	1200
	CTATGTTTAT	TCTATAGAAG	AAATGCAAA	TATCACTGTA	TTTAAATATT	TGTTATTCTC	1260
20	TCATGAATAG	AAATTTATGT	AGAAGCAAA	AAAATACTTT	TACCCACTTA	AAAAGAGAAT	1320
	ATAACATTTT	ATGTCACTAT	AATCTTTTGT	TTTTTAAGTT	AGTGATATAT	TGTTGTGTAT	1380
	TATCTTTTGT	TGGTGTGAAT	AAATCTTTTA	TCTTGAATGT	AATAAGAATT	TGGTGGTGTC	1440
	AATTGCTTAT	TGTTTTCCTC	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTTTACT	1500
25	GCCTAAAAAA	AAAAAAA	AAAA				

Seq ID NO: 655 Protein sequence

Protein Accession #: NP_000573

30	1	11	21	31	41	51	
	MRIAVICFL	LGITCAIPVK	QADSGSSEK	QLYNKYFDAV	ATWLNPDPSQ	KQNLLAPQTL	60
	PSKSNESHDD	MDMDDEDD	DHVDSDSID	SNDSDVDVDT	DDSHQSDSH	HSDESDELVT	120
	DFPTDLPLATE	VFTPVVPTVD	TYDGRGDSVV	YGLRSKSKKF	RRPDIQYFDA	TDEDITSHME	180
	SEELNGAYKA	IPVAQDLNAP	SDWDSRGKDS	YETSQLDDQS	AETHSHRQSR	LYKRKANDES	240
35	NEHSDVDSQ	ELSKVSREPH	SHEPHSHEDM	LVVDPKSKES	DKHLKFRISH	ELDSASSEVN	

Seq ID NO: 656 DNA sequence

Nucleic Acid Accession #: NM_003108.1

Coding sequence: 76..1401

40	1	11	21	31	41	51	
	GGGGTGGGAG	GGGGAGGGGG	ACCTCCGCAC	GAGACCCAGC	GGCCCGGGTT	GGAGCGTCCA	60
45	GCCTTCGAAC	GGATCATGTT	GCAGCAGGCG	GAGAGCTTGG	AAGCGGAGAG	CAACCTGCCC	120
	CGGGAGGCGC	TGACACACGA	GGAGGGCGAA	TTTATGGCTT	GCAGCCCGGT	GGCCCTGGAC	180
	GAGAGCGACC	CAGACTGGTG	CAAGACGCGC	TCGGGCCACA	TCAAGCGGCC	GATGAACGCG	240
	TTTATGGTAT	GGTCCAAGAT	CGAACGCGAG	AAGATCATGG	AGCAGTCTCC	GGACATGCAC	300
	AACGCGCAGA	TCTCCAAGAG	GCTGGGCAAG	CGCTGGAAAA	TGCTGAAGGA	CAGCGAGAAG	360
50	ATCCCGTTCA	TCGGGAGAGC	GGAGCGGCTG	CGGCTCAAGC	ACATGGCCGA	CTACCCGAC	420
	TACAAGTACC	GGCCCGCGAA	AAAGCCCAAA	ATGGACCCCT	CGGCCAAGCC	CAGCGCCAGC	480
	CAGAGCCAG	AGAAGAGCGC	GGCCGCGCGC	GGCGGCGGGA	GCGCGGCGG	AGGCGCGGGC	540
	GGTGCCAAAG	CCTCCAAGGG	CTCCAGCAAG	AAATGCGGCA	AGCTCAAGGC	CCCCGCGGCC	600
	CGCGGGCCCA	AGGCGGGGCG	GGGCAAGGCG	GCCCAAGTCC	GGGACTACGG	GGGCGCGGGC	660
55	GACGACTAGC	TGCTGGGCGC	CCTGCGCTGT	AGCGGCTCGG	CGCGGCGCGG	CGCGGGCAAG	720
	ACGCTCAAGT	GGTGTCTTCT	GGATGAGGAC	GACGACGAGC	ACGACGACGA	CGACGAGCTG	780
	CAGCTGCGAG	TCAACACAGA	GCCGGAACAG	GAGGACGAGG	AACCAACGCA	CCAGCAGCTC	840
	CTGCAGCCGC	CGGGGCGAGCA	GCCGTGCGAG	CTGCTGAGAC	GCTACAAAGT	CGCCAAAGTG	900
	CCGCGCCAGC	CTACGCTGAG	CAGCTCGGCG	GAGTCCCGCG	AGGGAGGAGG	CCTCTACGAC	960
60	GAGGTGCGGG	CCGCGCGGAC	CTCGGGCGCC	GGGGGCGGCA	CGCGCCTCTA	CTACAGCTTC	1020
	AAGAACATCA	CCAAGCAGCA	CCCGCGCGCG	CTCGCGCAGC	CCGCGCTGTC	GCCCGGCTCC	1080
	TGCGGCTCGG	TGTCCACCTC	CTCGTCCAGC	AGCAGCGGCA	GCAGCAGCGG	CAGCAGCGGC	1140
	GAGGACGCGG	ACGACCTGAT	GTTGACCTTG	AGCTTGAATT	TCTCTCAAAG	CGCGCACAGC	1200
	GCCAGCGAGC	AGCAGCTGGG	GGGCGGCGCG	GCGCGCGGGA	ACCTGTCCCT	GTCGCTGGTG	1260
65	GATAAGGATT	TGGATTCTGT	CAGCGAGGGC	AGCCTGGGCT	CCCACTTCGA	GTTCGCCGAC	1320
	TACTGCAACG	CGGAGCTGAG	CGAGATGATC	GCGGGGAGCT	GGCTGGAGGC	GAACTTCTCC	1380
	GACCTGGTGT	TCACATATTG	AAAGGCGGCC	GCTGCTCGCT	CTTTCTCTCG	GAGGGTGCAG	1440
	AGCTGGGTTT	CTTGGGAGGA	AGTTGTAGTG	GTGATGATGA	TGATGATGAT	AATGATGATG	1500
	ATGATGGTGG	TGTTGATGTT	GGCGGTGTTA	GGGTGGAGGG	GAGAGAAGAA	GATGCTGATG	1560
70	ATATTGATAA	GATGTGCTGA	CGCAAAGAAA	TTGGAAAACA	TGATGAAAAT	TTTGGTGGAG	1620
	TTAAAGTGAA	ATGAGTAGTT	TTTAAACATT	TTTCTGTCTC	TTTTTTTGTC	CCCCCTCCCT	1680
	TCCTTTATCG	TGCTCAAGG	TAGTTGCATA	CCTAGTCTCG	AGTTGTGATT	ATTTTCCCAA	1740
	AAAAATGTGT	TTTGTAAATTA	CTATTTCTTT	TTCTGAAAT	TCGTGATTGC	AACAAAGGCA	1800
	GAGGGGCGCG	CGCGGCGGAG	GGGAGGTAGG	ACCCGCTCCG	GAAGGCGCTG	TTTGAAGCTT	1860
75	GTCGGTCTTT	GAAGTCTGGA	AGAAGTCTGC	AGAGGACCCCT	TTTGGCAGCA	CAACTGTTAC	1920
	TCTAGGAGAT	TGGTGGAGAT	ATTTTTTTTT	CTTAAGAGAA	CTTAAAGAAC	TGGTGAATTT	1980
	TTTTTAACAA	AAAAAGGG					

Seq ID NO: 657 Protein sequence

Protein Accession #: NP_003099.1

80	1	11	21	31	41	51	
	MVQAESLEA	ESNLPREALD	TEEGEFMACS	FVALDESDPD	WCKTASGHIK	RPMNAPMVVS	60
85	KIERRKIMQ	SPMDHVAEIS	KRLGKRWMKL	KDSEKIPFIR	EAERLRLEKH	ADYDPVKYRP	120
	RKKPKMDPSA	KPSASQSPKE	SAAGGGGSSA	GAGAGGAKTS	KGSSKKCGKL	KAPAAAGAKA	180
	GAGKAAQSGD	YGGAGDDYVL	GSLRVSGSGG	GGAGKTVKCV	FLDEDDDDDD	DDDELQLQIK	240

QEPDEEDBP PHQQLLPFG QPQSLLRRY NVAIVPASPT LSSSAESPES ASLYDEVRAE 300
ATSGAGGGR LYYSPFNITK QHPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGSDADD 360
LWFDLSLNTS QSAHSASEQQ LGGGAAAGNL SLSLVDRDL SPSGSLGSH FRFPDYCTPE 420
LSEMIAGDWL EANFSDLVFT Y

Seq ID NO: 658 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGGCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCAGTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
COCTGTTCCT GCTGCGCTCC GCGCTGGCGG ACTTCAGCCT GGACCAACAG GTGCACTCGA 240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTCGCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGCACTG TACAACGCCA TGGCGGTGGA GGGGGGCGG GGGCCCGCGG 420
GCCAGGCTCT TCCTACCCG TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
TGGAAACATG CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGSTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCGGA ATTCGGGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCTGG 780
AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAAGCA CCAGTGGGTG GTCAATCCGC 840
GGCACAACCT GGGCGTCCAG CTCTGGGTGG AGACGTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CTTGAGTTGG GGCACGGGG CCCAGAACAA GCAGCCCTTC ATGTTGGCTT 960
TCTTCAAGGC CACGAGGTC CACTTCCGCA GCATCCGTC CAOGGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCACAGAG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACCTGGCAG 1080
AGAACAGCG TAGCCACAG AGGCAGGCT GTAAAGAGCA CGAGCTGTAT GTCACTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGAGTG TGCTTCCCT CTGAACCTCT ACATGAACCG CACCAACCA GCCATCGTGC 1260
AGACGCTGCT CCACTTCATC AACCCGGAAG CGGTGCCCAA GCGCTGCTGT GCGCCACGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAACGTATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCGTGTGGCT GCGACTAGCT CCTCGAGAA TTCAGACCTC 1440
TTGGGGCCAA GTTTTCTCG ATCTCTCAT GCTCGCCTTG GCCAGGAAC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCTTCCCTAT CCGCACTTT AAAGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCCTACAAGC TGTGACAGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCAATTGGT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACAGGACA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGTCGTGTC GAAAGGAAAA TTGACCCGGA AGTTCTCTGA ATAAATGTCA 1860
CAATAAAGC AATGAATG

Seq ID NO: 659 Protein sequence
Protein Accession #: NP_001710

1 11 21 31 41 51
MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRLSQBE RREMQREILS 60
ILGLPFRPRP HLGCKENSAP MFMLDLNAM AVEEGGGPGG QGFSYPYKAV PSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREPRFOL SKIPEGEAVT AAEPRYIKDY 180
IRERFNTBTF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGMVLVFDITA TSNHVVNPR 240
HNLGLQLSVE TLDOQSINFK LAGLIGRHGP QNKQPPMVAF FKATEVHPRS IRSTGSKQRS 300
QNRSKTPKQ BALKMANVAE NSSSDQROAC KHELYVVSFR DLGWQDWIIA PEGYAAYYCE 360
GECAFLPNYS MNATNHAIVQ TLVHFINPST VPKPCCAPTQ LNAISVLVYFD DSSNVILKRY 420
RNMVVRACGC H

Seq ID NO: 660 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 211..1895

1 11 21 31 41 51
GGATCTGAGG GGGGCCAGT CACTTCTCTC ACGTCTCTGT GCTGGGGGGG AGGAGCGGAT 60
GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTT TTGGGTGGGA 120
GAGGAATTAT CTGATAAAAT TCCTGGGTGA ATATTTTAA AAAAGGAGAG TTTTAAAAA 180
TGATTTTTTT CCCTCGAAAA TGACCTTTTT ATGCTTGAAG GCAGTTTGTG AACCAAGATA 240
GTGCTTTTTT TTTTCTCTTC TTTTCTTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
CTTGCTCTGA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCACT CCAGGAGGGA 420
GAAGGTAAIT GTTTCCTGTA ATGGGATGGA CTCATTGTGT GGGCCAGAGG AACAGTGGG 480
AAATATATGG CTGTTCCTGA CCTTCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
TTCCGACACT GTAACCCCAA TGGAAACATG GATTTTATGC ACAGCTTAAA TAAACATAGG 600
GCCAATTATT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCTTGT 720
GCTGTGGCTA TTCTCATCAT TGGTTACTTC AGACGATGTC ATTGCCTAG GAACATATC 780
CACATCACT TATTTGTGTC TTTCTGCTG AGAGCTACAA GCATCTTTGT CAAGACAGA 840
GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
CAAAATTCCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGT CAAGATTGCT 960
GTTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC 1020
TACTGCATA ATCTCATCTT TGTGGCTTTC TTTTGGGACA CCAATACTCT GTGGGGCTTC 1080
ATCTTGATAG GCTGGGGGTG TCCAGCAGCA TTTGTTGCAG CATGGGCTGT GGCACGAGCA 1140
ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGTCTGAG ACATCAAGTG GATTATCAA 1200
GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTCTG TTCTGAATAC GTTTAGAGTT 1260
CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGA GCAATACAGG 1320
AAACTGGCCA AATGACACT GGTCTGGTCT CTAGTCTTTG GAGTGCAATTA CATGTTGTC 1380

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GTATGCTGCTC CTCATCTCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 GTTCAGGCGAG AGGTGAAGAA GATGTGGAGT CGGTGGGAATC TCTCCGTGGA CTGGAAAAGG 1560
 ACACCCGCAT GTGGCAGCCG CAGATGGCGC TCAGTGTCTA CCAOCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA GCATGTGTG TTAATCTCTG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCTTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGGAACTCAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 661 Protein sequence
 Protein Accession #: Eos sequence

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1 11 21 31 41 51
 | | | | | |
 MLRSSLSSTSI VLFLFSSPST INESISSRKR HRFLEQLDSD GTITIEEQIV LVLLKAKVQCE 60
 LNIITQLQGG EGNCFPEMDG LIOWPRGTVG KISAVPCPPY IYDFNHRGVA FRHCNPNGTW 120
 DFMHSIWKTY ANYSDCLRLF QPDISIGKQE FFERLYVMYV VGYISIFPSL AVAILIIGYF 180
 RRLHCTRNYY RMHLFVSFPL RATSIFVKDR VVHARIGVKE LESLIMQDDP QNSIEATSVD 240
 KSQYIGCKIA VVMPYIFLAT NYWILVEGL YLHNLIFVAF PSDTKYLWGF ILIGWGFPA 300
 FVAANAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILPLNTVRV LATKIWETNA 360
 VGHDTKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL PFNSFQGFV 420
 SIICYCNGE VQAEVKKMWS RMNLSVDWKR TPCGSRROG SVLITVTHTS SSQSQVAAST 480
 RMVLISGKAA KIASRQPDHS ITLPGYVWSN SEQDCLPHSP HEETKEDSGR QGDILMEKP 540
 SRPMESNPDT EGCGSTEDV L

Seq ID NO: 662 DNA sequence
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143..1795

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1 11 21 31 41 51
 | | | | | |
 GGCCTGTGGC CCGGGCCCGA CCACCCAGC TGGCGTCTGT TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTTACA GCGGTTCGGG GCATGGCCGG GCTGGGGGGG TCGCTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCCGACGT GATTCTGATG GCACCATTAC 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTG 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGTC CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCCTG AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAA TCTTTGAAAG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCCTGG CTGTGGCTAT TCTCATCAIT GGTACTTCA GACGATTGCA 660
 TTGCATAGG AACATATACC ACATGCACIT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGACG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
 TATGGGTGAG AAGATTGCTG TTGTGATGTT TATTACTTTC CTGGCTACAA ATTATTATTG 900
 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCTT TTTGGACAC 960
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TGTGTGACG 1020
 ATGGGCTGTG GCAGAGCAAC CTCTGGCTGA TGGGAACTTA GTGCTGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGCATGA 1200
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG 1260
 AGTGCAATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TCTTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCGTGAGC TGGAAAGAGA CACCGCCATG TGGCAGCCCG AGATGCGGCT CAGTGCTCAC 1500
 CACCGTACG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGCG AAGAGCTGCC AGATGGCCAG CAGACAGCCT GACAGGCCA TCACTTTACC 1620
 TGGCTATGTG TGGAGTAACT CAGAGCAGGA CTGCTGCCCA CACTCTTTCC ACGAGGAGAC 1680
 CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGCTT TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTTGAAGTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980
 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTCTCTT TAAATTAATG TATGGTATT 2040
 GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCC TAAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTCTCTTT TAGAAACTAG TATTCTCTTA TTTCTTACT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAATTT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAAATT CTCAAAAAAG AATATTTCAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 TTCTTTGATA ACCATGTCAT GTGGAAAGAT TTCTCAGTT AGTGAGCTTG TGTCTGCAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCCTTG 2580
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGATCAA TTAATAATTT GTTTTAAAA 2640
 T

Seq ID NO: 663 Protein sequence
 Protein Accession #: NP_005039

85

1 11 21 31 41 51
 | | | | | |
 MAGLQASLEW WGNLNLGSL LARAQLDSDG TITIEEQIVL VLKAKVQCEL NITLQLQEGE 60
 GNCFPEDGL ICWPRGTGK ISAVPCPPYI YDFNHRGVAF RHCHNPNGTW FMSLNTKWA 120
 NYSDCLRLFQ PDISIGKQEF FERLYVMYTV GYSISPSGLA VAILIIGYFR RLHCTRNYYH 180
 MELFVSPMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240

VMFIYFLATN YYWILVEGLY LHNLFVFAFF SDTRYLWGFPI LIGWGFPAAP VAAWAVARAT 300
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILPLNTVRVL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLVVLV VFGVHVIVFV CLPHSPTGLG WEIRMECELF FNSPQGFVVS IYCYCNGEV 420
 QAEVKMWSR WNLSDWKRT PPGSRRCGS VLTTVTHTS SQQSVAASR MVLISGKAAR 480
 5 IASRQPDISH TLPQVWSNS BQDCLPHSFH SETKEDSGRQ GDDILMEKPS RPFMESNPDTE 540
 GCGGETEDVL

Seq ID NO: 664 DNA sequence
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43..1104

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1	11	21	31	41	51	
CTTCTTTAAA	TTTCTTTCTA	GGATGTTTAC	TTCTTCTCCA	CAATGAATGA	GTGTCACTAT	60
GACAAGCACA	TGGACTTTTT	TTATAATAGG	AGCAACACTG	ATACTGTGGA	TGACTGGACA	120
GGAAACAAGC	TTGTGATTGT	TTGTGTGTGT	GGGACGTTTT	TCTGCCTGTT	TATTTTTTTT	180
TCTAATTCTC	TGGTCATCGC	GGCAGTGATC	AAAAACAGAA	AATTTCATTT	CCCTTCTTAC	240
TACCTGTTGG	CTAATTAGC	TGCTGCGGAT	TTCTTGGCTG	GAAATGCTTA	TGTATTCTCT	300
ATGTTTAAAC	CAGGCCCACT	TTCAAAAAC	TTGACTGTCA	ACCGCTGTTT	TCTCGTCAG	360
GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCACCT	TGCTGGTTAT	CGCGTGGAG	420
AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTTATGG	GGGCGTCC	CACACTGGGC	540
TGGAATTGCC	TCTGCAACAT	CTCTGCTGTC	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
TACCTTGTGT	TCTGGACAGT	GTCCAACTTC	ATGGCCCTTC	TCATCATGGT	TGTGGTGATC	660
CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAACGTCT	TGCTCTCGCA	TACAAGTGGG	720
TCCATCAGCC	CGCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
GCGTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTCTGTC	TCTCTGACGG	CCTGAACCTC	840
AGGCAGTGTG	GCGTGCAGCA	TGTGAAAAGG	TGGTTCCTGC	TGCTGGCGCT	GCTCAACTCC	900
GTGCTGAACC	CCATCATCTA	CTCCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGGGTC	CCTCTCGCAT	CCCTTCCACA	1020
GTCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
GTCTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCCTCT	GGCCCAACCA	GGTGATGACT	1140
GTCTTAGG						

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Seq ID NO: 665 Protein sequence
 Protein Accession #: NP_036284

1	11	21	31	41	51	
MNECHYDKHM	DFPNRSTND	TVDDWTGTL	VIVLCVGTFF	CLFIFFPSNSL	VIAAVIRNRK	60
FHPFFYYLLA	NLAADFFPAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIASERHMS	IMMRVHSMG	TKRVTLLIL	LWMAIAIFMG	AVPTLGNLNL	CNISACSSLA	180
PIYSRSYLVF	WTVSNLMAFL	IMVVVYLRIV	VYVKRKTNVL	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFV	CWTPGLVLL	LDGLNCRQCG	VQHVIRWFL	LALLNSVVP	IISYKDEDM	300
YGTMKMICCC	FSQENPERP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

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Seq ID NO: 666 DNA sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150..3362

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1	11	21	31	41	51	
AACGCCCGCC	TCGGGAGCGC	TCGGGGTGGG	GCTCCGCGTG	CGGCTGCTGC	TGCGGCGCCC	60
CGGCTCCGGT	GCGTCCGCGT	CCTGTGCCCC	CGCGGAGCA	GTCTGCGGCC	CGCGGTGGCC	120
CCTCAGCTCC	TTTCTCTGAG	CCGCGCGCGA	TGGGAGCTGC	CGCGGGATCC	CGCGCCAGAC	180
CCGCGCGGTT	GCTCTGCTGC	AGCGTCTGTC	TGCTGCGCGT	GCTGGCGGGT	ACCCAGACAG	240
CCATTGTCTT	CATCAAGCAG	CGGTCTCTCC	AGSATGCACT	GCAAGGGGCG	CGGGCGCTGC	300
TTGCTGTGA	GGTGAGGGCT	CGGGGCCCGG	TACATGTGTA	CTGGCTGCTC	GATGGGGCCC	360
CTGTCCAGGA	CACGAGCGCG	CGTTTCCGCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG	420
ACCGGCTGCA	GGACTCTGCG	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAA	480
AAGCCGCGAG	TGCCAACGCC	TCCTTCAACA	TCAAATGGAT	TGAGGCAGGT	CCTGTGGTCC	540
TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGTGCACA	CTTGGTTGCC	600
ACATTGATGG	GCACCTCGG	CCCACCTACC	AATGGTTCCG	AGATGGGACC	CCCCTTTCTG	660
ATGGTCAGAG	CAACCAACCA	GTCAGCAGCA	AGGAGCGGAA	CCTGACGCTC	CGGCCAGCTG	720
GTCTGAGCA	TAGTGGGCTG	TATTCCTGCT	GCGCCACAG	TGCTTTTGGC	CAGGCTTGCA	780
GCAGCCAGAA	CTTCACTCTG	AGCATTGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
CCCAGGACGT	GGTAGTAGCG	AGGTATGAGG	AGGCCATGTT	CCATTGCCAG	TCTCAGCCCC	900
AGCCACCCCC	GAGCCTGCAG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCGCAGTC	960
GCCTCCACCA	CCTCCGAGA	GCCACAGTGT	TTGCCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
TCGCGCCACG	CAATGCAGGG	ATCTACCGCT	GCAATTGGCCA	GGGGCAGAGG	GGCCCAACCA	1080
TCATCTCGGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
GGGTGTTTAC	AGCTGGCAGC	GAGGAGGCTG	TGACCTGCCT	TCCCCCAAG	GGTCTGCCAG	1200
AGCCAGAGCT	GTGGTGGGAG	CACGCGGGAG	TCCGGCTGCC	CACCCATGGC	AGGGTCTACC	1260
AGAAGGGCCA	CGAGCTGGTG	TTGGCCAAAT	TTGCTGAAAG	TGATGCTGGT	GTCTACACCT	1320
GCCACGCGCG	CAACCTGGCT	GCTCAGCGGA	GACAGGATGT	CAACATCACT	GTGGCCACTG	1380
TGCCCTCTCT	GCTGAAGAAG	CCCCAAGACA	GCCAGCTGGA	GGAGGGCAAA	CCCGGCTACT	1440
TGGATTGCTT	GACCCAGGCC	ACACAAAAC	CTACAGTTGT	CTGGTACAGA	AACCAAGATG	1500
TCATCTCAGA	GGACTCAACG	TTGAGGTTCT	TCAAGAAATG	GACCTTGCGC	ATCAACAGCG	1560
TGGAGGTGTA	TGATGGGACA	TGGTACCGTT	GTATGAGCAG	CACCCAGGCC	GGCAGCATCG	1620
AGGCGCAAGC	CGGTGTCCAA	GTGCTGGAAA	AGCTCAAGTT	CACACCAACA	CCCCAGCCAC	1680
AGCAGTGCTAT	GGAGTTTGAC	AAGGAGGCCA	CGGTGCCCTG	TTCAGCCACA	GGCGGAGAGA	1740
AGCCCACTAT	TAAGTGGGAA	CGGGCAGATG	GGAGCAGCCT	CCCAGAGTGG	GTGACAGACA	1800
ACGCTGGGAC	CCTGCATTTT	GCCCGGGTGA	CTCGAGATGA	CGCTGGCAAC	TACACTTGCA	1860
TTGCTTCCAA	CGGCGCGCAG	GGCCAGATTC	GTGCCCATGT	CCAGCTCACT	GTGGCAGTTT	1920
TTATCACTTT	CAAGTGGGAA	CCAGAGGCTA	CGACTGTGTA	CCAGGGCCAC	ACAGCCCTAC	1980
TGCACTGCGA	GGCCAGGGGG	GACCCCAAGC	CGCTGATTCA	GTGGAAAGGC	AAGGACCGCA	2040
TCTTGAACCC	CACCAAGCTG	GGACCCAGGA	TGCACATCTT	CCAGAAATGG	TCCCTGGTGA	2100

85

	TCCATGACGT	GGCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
	ACATCAAGCA	CACGGAGGCC	CCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
	AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTG	2280
5	CCGCTGTGGC	CTACATCAT	GCGGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
	AAGCCAGCG	GCTGCAAGG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCACGGTGT	TAGCCTGCG	CCCATCACC	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
10	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCCTGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAGGATGAG	CAGCAGCAGC	TGGACTTCGG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAGCTGAA	CCAGCCCAAC	GTGGTGCGGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTTCTG	AGGATTTCCA	2820
	AGAGCAAGGA	TGAAAAATTG	AAGTCAAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
15	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACTGCCTG	GTCACTGCC	AGAGACAAGT	GAAGGTGTCT	GCCTTGGGCC	3000
	TCAGCAAGGA	TGTTGACAA	AGTGAGTACT	ACCACTTCGG	CCAGGCGCTG	GTGCCGTGCG	3060
	GCTGGATGTC	CCCGAGGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CTTTCGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCCAT	GGTGGGCAGG	3180
20	CAGATGATGA	AGTACTGAGG	GATTGACAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCGAGG	3240
	GCTGCCCTTC	CACACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCCCTGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
	CAGCATGATG	GGCAAGATCC	CTGTCTCCTC	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
25	TTGCTGAGTG	CTCAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCCCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGGAGCTAG	GGCTTTGAGC	TGGGCAGTTT	CCCTGCGCAC	3600
	CTCTTCTCTG	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTCT	GGCCTTCAAC	3660
	TTCTCCCTCT	GACCGCTGAC	AACTCTGCCA	CTCATCTGCC	AACTTTGCC	GGGGAGGGCT	3720
	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTTAATA	TTCTCAAGTT	CTGGGCACAC	3780
30	AGGCTTAATG	AGTACTCTTC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTGTGCACAC	CTGACCCAGA	CCCACTCTCT	3900
	CCCCACCTTT	CTCTCCTTTC	CTCATCTTAA	GTGCCTGGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACG	GCCTTTTGTG	TATGCACAC	GGCGGGCTTT	TATATGTAAT	4020
	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
35	GCCATCCTTA	CCCCACACTT	TTATTGTTGT	CGTTTTTTGT	TTGTTTTTGT	TTTTTGTITT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTTA		

Seq ID NO: 667 Protein sequence
Protein Accession #: NP_002812

40	1	11	21	31	41	51	
	MGAARGSPAR	PRRLPLLSVL	LLPLLGGTQT	AIIVFIKQPS	QDALQRRAL	LRCEVEAPGP	60
	VHVVYLLDGA	PVQDTERFPA	QSSLSFAAV	DRLQDSGTFO	CVARDDVTGE	EARSANASFN	120
	IKWIEAGFPV	LKHPASEAEI	QPQTQVTLRC	HIDGHPRTY	QWFRDGTPLS	DGQSNHTVSS	180
45	KERNLTLRPA	GPEHSGLYSC	CAHSAPQAC	SSQNFTLSIA	DESFAVVLA	PQDVVVARYE	240
	EAMFHCQSPA	QPPPSLQWLF	EDETPIITNS	RPPHLRRATV	FANGSLLLTQ	VRPRNAGIYR	300
	CIQGGGRGPP	IILEATLHLA	EIEDMPLFEP	RVFTAGSEER	VTCLPPKGLP	EPSVWWEHAG	360
	VRLEPTGRRVY	QKGEHLVLAN	IAESDAGVYT	CHAANLAGOR	RQDVNITVAT	VPSWLKKPQD	420
50	SQLEBCKPGY	LDCLTQATPK	PTVVVYRNQM	LISEDSPFEV	FKNGTLRLNS	VEVDGTWYR	480
	CMSSTPAGSI	BAQARQVQLE	KLKFTPPPQF	QQCMFDPKEA	TVPCSATGRE	KPTIKWERAD	540
	GSSLPFWITD	NAGTLHFARV	TRDDAGNYTC	IASNGPQQOI	RAHVQLTVAV	FITFKVEPER	600
	TTVYQGHYAL	LQCEAGGDPK	PLIQWKGKDR	ILDPTKLGRP	MHIFQNGSLV	IHDVAPEDSG	660
	RYTCAIAGNSC	NIKHTEAPLY	VVDKPVPEES	BPGSPPPFYK	MIQTIIGLSV	AAVAYI IAVL	720
55	GLMFYCKPGY	KAKRLQKQPE	GEPEMECLN	GGPLQNGQPS	AEIQEEVALT	SLGSGPAATN	780
	KRHSTSDKME	FRRSSLPQIT	TLGKSEFGEV	FLAKAQGLEE	GVAETLVLVK	SLQTKDBQQQ	840
	LDPRRELEMF	GKLNHANVVR	LLGLCREABP	HYMVLEYVDL	GDLLQFLRLS	RSKDEKLKSO	900
	PLSTKQKVAL	CTQVALGMEH	LSNNRFVHKD	LAARNCLVSA	QRQVKVSALG	LSKDVYNSEY	960
	YHFRQAWVPL	RWMSPEALLE	GDFSTKSDVM	AFGVLMWEVF	THGEMPHGGQ	ADDEVLLADLQ	1020
60	AGKARLPQPE	GCPSKLYRLM	QRKWLSPKID	RPSFSEIASA	LGDSTVDSKP		

Seq ID NO: 668 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1389

65	1	11	21	31	41	51	
	ATGGGCTACC	AGAGGCAGGA	GCCTGTCACT	CGGCCGACAG	GAGATTAGAA	TGACAGAGAA	60
	ACCCTGTGTT	CTGAACATGA	GTATAAAGAG	AAAACCTGTC	AGTCTGCTGC	TCCTTTTAAT	120
	GTGTGCAACT	CGATTATAGG	ATCTGGTATA	ATAGGATTGC	CTTATTCAAT	GAAGCAAGCT	180
70	GGGTTTCCTT	TGGGAATATT	GCTTTTATTC	TGGGTTCAT	ATGTTACGGA	CTTTCCCTTT	240
	GTTTATTGTA	TAAAGGAGG	GGCCCTCTCT	GGAACAGATA	CCTACCACTC	TTTGTCATAT	300
	AAAACCTTCG	GCTTTCCAGG	GTATCTGCTC	CTCTCTGTTT	TTCACTTTT	GTATCCTTTT	360
	ATAGCAATGA	TAAATTACAA	TATAATAGCT	GGAGATACTT	TGAGCAAGAT	TTTTCAAAGA	420
75	ATCCAGGAG	TTGATCTCGA	AAACGTGTTT	ATTGGTGGCC	ACTTCATTAT	TGGACTTTCC	480
	ACAGTTACCT	TTACTCTGCC	TTTATCTCTG	TACCGAAATA	TAGCAAGACT	TGGAAAGGTC	540
	TCCTCATCT	CTACAGGTTT	AACAACCTCT	ATTCTTGGAA	TTGTAATGGC	AAGGGCAATT	600
	TCACTGGGTC	CACACATACC	AAAAACAGAA	GACGCTTGGG	TATTTGCAAA	GCCCAATGCC	660
	ATTCAAGCGG	TCGGGTTAT	GTCTTTTGCA	TTTATTGGCC	ACCATAACTC	CTTCTTAGTT	720
	TACAGTTCTC	TAGAAGAACC	CACAGTAGCT	AAGTGGTCCC	GCCTTATCCA	TATGTCCATC	780
80	GTGATTCTG	TATTTACTGT	TATATTCTTT	GCTACATGTG	GATACTTGAC	ATTTACTGGC	840
	TTCACCCAAG	GGGACTTATT	TGAAAATTAC	TGCAGAAATG	ATGACCTGGT	AACATTTGGA	900
	AGATTTTGTT	ATGGTGTCAC	TGTCAATTTT	ACATACCCCTA	TGGAATGCTT	TGTGACAAGA	960
	GAGGTAATTG	CCAATGTGTT	TTTTGGTGGG	AATCTTTCAT	CGGTTTTCCT	CATTGTGTGA	1020
85	ACAGTAGTGG	TCATCACTGT	AGCCAGGCTT	GTGTCAATGC	TGATTGATTG	CCTCGGGATA	1080
	GTTCATGAC	TCATGAGGTT	GCTCTGTGCA	ACTCCCTCTA	TTTTTATCAT	TCCATCAGCC	1140
	TGTTATCTGA	AACGTGCTGA	AGAACAAGG	ACACACTCCG	ATAAGATTAT	GTCTTGTGTC	1200
	ATGCTTCCCA	TTGGTGCRTG	GGTGATGGTT	TTTGGATTGG	TCATGGCTAT	TACAAATACT	1260

CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAAATT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC 1380
 TTCAATGA

5 Seq ID NO: 669 Protein sequence
 Protein Accession #: Eos sequence

	1	11	21	31	41	51	
10	MGYQRQEPVI	PPQRDLDDRE	TLVSEHEYKE	KTCQSAALFN	VVNSIIIGSGI	IGLPYSMKQA	60
	GFPLGILLLF	WVSVDYDFSL	VLLIKGGALS	GTDYQSLVN	KTFGPGYLL	LSVLQFLYPF	120
	IAMISYNIIA	GDYLSKVPQR	IPGVDPENVF	IGRRPIIGLS	TVPTPLPLSL	YRNIAKLGV	180
	SLISTGLTTL	ILGIVMARAI	SLGPHIPKTE	DAWVFAKPNA	IQAVGVMSFA	FICHENSFLV	240
15	YSSLEPTVA	KWSRLIHMSI	VISVFICIFP	ATCGYLTFTG	PTQGDLPENY	CRNDDLVTGP	300
	RFQCYGTVIL	TYPMCEFTVR	EVIANVFPGS	NLSSVPHIVV	TVMVITVATL	VSLILDCLGI	360
	VLELNGVLCA	TLPLIFIIPA	CYLKLSSEPR	THSDKIMSCV	MLPIGAVVMV	PGFVMAITNT	420
	QDCTHGEKMF	YCFDFNPSLT	NTSESHVQQT	TQLSTLNIISI	FQ		

20 Seq ID NO: 670 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1284

	1	11	21	31	41	51	
25	ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCGCAGCA	GAGGATTGCC	TTATTCAATG	60
	AAGCAAGCTG	GGTTTCCCTT	GGGAATATTG	CTTTTATTCT	GGGTTTCATA	TGTTACAGAC	120
	TTTCCCTCTG	TTTATTGTAT	AAAAGGAGGG	GCCCTCTCTG	GAACAGATAC	CTACCACTCT	180
	TTGGTCAATA	AAACTTTCGG	CTTTCAGGG	TATCTGCTCC	TCTCTGTCTC	TCAGTTTTTG	240
	TATCCTTTTA	TAGCAATGAT	AAGTTACAAT	ATAATAGCTG	GAGATACTTT	GAGCAAAAGT	300
30	TTTCAAGAA	TCCAGGAGT	TGATCCTGAA	AACTGTGTTA	TTGGTCGCCA	CTTCATTATT	360
	GGACTTTCCA	CAGTTACCTT	TACTCTGCCT	TTATCCTTGT	ACCGAAATAT	AGCAAAGCTT	420
	GGAAAGGCTC	CCCTCATCTC	TACAGGTTTA	ACAACTCTGA	TTCTTGAAT	TGTAATGGCA	480
	AGGGCAATTT	CATGGGTCC	ACACATACCA	AAAACAGAAG	ACGCTTGGGT	ATTTGCAAGG	540
	CCCAATGCCA	TTCAAGCGGT	GGGGTTATG	TCTTTTGCAT	TTATTTGCCA	CCATAACTCC	600
35	TTCTTAGTTT	ACAGTTCTCT	AGAAGAAGCC	ACAGTAGCTA	AGTGGTCCCG	CCTTATCCAT	660
	ATGTCCATCG	TGATTTCTGT	ATTATCTCTG	ATATTCTTTG	CTACATGTGG	ATACCTTGACA	720
	TTTACTGGCT	TCACCAAGG	GGACTTATTT	GAAAATTACT	GCAGAAATGA	TGACCTGGTA	780
	ACATTTGGAA	GATTTTGTGA	TGGTGTCACT	GTCATTTTGA	CATACCCAT	GGAATGCTTT	840
	GTGACAAGAG	AGGTAATGCG	CAATGTGTTT	TTTGGTGGGA	ATCTTTCATC	GGTTTCCAC	900
40	ATTGTTGTAA	CAGTGATGGT	CATCACTGTA	GCCACGCTTG	TGTCATTGCT	GATTGATTGC	960
	CTGGGATAGT	TTCTAGAACT	CAATGGTGTG	CTCTGTGCAA	CTCCCTCAT	TTTTATCAAT	1020
	CCATCAGCCT	GTTATCTGAA	ACTGTCTGAA	GAACCAAGGA	CACACTCOGA	TAAGATTATG	1080
	TCTTGTGTCA	TGCTTCCCAT	TGGTGTCTGT	GTGATGTTT	TTGATTGCT	CATGGCTATT	1140
	ACAAATATCT	AAGACTGCAC	CCATGGGCAG	GAAATGTTCT	ACTGCTTTCC	TGACAATTC	1200
45	TCTCTCACAA	ATACCTCAGA	GTCTCATGTT	CAGCAGACAA	CACAACTTTC	TACTTTAAAT	1260
	ATTAGTATCT	TTCAACTCGA	GTAA				

50 Seq ID NO: 671 Protein sequence
 Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MGYQRQEPVI	PPQRGLFYSM	KQAGFPLGIL	LLFWVSVDY	FSLVLLIKGG	ALSGTDYQS	60
55	LVNKTGPPGP	YLLSLVQLPL	YPLIAMISYN	IIAGDTLSKV	QRIIPGVDP	NVFIHRHPII	120
	GLSTVTPLLP	LSLYRNIAKL	GKVSLLISTGL	TTLLIGIVMA	RAISLGPPIP	KTEDAWVFAK	180
	PNAIQAVGVM	SFAFICHMS	FLVYSLEEF	TVAKWSRLH	MSIVISVFIC	IFPATCGYLT	240
	FTGFTGDLF	ENVCRDDLIV	TGPRFCYGV	VILTYPMCEP	VTRVIANVF	PGNLSVPH	300
	IVTVVMTIV	ATVLSLLIDC	LGIIVLELNG	LCATPLIFII	PSACYLKLSE	EPRTSHDKIM	360
60	SCVMLPIGAV	VMVFGPVMAI	TNTQDCTHQ	EMFYCPDFNF	SLTNTSESHV	QQTQLSTLN	420
	ISIFQLB						

65 Seq ID NO: 672 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1203

	1	11	21	31	41	51	
	ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCGCAGT	TTTCCCTTGT	TTTATTGATA	60
70	AAAGGAGGGG	CCCTCTCTGG	AACAGATACC	TACCAGTCTT	TGGTCAATAA	AACTTTCGGC	120
	TTTCCAGGGT	ATCTGTCTCT	CTCTGTCTCT	CAGTTTCTGT	ATCCTTTTAT	AGCAATGATA	180
	AGTTACAATA	TAATAGCTGG	AGATACTTTG	AGCAAGTTT	TTCAAGAAT	CCCAGGAGTT	240
	GATCCTGAAA	ACGTGTTTAT	TGGTCGCCAC	TTCAATTATG	GACTTTCCAC	AGTTACCTTT	300
	ACTCTGCCTT	TATCCTTGTA	CCGAAATATA	GCAAGCTTG	GAAAGGTCTC	CCTCATCTCT	360
75	ACAGGTTTAA	CAACTCTGAT	TCTTGGAAAT	GTAATGGCAA	GGGCAATTTC	ACTGGGTCCA	420
	CACATACCAA	AAACAGAAGA	CGCTTGGGTA	TTTGCAAGC	CCAATGCCAT	TCAAGCGGTC	480
	GGGGTTATGT	CTTTTGCAAT	TATTTGCCAC	CATAACTCCT	TCTTAGTTTA	CAGTTCTCTA	540
	GAAGAACCAC	CAGTAGCTAA	GTGGTCCCGC	CTTATCCATA	TGTCCATCGT	GATTTCTGTA	600
	TTTATCTGTA	TATTTCTTGC	TACATGTGGA	TACTTGACAT	TTACTGGCTT	CACCAAGGG	660
	GACTTATTTG	AAAATTACTG	CAGAAATGAT	GACCTGGTAA	CATTTGGAAG	ATTTTGTATT	720
80	GGTGTCACTG	TCATTTTGAC	ATACCTATG	GAATGCTTTG	TGACAAGAGA	GGTAATTGCC	780
	AATGTGTTT	TTGGTGGGAA	TCTTTTCATG	GTTTTCACCA	TTGTTGTAAC	AGTGATGGTC	840
	ATCACTGTAG	CCACGCTTGT	GTCAATGCTG	ATTGATTGOC	TGGGATAGT	TCTAGAACTC	900
	AATGGTGTGC	TCTGTGCAAC	TCCCTCAT	TTTATCATTC	CATCAGCCTG	TTATCTGAAA	960
	CTGTCTGAAG	AACCAAGGAC	ACACTCOGAT	AAGATTATGT	CTGTGTCTAT	GCTTCCCAT	1020
85	GGTGTGTGG	TGATGTTT	TGGATTCTGC	ATGGCTATTA	CAAAATCTCA	AGACTGCAAC	1080
	CATGGGCAGG	AAATGTTCTA	CTGCTTTCCT	GACAATTTCT	CTCTCACAAA	TACCTCAGAG	1140
	TCTCATGTTT	AGCAGACAC	ACAACTTTCT	ACTTTAAATA	TAGTATCTT	TCAACTCGAG	1200

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

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1	11	21	31	41	51	
MGYQRQEPVI	PPQPSLVLLI	KGGALSGTDT	YQSLVNKTFG	FPGYLLLSVL	QFLYPFIAMI	60
SYNIIAGDTL	SKVFPQIPGV	DPENVFIGRH	FIIGLSTVTF	TLPLSLYRNI	AKLGKVSLSIS	120
TGLTTLILGI	VMARAIISLGP	HIPKTEDAWV	FAKPNAIQAV	GVMSFAPICH	HNSFLVYSSL	180
EEPTVAKWSR	LIHMSIVISV	PICIFFATCG	YLTPGTPTQG	DLFENYCRND	DLVTFGRFCY	240
GVTVILTYPM	ECFVTREVIA	NVFFGGNLSS	VFHIVVTVMV	ITVATLVSL	IDCLGIVLEL	300
NGVLCAATPLI	FIIPSACYLK	LSEEPRTSD	KIMSCVMLPI	GAVVMVFPV	MAINTNQDCT	360
HGQEMFYCFP	DNPSLINTSE	SHVQQTQLS	TLNISIFQLE			

Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

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1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCCGCAGG	TCAATAAAAC	TTTGGGCTTT	60
CCAGGGTATC	TGCTCTCTCT	TGTTCTTCAG	TTTTTGTATC	CTTTTATAGC	AATGATAAGT	120
TACAATATAA	TAGCTGGAGA	TACTTTGAGC	AAAGTTTTTC	AAAGAATCCC	AGGAGTTGAT	180
CCTGAAAGAG	TGTTTATTTG	TGCCCACTTC	ATTATTGGAC	TTTCCACAGT	TACCTTTACT	240
CTGCCCTTAT	CCTTGTACCG	AAATATAGCA	AAGCTTGGAA	AGGCTCCCT	CATCTCTACA	300
GGTTTAACAA	CTCTGATTCT	TGGAATTGTA	ATGGCAAGGG	CAATTTCACT	GGGTCCACAC	360
ATACCAAAAA	CAGAAGACGC	TTGGGTATT	GCAAGGCCCA	ATGCCATTCA	AGCGGTGGGG	420
GTATGTCTT	TTGCCATTAT	TTGCCACCAT	AACCTCTTCT	TAGTTTACAG	TTCTCTAGAA	480
GAACCCACAG	TAGCTAAGTG	GTCCCGCCTT	ATCCATATGT	CCATGTGAT	TTCTGTATTT	540
ATCTGTATAT	TCTTTGCTAC	ATGTGGATAC	TTGACATTTA	CTGGCTTCAC	CCAAGGGGAC	600
TTATTTGAAA	AATTAGTGAC	AAATGATGAC	CTGGTAACAT	TTGGAAGATT	TTGTATATGT	660
GTCACTGTCA	TTTGTACATA	CCCTATGGAA	TGCTTTGTGA	CAAGAGAGGT	AATTGCCAAT	720
GTGTTTITTT	TGCGGAATCT	TTCAATCGTT	TTCCACATTG	TTGTAACAGT	GATGGTCATC	780
ACTGTAGCCA	CGCTTGTGTC	ATTGCTGATT	GATTGCCTCG	GGATAGTTCT	AGAAGTCAAT	840
GGTGTGCTCT	GTGCACTCC	CCTCATTTT	ATCATTCCAT	CAGCGTGTTA	TCTGAAACTG	900
TCTGAAGAAC	CAAGGACACA	CTCCGATAAG	ATTATGTCTT	GTGTCACTGT	TCCCATTTGT	960
GCTGTGGTGA	TGGTTTITTT	ATTGCTCATG	GCTATTACAA	ATACTCAAGA	CTGCACCCAT	1020
GGCAGGAAA	TGTTCTACTG	CTTTCCTGAC	AATTTCTCTC	TCACAAATAC	CTCAGAGTCT	1080
CATGTTTCAG	AGACAACACA	ACTTTCTACT	TTAAATATTA	GTATCTTTCA	ACTOGAGTAA	

Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

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1	11	21	31	41	51	
MGYQRQEPVI	PPQVNTKTFP	PGYLLLSVLQ	FLYPFIAMIS	YNIIAGDTLS	KVFQRIQVVD	60
PENVFIGRHF	IIGLSTVTF	LPLSLYRNIA	KLKVSLSIST	GLTTLILGIV	MARAIISLGP	120
IPKTEDAWVF	AKPNAIQAVG	VMSFAPICH	NSFLVYSSLE	EPTVAKWSRL	IHMSIVISVP	180
ICIFPATCGY	LTFPTGTQGD	LFENYCRND	LVTGFRFCY	VTIVILTYPM	CFVTREVIAN	240
VFFPGNLSSV	FHVIVVTVMV	TVATLVSLLI	DCLGIVLELN	GVLCATPLIF	IIPSACYLKL	300
SEEPRTSDK	IMSCVMLPIG	AVVMVFPFVM	AITNTQDCTH	GQEMFYCFPD	NPSLNTSSES	360
HVQQTQLST	LNISIFQLE					

Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

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1	11	21	31	41	51	
AGGAATCTGC	GCTGGGTTTC	CGCAGATGCA	GAGGTGAGG	TGGCTGCGGG	ACTGGAAGTC	60
ATCGGGCAGA	GGTCTCACAG	CAGCCAAAGG	ACCTGGGGCC	CGCTCCTCCC	COCTCCAGGC	120
CATGAGGATT	CTGCAGTTAA	TCCTGCTTGC	TCTGGCAACA	GGGCTGTAG	GGGGAGAGAC	180
CAGGATCATC	AAGGGGTTCC	AGTGCAAGCC	TCACTCCCAG	CCCTGGCAGG	CAGCCCTGTT	240
CGAGAAGACG	CGGCTACTCT	GTGGGGCGAC	GCTCATCGCC	CCCAGATGGC	TCCTGACAGC	300
AGCCCATGCG	CTCAAGCCCC	GCTACATAGT	TCACTGGGG	CAGCACAACC	TCCAGAAGGA	360
GGAGGGCTGT	GAGCAGACCC	GGACAGCCAC	TGAGTCCTTC	CCCCACCCCG	GCTTCAACAA	420
CAGCCTCCCC	AACAAGACCC	ACCGCAATGA	CATCATGCTG	GTGAAGATGG	CATGCCCAGT	480
CTCCATCACC	TGGGCTGTGC	GACCCCTCAC	CCTCTCCTCA	CGCTGTGTCA	CTGCTGGCAC	540
CAGCTGCTCT	ATTTCCGGCT	GGGGCAGCAC	GTCCAGCCCC	CAGTTACGCC	TGCTCACAC	600
CTTGCGATGC	GCCAACATCA	CCATCATTTA	GCACCAAGAG	TGTGAGAAAG	OCTACCCCGG	660
CAACATCACA	GACACCATGG	TGTGTGCCAG	GTGCAGGAA	GGGGGCAAGG	ACTCTGCCCA	720
GGGTGACTCC	GGGGGCCCTC	TGGTCTGTAA	CCAGTCTCTT	CAAGGCATTA	TCTCTGGGG	780
CCAGGATCCG	TGTGCGATCA	CCCGAAAGCC	TGGTGTCTAC	ACGAAAGTCT	GCAAATATGT	840
GGACTGGATC	CAGGAGACGA	TGAAGAACAA	TTAGACTGGA	CCCACCCACC	ACAGCCCATC	900
ACCTCCATTT	TCCACTTGGT	GTTTGGTTCC	TGTTCACTCT	GTTAATAAGA	AACCTTAAGC	960
CAAGACCTCT	TACGAACATT	CTTTGGGCTC	CCTGGACTAC	AGGAGATGCT	GTCACTTAAT	1020
AATCAACCTG	GGGTTGGAAG	TCAGTGAGAC	CTGGATTCAA	ATTCTGCCTT	GAAATATTGT	1080
GACTCTGGGA	ATGACAACAC	CTGGTTTGTT	CTCTGTGTGA	TCCCAGCCCC	CAAGACAGC	1140
TCTGCGCCAT	ATATCAAGGT	TTCAATAAAT	ATTGTCTAAA	TGAGTG		

Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

85

1	11	21	31	41	51	
MRILQLILLA	LATGLVGGET	RIIKGFECIP	HSQFWQAALP	EKTRLLCGAT	LIAPRWLLTA	60

AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESPPHPGFNN SLPNKDHEND IMLVWASPV 120
 SITNAVEPLT LSSRCVTAQT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCNAYPG 180
 NITDTMVCAS VQEGGKDSQ GDSSGPLVCN QSLQGIISWG QDPCAITRKP GVIYTRVCKYV 240
 DWIQETMKN

5

Seq ID NO: 678 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..933

10 1 11 21 31 41 51
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 ATGTGCAGCA ATGGACGGTG CATCCCGGGC GCCTGGCAGT GTGACGGGCT GCGTGAAGTC 60
 TTCGACAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCGACCTTC 120
 TTCCCTGTG CCAGCGGCAT CCATTGCATC ATTGGTCGCT TCCGGTGCAA TGGGTTTGAG 180
 15 GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240
 GCCCGCTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG OGATGGACAG 300
 AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT 360
 GGGCAGGTGT TTGTGACTTC AGAGAACCAG CTTGTGTATT ACCCCAGCAT CACCTATGCC 420
 ATCATOGGCA GCTCGTCAT TTTTGTGCTG GTGGTGCCCT TGCTGGCACT GGTCTTGAC 480
 20 CACGAGCGGA AGCGGAACAA CCTCATGACG CTGCCCGTGC ACCCGCTGCA GCACCTGTG 540
 CTGCTGTCCC GCCTGGTGGT CCTGGACCAC CCCCACCACT GCAACGTGAC CTACAACGTC 600
 AATAATGSCA TCAGTATGT GGCACGCCAG GCGGAGCAGA ATGCGTGGGA AGTAGGCTCC 660
 CCACCTCTCT ACTCGAGGC CTTCTGTGAC CAGAGGCGCT CGTGGTATGA CCTTCTCCA 720
 CGCCCTACT CTTCTGACAC GGAATCTCTG AACCAAGCGG ACCTGCCCCC CTACCGCTCC 780
 25 CGGTCGCGGA GTGCCAACAG TGCCAGCTCC CAGGACGCCA GCAGCTCTCT GAGCGTGAA 840
 GACACGAGCC ACAGCCCGGG GCAGCTGGC CCCCAGGAG GCACCTGTGA GCCCAGGAG 900
 TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

30 Seq ID NO: 679 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MCSNGRCIPG AWQCDGLPDC FDKSDEKECP KAKSKCGPTF PFCASGIHCI IGRFRONGFE 60
 35 DCPDGSDEEN CTANPLLCST ARYHCKNGLC IDKSPICDQ NNCQDNDSEE SCESSQEPGS 120
 GQVFTSENG LVVYPSITYA IIGSSVIFVL VVALLALVLH HQRKRNLMT LPVHRLQHPV 180
 LLSRLVVLDE PHHCNVTYV NNGIQYVASQ AEQNASEVGS PPSYSEALLD QRPAMYDLPP 240
 PPSYSDTESL NQADLPYRS RSGSANSASS QAASSLLSVE DTSHPGQPG PQEGTAEPED 300
 SEPSQTEEV

40

Seq ID NO: 680 DNA sequence
 Nucleic Acid Accession #: S78203.1
 Coding sequence: 1..2190

45 1 11 21 31 41 51
 | | | | |
 ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTCACCTGT CTCCATGAA 60
 GAGGTACCAC CTGACACCAC TAGCCCTCCA AAGAAGCCAT CTCGACAAT CTGTGGCTCC 120
 50 AACTATCCAC TGAGCATTGC CTTCAATGTG GTGAATGAAT TCTCGAGCG CTCTTCTAT 180
 TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCTGTATT TCCTGCACGT GAATGAAGAT 240
 ACCTCCACAT CTATATAACA TGCCCTCAGC AGCCTCTGTT ATTTTACTCC CATCTGGGA 300
 GCAGCCATTG CTGACTCGTG GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCCTGGTG 360
 TATGTGCTTG GCCATGTGAT CAAGTCCCTG GGTGCCCTAC CAATACTGGG AGGACAAGTG 420
 55 GTACACACAG TCCTATCATT GATOGGCTG AGTCTAATAG CTTTGGGAC AGGAGGCATC 480
 AAACCTCTGT TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAACATGC AGAGGAACGG 540
 ACTAGTACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATT 600
 ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTTGGAG AAGACTGCTA TGCATTGGCT 660
 TTTGGAGTTC CAGGACTGCT CATGGTAATT GCACCTTGTG TGTTTGCAAT GGGAGCAAA 720
 60 ATATACAATA AACACACCCC TGAAGGAAAC ATAGTGGCTC AAGTTTTCAA ATGTATCTGG 780
 TTTGCTATT CCAATCGTTT CAAGAACCGT TCTGGAGACA TTCCAAAGCG ACAGCACTGG 840
 CTAGACTGGG CAGCTGAGAA ATATCCAAAG CAGCTCATT TGGATGTAAA GGCACGTACC 900
 AGGGTACTAT TCCTTTATAT CCCATTGCCC ATGTTCTGGG CTCTTTTGA TCAGCAGGT 960
 TCAOGATGA CTTTGAAGC CATCAGGATG AATAGGAATT TGGGGTTTTT TGTGCTTCAG 1020
 65 CCGGACCAGA TGCAGGTTCT AAATCCCTTT CTGGTTCTTA TCTTCATCCC GTTGTGAC 1080
 TTTGTATT ATCGTCTGGT CTCCAAGTGT GGAATTAAT TCTCATCACT TAGGAAAAATG 1140
 GCTGTGTTA TGATCCTAGC GTGCCTGGCA TTTGCAGTTG OGGCAGCTGT AGAGATAAAA 1200
 ATAAATGAAA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TTTTCTACA AGTCTTGAAT 1260
 CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAAATG AAAACAATTC TCTGTTGATA 1320
 70 GAGTCCATCA AATCCTTTCA GAAACACCA CACTATTCCA AACTGCACCT GAAACAAAA 1380
 AGCCAGGATT TTCATTCCA CCTGAAATAT CACAAATTGT CTCTCTACAC TGAGCATTT 1440
 GTGCAGGAGA AGAAGTGTG CAGTCTGTG ATTGTGAAG ATGGGAACAG TATCTCCAGC 1500
 ATGATGTTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGT 1560
 AACACTTTG ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
 75 GAAGACTATG GTGTGCTGCT TTATAGAACT GTGCAAGAG GAGAATACCC TGCACTGCAC 1680
 TGTAGAACAG AAGATAAGAA CTTTCTCTG AATTTGGGTC TTCTAGACT TGGTGACGA 1740
 TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGCTCTC AGGCCTGGAA GATTGAAGAC 1800
 ATTCAGGCA ACAAAATGTC CATTGCGTGG CAGCTACCA ATATGCCCCT GGTACAGCT 1860
 GGGGAGGTCA TGTCTCTGT CACAGGCTT GAGTTTCTT ATTCTCAGG TCCTCTAGC 1920
 80 ATGAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCTG 1980
 CTGTGTTGG CACAGTTCAG TGGCTGGTA CAGTGGGCGG AATTCATTT GTTTCTCTG 2040
 CTCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG 2100
 ACAGAGGATA TGGGGGTCC AGCAGATAAG CACATTCTCT ACATCCAGG GAACATGATC 2160
 AAACATAGAGA CCAAGAGAC AAAACTCTGA

85 Seq ID NO: 681 Protein sequence
 Protein Accession #: AAB34388.1

1 11 21 31 41 51
| | | | |
MNPFQKNESK ETLFSPVSIE EVFPRPPSP KPSPTICGS NYPLSIAFIV VNEFCERFSY 60
YGMKAVLILY FLYPLHWNED TSTSIYHAFS SLCYFTPILG AALADSWLKG FKTIIVLSLV 120
5 YVLGEVIKSL GALPILGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QFEKHAEER 180
TRYFSVFFLS INAGSLISTP ITPMLRGDVQ CFGEDCYALA FGVPGLLMVI ALVVPAMGSK 240
IYNKPPPGSN IVAQVFKCIW FAISNRPKNR SGDIKPRQHW LDWAAEKYK QLMIDVKALT 300
RVLPFLYIPL MFWALLDQGG SRWTLQAI RM NRNLGPFVLQ PQDMQVINF LVLIFIPLFD 360
FVIYRLVSKC GINFSLSLRM AVGMILACLA FAVAAVEIK INEMAPAQSG PQEVFLQVLN 420
10 LADDEVKVTV VGNENNSLLI ESIKSPQKTP HYSKLHLKTK SQDPHFLKY HNLSLYTES 480
VQEKWYSLV IREDGNSISS MMVKDTEKRT TNGMTTVRFV NTLKDVNIS LSTDTSLNVG 540
EDYGVSAIRT VQGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600
IPANKMSIAM QLFOYALVTA GEVMSVTGL EFSYSQAPSS MKSVLQAOWL LTIAGNIIIV 660
15 LVVAQFSGLV QWAEFILPSC LLLVICLIFS IMGYIVPVK TEDMRGPADK HIPHIQGNMI 720
KLETKKTKL

Seq ID NO: 682 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

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TGGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCGGGAAG AGGTAGCTCA 60
CGGATAGAA ACCTGTTGCG TTGCCAGAA GAAGGGAAGG CGCGAGTGA GAAAGAGGT 120
25 ACTGTAGATG CCTCCAAAT CCTTGGTTAT GGAATATTG GCTCATCCA GTACACTCGG 180
CTTGCTGTTT GAGTGTGCTT GTGGCATGTG CTTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
CTTGGGAGAC AGCGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360
30 AAAAGGGAAG GTGGCTGCCC AGTGCTCTCA TGCTGCTGTT TCAGCCTACA AGCAGATTCA 420
AAGAAGAAAT CCTGAAATGC TCAAACAATG GGAATACTGT GGCCAGCCCA AGTGGTGGT 480
CAAAGCTCCT GATGAAGAAA CCTGATTGCG ATTATTGGCC CATGCAAAAA TGCTGGGACT 540
GACTGTAAGT TTAATTCAAG ATGCTGGAGC TACTCAGATT GCACCAGGCT CTCAAACGTG 600
CCTAGGGAAT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAACT 660
35 TTAGTAGGTG GACTTTGATA TGACAACAC CCCTCCATCA CAAGTGTGTT AAGCCTGTCA 720
GATTCTAACA ACAAAAGCTG AATTTCTTCA CCCAACTTAA ATGTTCTTGA GATGAAATA 780
AAACCTATTC CCATGTTCTA AAAAA

Seq ID NO: 683 Protein sequence
Protein Accession #: NP_057161.1

40 1 11 21 31 41 51
| | | | |
MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60
45 DSGEYKMLLV VRNDLKMKGK KVAQAQCSHAA VSAYKQIQRR NPMLKQWEY CGQPKVVVKA 120
PDEETLIALL AHAKMLGLTV SLIQDAGRTO IAPGSQTVLG IGPSPADLID KVTGHLKLY

Seq ID NO: 684 DNA sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26..952

50 1 11 21 31 41 51
| | | | |
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TCAGATGCTC CTGGTGTGTC TGCTGCTCTC GTGGCTGCCG CATGGGGGGG CCTGTCTCT 120
55 GGCCGAGGCG AGCCCGCGCA GTTCCOOGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
ATTCCGAGAG TTGCGGAAC GCTACGAGGA CTGCTAACCC AGGCTCGGGG CCAACGAGAG 240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCTGCA GTCCGATAC TCACGCCAGA 300
AGTGGCGCTG GGATCGGCGG GCCACCTGCA CCTGCGTATC TCTCGGGCGG CCTTCCCGA 360
GGGGCTCCCC GAGGCTCCCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGGGTC 420
60 AAGGTCGTGG GACGTGACAC GACCGCTGCG CGCTCAGCTC AGCCTTGCAA GACCCCAAGC 480
GCCCGCGCTG CACCTGCGAC TGTGCGCGCC GCGCTGCGAG TCGGACCAAC TGCTGGCAGA 540
ATCTCTGCTC GCACGGCCCC AGCTGGAGTT GCACTTGGG CGCAAGCCG CCAGGGGGCG 600
CGCAGAGAGG GTGCGCGCA ACGGGGAAGA CTGTCCGCTC GGGCCCGGGG GTTGTGCTCG 660
TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCGGATTGGG TGCTGTGCGC 720
65 ACGGAGAGTG CAAGTGACCA TGTGATCGG CGCGTGGCGG AGCCAGTTCC GGGCGGCAAA 780
CATGCAACGG CAGATCAAGA CGAGCCTGCA CGGCTGAAG CCGGACCGG AGCCAGCGCC 840
CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT 900
GTGCTCCAGG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCTC 960
GGTCTCTCCA CTGTGCACTT GCGCGGGGGA GCGGACCTCA GTTGTCTGCT CCTGTGGAAT 1020
70 GGGCTCAAGG TTCCTGAGAC ACCGATTCC TGCCCAACA GCTGTATTTA TATAAGTCTG 1080
TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140
ACTGTGTATT TATTIAAAAC TCTGGTGATA AAAATAAAGC TGCTGTAAC GTTAAAAAAA 1200
AAAA

Seq ID NO: 685 Protein sequence
Protein Accession #: NP_004855.1

75 1 11 21 31 41 51
| | | | |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRAEF PGPSELHSED SRFRELKRY 60
80 EDLLTRLRAN QSWEDNTDL VPAPAVRILT FEVRLGSGGH LHLRISRAAL PEGLPASRL 120
HRLRPLSPT ASKSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQDQLL AESSSARPQL 180
ELHLRPQAR GRRRARARNG DDCLGPGRC CRHITVRASL EDLGWADWVL SPREVQVIMC 240
85 IGACPSQFRA ANMHAQIKTS LHLRKPDTPE APCCVPASYN PMVLIQKEDT GVSLLQTYDDL 300
LARDCHCI

Seq ID NO: 686 DNA sequence

	1	11	21	31	41	51	
5	ACCAAATCAA	CCATAGGTCC	AAGAACAATT	GTCTCTGGAC	GGCAGCTATG	CGACTCACCG	60
	TGCTGTGTGC	TGTGTGCGCT	CTGCCTGGCA	GCCTGSCCCT	GCGCTGCGCT	CAGGAGGCGG	120
	GAGGCATGAG	TGGACTACAG	TGGCAACAGG	CTCAGGACTA	TCTCAAGAGA	TTTATTCTCT	180
	ATGACTCAGA	AACAAAAAAT	GCCACAGT	TAGAAAGCAA	ACTCAAGGAG	ATGCAAAAAT	240
10	TCTTTGGCCT	ACCTATAACT	GGAATGTAA	ACTCCCGCGT	CATAGAAATA	ATGCAGAAGC	300
	CCAGATGTGG	AGTGCCGATG	GTTCGCAGAT	CTCCAAATAGC	CAAGAAATGGA		360
	CTTCCAAAGT	GGTCACTAC	AGGATCGTAT	CATATACTCG	AGACTTACCG	CATATTACAG	420
	TGGATCGATT	AGTGTCAAAG	GCTTTAAACA	TGTGGGGGCA	AGAGATCCCC	GTCGATTCTA	480
	GGAAGATTGT	ATGGGGAAAT	GCTGCATCA	TGATTGCTCT	TGCGCGAGGA	GCTCATGGGG	540
15	ACTCCTACCC	ATTGTATGGG	CCAGAAACA	CGCTGGCTCA	TGCGTTTGCG	CTCTGGGACG	600
	GTCTCGGAGG	AGATGCTCAT	TTCGATGAGG	AATCAACGCTG	GACGCGATGGT	AGCACTCTAG	660
	GGATTAACTT	CTGTATGTCT	CGCACTCATG	ATGTGCGCCA	TTCTTTGGGT	ATGGGCACAT	720
	CTCTCGATCC	TAA'TGCAATG	ATGTATCCAA	ACTATGGAAA	TGGAGATCCC	CAAAATTTTA	780
	AAC'TTCCCA	GGATGATAGT	AAAGCATTC	AGGAAC'TATA	TGGAAGAGA	AGAAATTCAA	840
20	GAAAGAACAA	GAAACTTCAG	GCAGAACATC	CATTCAATCA	TCATTGGAT	TGTATATCAT	900
	TGTTGGACAA	TCAGAA'TTTC	TAAGCACTGT	TCTTCCACTC	CATT'TAGCAA	TTATGTCA'CC	960
	CTTTT'TTAT	GCAGTGGT'T	TTTGAATGTC	TTTCACTCCT	TTTAT'TGGT	AGGATCCCTT	1020
	ATGTTGTGAC	TGTTGCTTAT	TCCATCTATG	AGCTT'TGTCA	GTGCGCGTAG	ATGTCAATAA	1080
	TGTTGTCATCA	TCAAAATAAA	TAAATAGT'TT	ATTCCATGGT	AAATTTTA		

	1	11	21	31	41	51	
30	MRLTVLCAVC	LLPGSLALPL	PQEAGGMSEL	QWEQAQDYLK	RPFLYDSETK	NANSLEAKLK	60
	EMQKFGFLPI	TGLMNSRVIE	IMQKPRGVGP	DAVSI SLFPN	SPKHTSKVVT	YRIVSYTRDL	120
	PHITVDRLVS	KALNMGKKEI	PLHFRKVVVG	TDADIMIGFAR	GAHGDSYFPD	PGPNTLAHAF	180
	APGTGLGSDA	HFDDEDERWT	GSSLGINFLY	AATHELGHSL	GMGHSSDPNA	VMYPTYGNGD	240
35	PONFKLSDD	IKGIOLKYGT	RNSRKK				

Coding sequence: 1..870

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ATGACAGGAG	TGTTTGACAG	AAGGGTCCCC	AGCATCGCAT	CCGGCGACTT	CCAAGCTCCG	60
TTCCAGACGT	CCCGCAGCTAT	GCACCATCGC	TCTCAGGAAT	CGCCAACTTT	GCCCGAGTCT	120
TACGCTACCG	ATTCTGATCA	CTACAGCCCT	ACGGGGGGAG	CCCGCGCAGG	CTAGCTGCTT	180
CTCACTCGTG	CTTCTATATG	CAAAAGCTCT	AACCCCTACG	AGTATACGTA	TCACGGGGTG	240
AACGGCTCCG	CCGGGAGCTA	CCAGCCAAAC	CGTTATGCGC	ACTATAGCTG	CGCTAGCTCC	300
TACCAACCA	ACGGCGGGGC	CTACAACCGC	GTCCTCAAGC	CCACCAACCA	GCCAGAGAAA	360
GAAGTGACCG	AGCCCGAGGT	GAGAAATGGT	AATGGCAACG	CAAAAGAAAT	TGGTAAACCC	420
AGGAATATT	ATTCAGCTTT	TCACTCGGCG	GCATTACAGA	GAAAGTTGAT	GAAGACTCAG	480
TACTTCGCGT	TGCGGGAAGC	CGCGCAGCTG	CGCCGCTCGC	TGGGATATGAC	ACAAACACAG	540
GTGAAATCT	GGTTTCAGAA	CAAAAGATCC	AGGATCAAGA	AGATCATGAA	AAACGGGGAG	600
ATGCCCCCGC	AGACACAGTC	CAGCTCCAGC	GACCCAATGG	CGTGTAACCT	GCCCGAGTCT	660
CCAGCGGTGT	GGGACGCCCC	GGGCTCGTCC	CGCTCGCTCA	GCCACCAACC	TCATGTCCAC	720
CCTCGACACT	CCAAACCACT	CCAGCGGTCC	AGCTACCTGC	AGAACTCTGC	ATCCTGTGAT	780
ACAAAGTCAG	CCAGCTCAAT	CAATTCCAC	CTGCGCGCGC	CGGGCTCCTT	ACAGCACCCG	840
CTGGGCGCTG		ACTCTATTAG				

65

1	11	21	31	41	51	
MTGVFDRRPV	SIRSGDFQAP	FQTSAAHHHP	SQESPTLPES	SATDSYYSP	TGGAPHGYS	60
PTSAISYKAL	NPYQYQYHGV	NGSAISYPAK	AYADYSYASS	YHQYGGAYNR	VPASATQPEK	120
ETPEVPERNV	GMGPKKVRFP	LT1YSSQLA	ALRRPQFTQ	YLALPERAEL	AASLGILTOQT	180
VKIWFQNKRS	KIKKIMKNGE	MPPEHSPSSS	DPMACNSPOS	PAVWEQCGSS	RSLSEHPHAR	240
PVTNSQSPAS	SYLNSASVY	TSAASSINSH	LPPMCSLOHP	LALASGLTY		

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung
2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated antibody in the biological
6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9 antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 18. The method of claim 16, wherein the patient is a human.

1 19. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby
9 monitoring the efficacy of the therapy.

1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated
3 polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 21. The method of claim 19, wherein the patient is a human.

1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1A-16.

1 23. The nucleic acid molecule of claim 22, which is labeled.

1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label

1 25. An expression vector comprising the nucleic acid of claim 22.

1 26. A host cell comprising the expression vector of claim 25.

1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1A-16.

1 28. An antibody that specifically binds a polypeptide of claim 27.

1 29. The antibody of claim 28, further conjugated to an effector component.

1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.

1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.

1 32. The antibody of claim 29, which is an antibody fragment.

- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a lung cancer cell in a biological sample from a
2 patient, the method comprising contacting the biological sample with an antibody of claim
3 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to lung cancer in a patient,
2 the method comprising contacting a biological sample from the patient with a polypeptide
3 encoded by a nucleic acid comprises a sequence from Tables 1A-16.
- 1 38. A method for identifying a compound that modulates a lung cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a lung cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1A-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.
- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.

1 44. A method of inhibiting proliferation of a lung cancer-associated cell to
2 treat lung cancer in a patient, the method comprising the step of administering to the subject a
3 therapeutically effective amount of a compound identified using the method of claim 38.

1 45. The method of claim 44, wherein the compound is an antibody.

1 46. The method of claim 45, wherein the patient is a human.

1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having lung cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of lung cancer.

1 48. The assay of claim 47, wherein the control is a mammal with lung
2 cancer or a cell therefrom that has not been treated with the test compound.

1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having lung cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having lung
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.